

(12) INTERNATIONAL APPLICATION PUBLISHED UNDER THE PATENT COOPERATION TREATY (PCT)

(19) World Intellectual Property Organization
International Bureau



(43) International Publication Date
27 December 2002 (27.12.2002)

PCT

(10) International Publication Number
WO 02/102235 A2

- (51) International Patent Classification⁷: A61B
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- (21) International Application Number: PCT/US02/19297
- (22) International Filing Date: 18 June 2002 (18.06.2002)
- (81) Designated States (*national*): AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CO, CR, CU, CZ, DE, DK, DM, DZ, EC, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, OM, PH, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TN, TR, TT, TZ, UA, UG, US, UZ, VN, YU, ZA, ZM, ZW.
- (25) Filing Language: English
- (26) Publication Language: English
- (30) Priority Data:
- | | | |
|------------|-------------------------------|----|
| 60/299,234 | 18 June 2001 (18.06.2001) | US |
| 60/315,287 | 27 August 2001 (27.08.2001) | US |
| 60/317,544 | 5 September 2001 (05.09.2001) | US |
| 60/350,666 | 13 November 2001 (13.11.2001) | US |
| 60/372,246 | 12 April 2002 (12.04.2002) | US |
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- (84) Designated States (*regional*): ARIPO patent (GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZM, ZW), Eurasian patent (AM, AZ, BY, KG, KZ, MD, RU, TJ, TM), European patent (AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, TR), OAPI patent (BF, BJ, CF, CG, CI, CM, GA, GN, GQ, GW, ML, MR, NE, SN, TD, TG).

Published:

— without international search report and to be republished upon receipt of that report

For two-letter codes and other abbreviations, refer to the "Guidance Notes on Codes and Abbreviations" appearing at the beginning of each regular issue of the PCT Gazette.

(54) Title: METHODS OF DIAGNOSIS OF OVARIAN CANCER, COMPOSITIONS AND METHODS OF SCREENING FOR MODULATORS OF OVARIAN CANCER

(57) Abstract: Described herein are genes whose expression are up-regulated or down-regulated in ovarian cancer. Related methods and compositions that can be used for diagnosis and treatment of ovarian cancer are disclosed. Also described herein are methods that can be used to identify modulators of ovarian cancer.

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METHODS OF DIAGNOSIS OF OVARIAN CANCER, COMPOSITIONS AND
METHODS OF SCREENING FOR MODULATORS OF OVARIAN CANCER

CROSS-REFERENCES TO RELATED APPLICATIONS.

5 This application is related to USSN 60/299,234, filed June 18, 2001; USSN 60/315,287, filed August 27, 2001; USSN 60/317,544, filed September 5, 2001; USSN 60/350,666, filed November 13, 2001; and USSN 60/372,246, filed April 12, 2002, each of which is incorporated herein by reference for all purposes.

10 FIELD OF THE INVENTION

The invention relates to the identification of nucleic acid and protein expression profiles and nucleic acids, products, and antibodies thereto that are involved in ovarian cancer; and to the use of such expression profiles and compositions in the diagnosis, prognosis, and therapy of ovarian cancer. The invention further relates to methods for
15 identifying and using agents and/or targets that inhibit ovarian cancer.

BACKGROUND OF THE INVENTION

Ovarian cancer is the sixth most common cancer in women, accounting for 6% of all female cancers. It ranks fifth as the cause of cancer death in women. The American Cancer
20 Society predicts that there will be about 23,100 new cases of ovarian cancer in this country in the year 2000 and about 14,000 women will die of the disease. Because many ovarian cancers cannot be detected early in their development, they account for a disproportionate number of fatal cancers, being responsible for almost half the deaths from cancer of the female genital tract; more deaths than any other reproductive organ cancer.

25 Most patients with epithelial ovarian cancer, the predominant form, are asymptomatic in early-stage disease and usually present with stage III or IV disease. Their five-year survival is less than 25%, with lower survival among African-American women. The minority of patients discovered with early-stage disease have a five-year survival rate of 80%-90%. See, Parker, et. al.. (1997) "Cancer Statistics, 1997" CA Cancer J. Clin. 47:5-27.

30 In the absence of a family history of ovarian cancer, lifetime risk of ovarian cancer is 1/70. Risk factors include familial cancer syndromes (risk of up to 82% by age 70 in women

with hereditary breast/ovarian syndrome); family history (1.4% lifetime risk with no affected relatives, 5% with one affected relative, 7% with two affected relatives; Kerlikowske, et.al. (1992) Obstet. Gynecol. 80:700-707); nulliparity; advancing age; obesity; personal history of breast, endometrial, or colorectal cancer; fewer pregnancies; or older age (>35 years) at first pregnancy. However, 95% of all ovarian cancers occur in women without risk factors. Use of hormonal contraceptives, oophorectomy, and tubal sterilization reduce risk of ovarian cancer (Kerlikowske, et. al. (1992) Obstet. Gynecol. 80:700-707; Grimes (1992) Am J. Obstet. Gynecol. 166:1950-1954; Hankinson, et. al. (1993) JAMA 270:2813-2818); however, even bilateral oophorectomy may not be completely effective in preventing ovarian cancer.

Treatment of ovarian cancer consists largely of surgical oophorectomy, anti-hormone therapy, and/or chemotherapy. Although many ovarian cancer patients are effectively treated, the current therapies can all induce serious side effects which diminish quality of life. Deciding on a particular course of treatment is typically based on a variety of prognostic parameters and markers (Fitzgibbons, et al. (2000) Arch. Pathol. Lab. Med. 124:966-978; Hamilton and Piccart (2000) Ann. Oncol. 11:647-663), including genetic predisposition markers BRCA-1 and BRCA-2 (Robson (2000) J. Clin. Oncol. 18:113sup-118sup).

The identification of novel therapeutic targets and diagnostic markers is essential for improving the current treatment of ovarian cancer patients. Recent advances in molecular medicine have increased the interest in tumor-specific cell surface antigens that could serve as targets for various immunotherapeutic or small molecule strategies. Antigens suitable for immunotherapeutic strategies should be highly expressed in cancer tissues and ideally not expressed in normal adult tissues. Expression in tissues that are dispensable for life, however, may be tolerated. Examples of such antigens include Her2/neu and the B-cell antigen CD20. Humanized monoclonal antibodies directed to Her2/neu (Herceptin®/trastuzumab) are currently in use for the treatment of metastatic breast cancer. Ross and Fletcher (1998) Stem Cells 16:413-428. Similarly, anti-CD20 monoclonal antibodies (Rituxin®/rituximab) are used to effectively treat non-Hodgkin's lymphoma. Maloney, et al. (1997) Blood 90:2188-2195; Leget and Czuczman (1998) Curr. Opin. Oncol. 10:548-551.

Potential immunotherapeutic targets have been identified for ovarian cancer. One such target is polymorphic epithelial mucin (MUC1). MUC1 is a transmembrane protein, present at the apical surface of glandular epithelial cells. It is often overexpressed in ovarian cancer, and typically exhibits an altered glycosylation pattern, resulting in an antigenically

distinct molecule, and is in early clinical trials as a vaccine target. Gilewski, et al. (2000) Clin. Cancer Res. 6:1693-1701; Scholl, et al. (2000) J. Immunother. 23:570-580. The tumor-expressed protein is often cleaved into the circulation, where it is detectable as the tumor marker, CA 15-3. See, e.g., Bon, et al. (1997) Clin. Chem. 43:585-593. However, many
5 patients have tumors that express neither HER2 nor MUC-1; therefore, it is clear that other targets need to be identified to manage localized and metastatic disease.

Mutations in both BRCA1 and BRCA2 are associated with increased susceptibility to ovarian cancer. Mutations in BRCA1 occur in approximately 5 percent (95 percent confidence interval, 3 to 8 percent) of women in whom ovarian cancer is diagnosed before
10 the age of 70 years. See Stratton, et al. (1997) N.E.J. Med. 336:1125-1130. And, in BRCA1 gene carriers, the risk for developing ovarian cancer is .63. See Easton (1995) Am. J. Hum. Genet. 56:267-xxx; and Elit (2001) Can. Fam. Physician 47:778-84.

Other biochemical markers such as CA125 have been reported to be associated with ovarian cancer, but they are not absolute indicators of disease. Although roughly 85% of
15 women with clinically apparent ovarian cancer have increased levels of CA125, CA125 is also increased during the first trimester of pregnancy, during menstruation, in the presence of non-cancerous illnesses, and in cancers of other sites.

While industry and academia have identified novel gene sequences, there has not been an equal effort exerted to identify the function of these novel sequences. The elucidation of a
20 role for novel proteins and compounds in disease states for identification of therapeutic targets and diagnostic markers is essential for improving the current treatment of ovarian cancer patients. Accordingly, provided herein are molecular targets for therapeutic intervention in ovarian and other cancers. Additionally, provided herein are methods that can be used in diagnosis and prognosis of ovarian cancer. Further provided are methods that can
25 be used to screen candidate bioactive agents for the ability to modulate ovarian cancer.

SUMMARY OF THE INVENTION

The present invention therefore provides nucleotide sequences of genes that are up- and down-regulated in ovarian cancer cells. Such genes are useful for diagnostic purposes, and also as targets for screening for therapeutic compounds that modulate ovarian cancer, such as hormones or antibodies. The methods of detecting nucleic acids of the invention or their encoded proteins can be used for many purposes, e.g., early detection of ovarian cancers, monitoring and early detection of relapse following treatment, monitoring response to therapy, selecting patients for postoperative chemotherapy or radiation therapy, selecting therapy, determining tumor prognosis, treatment, or response to treatment (of primary or metastatic tumors), and early detection of pre-cancerous lesions. Other aspects of the invention will become apparent to the skilled artisan by the following description of the invention.

In one aspect, the present invention provides a method of detecting an ovarian cancer-associated transcript in a cell from a patient, the method comprising contacting a biological sample from the patient with a polynucleotide that selectively hybridizes to a sequence at least 80% identical to a sequence as shown in Tables 1-26.

In one embodiment, the present invention provides a method of determining the level of an ovarian cancer associated transcript in a cell from a patient.

In one embodiment, the present invention provides a method of detecting an ovarian cancer-associated transcript in a cell from a patient, the method comprising contacting a biological sample from the patient with a polynucleotide that selectively hybridizes to a sequence at least 80% identical to a sequence as shown in Tables 1-26.

In one embodiment, the polynucleotide selectively hybridizes to a sequence at least 95% identical to a sequence as shown in Tables 1-26.

In one embodiment, the biological sample is a tissue sample. In another embodiment, the biological sample comprises isolated nucleic acids, e.g., mRNA.

In one embodiment, the polynucleotide is labeled, e.g., with a fluorescent label.

In one embodiment, the polynucleotide is immobilized on a solid surface.

In one embodiment, the patient is undergoing a therapeutic regimen to treat ovarian cancer. In another embodiment, the patient is suspected of having metastatic ovarian cancer.

In one embodiment, the patient is a human.

In one embodiment, the ovarian cancer associated transcript is mRNA.

In one embodiment, the method further comprises the step of amplifying nucleic acids

before the step of contacting the biological sample with the polynucleotide.

In another aspect, the present invention provides a method of monitoring the efficacy of a therapeutic treatment of ovarian cancer, the method comprising the steps of: (i) providing a biological sample from a patient undergoing the therapeutic treatment; and (ii) determining the level of an ovarian cancer-associated transcript in the biological sample by contacting the biological sample with a polynucleotide that selectively hybridizes to a sequence at least 80% identical to a sequence as shown in Tables 1-26, thereby monitoring the efficacy of the therapy. In a further embodiment, the patient has metastatic ovarian cancer. In a further embodiment, the patient has a drug resistant form of ovarian cancer.

In one embodiment, the method further comprises the step of: (iii) comparing the level of the ovarian cancer-associated transcript to a level of the ovarian cancer-associated transcript in a biological sample from the patient prior to, or earlier in, the therapeutic treatment.

Additionally, provided herein is a method of evaluating the effect of a candidate ovarian cancer drug comprising administering the drug to a patient and removing a cell sample from the patient. The expression profile of the cell is then determined. This method may further comprise comparing the expression profile to an expression profile of a healthy individual. In a preferred embodiment, said expression profile includes a gene of Tables 1-26.

In one aspect, the present invention provides an isolated nucleic acid molecule consisting of a polynucleotide sequence as shown in Tables 1-26.

In one embodiment, an expression vector or cell comprises the isolated nucleic acid.

In one aspect, the present invention provides an isolated polypeptide which is encoded by a nucleic acid molecule having polynucleotide sequence as shown in Tables 1-26.

In another aspect, the present invention provides an antibody that specifically binds to an isolated polypeptide which is encoded by a nucleic acid molecule having polynucleotide sequence as shown in Tables 1-26.

In one embodiment, the antibody is conjugated to an effector component, e.g., a fluorescent label, a radioisotope or a cytotoxic chemical.

In one embodiment, the antibody is an antibody fragment. In another embodiment, the antibody is humanized.

In one aspect, the present invention provides a method of detecting an ovarian cancer cell in a biological sample from a patient, the method comprising contacting the biological

sample with an antibody as described herein.

In another aspect, the present invention provides a method of detecting antibodies specific to ovarian cancer in a patient, the method comprising contacting a biological sample from the patient with a polypeptide encoded by a nucleic acid comprising a sequence from

5 Tables 1-26.

In another aspect, the present invention provides a method for identifying a compound that modulates an ovarian cancer-associated polypeptide, the method comprising the steps of: (i) contacting the compound with an ovarian cancer-associated polypeptide, the polypeptide encoded by a polynucleotide that selectively hybridizes to a sequence at least 80% identical
10 to a sequence as shown in Tables 1-26; and (ii) determining the functional effect of the compound upon the polypeptide.

In one embodiment, the functional effect is a physical effect, an enzymatic effect, or a chemical effect.

In one embodiment, the polypeptide is expressed in a eukaryotic host cell or cell
15 membrane. In another embodiment, the polypeptide is recombinant.

In one embodiment, the functional effect is determined by measuring ligand binding to the polypeptide.

In another aspect, the present invention provides a method of inhibiting proliferation of an ovarian cancer-associated cell to treat ovarian cancer in a patient, the method
20 comprising the step of administering to the subject a therapeutically effective amount of a compound identified as described herein.

In one embodiment, the compound is an antibody.

In another aspect, the present invention provides a drug screening assay comprising the steps of: (i) administering a test compound to a mammal having ovarian cancer or to a cell sample
25 isolated from; (ii) comparing the level of gene expression of a polynucleotide that selectively hybridizes to a sequence at least 80% identical to a sequence as shown in Tables 1-26 in a treated cell or mammal with the level of gene expression of the polynucleotide in a control cell sample or mammal, wherein a test compound that modulates the level of expression of the polynucleotide is a candidate for the treatment of ovarian cancer.

In one embodiment, the control is a mammal with ovarian cancer or a cell sample that
30 has not been treated with the test compound. In another embodiment, the control is a normal cell or mammal, or is non-malignant tissue.

In one embodiment, the test compound is administered in varying amounts or

concentrations. In another embodiment, the test compound is administered for varying time periods. In another embodiment, the comparison can occur after addition or removal of the drug candidate.

In one embodiment, the levels of a plurality of polynucleotides that selectively hybridize to a sequence at least 80% identical to a sequence as shown in Tables 1-26 are individually compared to their respective levels in a control cell sample or mammal. In a preferred embodiment the plurality of polynucleotides is from three to ten.

In another aspect, the present invention provides a method for treating a mammal having ovarian cancer comprising administering a compound identified by the assay described herein.

In another aspect, the present invention provides a pharmaceutical composition for treating a mammal having ovarian cancer, the composition comprising a compound identified by the assay described herein and a physiologically acceptable excipient.

In one aspect, the present invention provides a method of screening drug candidates by providing a cell expressing a gene that is up- and down-regulated as in an ovarian cancer. In one embodiment, a gene is selected from Tables 1-26. The method further includes adding a drug candidate to the cell and determining the effect of the drug candidate on the expression of the expression profile gene.

In one embodiment, the method of screening drug candidates includes comparing the level of expression in the absence of the drug candidate to the level of expression in the presence of the drug candidate, wherein the concentration of the drug candidate can vary when present, and wherein the comparison can occur after addition or removal of the drug candidate. In a preferred embodiment, the cell expresses at least two expression profile genes. The profile genes may show an increase or decrease.

Also provided is a method of evaluating the effect of a candidate ovarian cancer drug comprising administering the drug to a transgenic animal expressing or over-expressing the ovarian cancer modulatory protein, or an animal lacking the ovarian cancer modulatory protein, for example as a result of a gene knockout.

Moreover, provided herein is a biochip comprising one or more nucleic acid segments of Tables 1-26, wherein the biochip comprises fewer than 1000 nucleic acid probes. Preferably, at least two nucleic acid segments are included. More preferably, at least three nucleic acid segments are included.

Furthermore, a method of diagnosing a disorder associated with ovarian cancer is

provided. The method comprises determining the expression of a gene of Tables 1-26 in a first tissue type of a first individual, and comparing the distribution to the expression of the gene from a second normal tissue type from the first individual or a second unaffected individual. A difference in the expression indicates that the first individual has a disorder associated with ovarian cancer.

In a further embodiment, the biochip also includes a polynucleotide sequence of a gene that is not up- and down-regulated in ovarian cancer.

In one embodiment a method for screening for a bioactive agent capable of interfering with the binding of an ovarian cancer modulating protein (ovarian cancer modulatory protein) or a fragment thereof and an antibody which binds to said ovarian cancer modulatory protein or fragment thereof. In a preferred embodiment, the method comprises combining an ovarian cancer modulatory protein or fragment thereof, a candidate bioactive agent and an antibody which binds to said ovarian cancer modulatory protein or fragment thereof. The method further includes determining the binding of said ovarian cancer modulatory protein or fragment thereof and said antibody. Wherein there is a change in binding, an agent is identified as an interfering agent. The interfering agent can be an agonist or an antagonist. Preferably, the agent inhibits ovarian cancer.

Also provided herein are methods of eliciting an immune response in an individual. In one embodiment a method provided herein comprises administering to an individual a composition comprising an ovarian cancer modulating protein, or a fragment thereof. In another embodiment, the protein is encoded by a nucleic acid selected from those of Tables 1-26.

Further provided herein are compositions capable of eliciting an immune response in an individual. In one embodiment, a composition provided herein comprises an ovarian cancer modulating protein, preferably encoded by a nucleic acid of Table 1-26 or a fragment thereof, and a pharmaceutically acceptable carrier. In another embodiment, said composition comprises a nucleic acid comprising a sequence encoding an ovarian cancer modulating protein, preferably selected from the nucleic acids of Tables 1-26, and a pharmaceutically acceptable carrier.

Also provided are methods of neutralizing the effect of an ovarian cancer protein, or a fragment thereof, comprising contacting an agent specific for said protein with said protein in an amount sufficient to effect neutralization. In another embodiment, the protein is encoded by a nucleic acid selected from those of Tables 1-26.

In another aspect of the invention, a method of treating an individual for ovarian cancer is provided. In one embodiment, the method comprises administering to said individual an inhibitor of an ovarian cancer modulating protein. In another embodiment, the method comprises administering to a patient having ovarian cancer an antibody to an ovarian cancer modulating protein conjugated to a therapeutic moiety. Such a therapeutic moiety can be a cytotoxic agent or a radioisotope.

5

DETAILED DESCRIPTION OF THE INVENTION

In accordance with the objects outlined above, the present invention provides novel methods for diagnosis and prognosis evaluation for ovarian cancer (OC), including metastatic ovarian cancer, as well as methods for screening for compositions which modulate ovarian cancer. Also provided are methods for treating ovarian cancer and related conditions, e.g., ovarian carcinoma (e.g., epithelial (including malignant serous tumors, malignant mucinous tumors, and malignant endometrioid tumors), germ cell (including teratomas, choriocarcinomas, polyembryomas, embryonal carcinoma, endodermal sinus tumor, dysgerminoma, and gonadoblastoma), and stromal carcinomas (e.g., granulosa stromal cell tumors)), fallopian tube carcinoma, and peritoneal carcinoma.

Tables 1-26 provide unigene cluster identification numbers for the nucleotide sequence of genes that exhibit increased or decreased expression in ovarian cancer samples. Tables 1-26 also provide an exemplar accession number that provides a nucleotide sequence that is part of the unigene cluster.

Definitions

The term "ovarian cancer protein" or "ovarian cancer polynucleotide" or "ovarian cancer-associated transcript" refers to nucleic acid and polypeptide polymorphic variants, alleles, mutants, and interspecies homologues that: (1) have a nucleotide sequence that has greater than about 60% nucleotide sequence identity, 65%, 70%, 75%, 80%, 85%, 90%, preferably 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% or greater nucleotide sequence identity, preferably over a region of over a region of at least about 25, 50, 100, 200, 500, 1000, or more nucleotides, to a nucleotide sequence of or associated with a gene of Tables 1-26; (2) bind to antibodies, e.g., polyclonal antibodies, raised against an immunogen comprising an amino acid sequence encoded by a nucleotide sequence of or associated with a gene of Tables 1-26, and conservatively modified variants thereof; (3) specifically hybridize under stringent hybridization conditions to a nucleic acid sequence, or the complement thereof of Tables 1-26 and conservatively modified variants thereof; or (4) have an amino acid sequence that has greater than about 60% amino acid sequence identity, 65%, 70%, 75%, 80%, 85%, 90%, preferably 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% or greater amino sequence identity, preferably over a region of over a region of at least about 25, 50, 100, 200, 500, 1000, or more amino acid, to an amino acid sequence encoded by a nucleotide sequence of or associated with a gene of Tables 1-26. A polynucleotide or polypeptide

sequence is typically from a mammal including, but not limited to, primate, e.g., human; rodent, e.g., rat, mouse, hamster; cow, pig, horse, sheep, or other mammal. An "ovarian cancer polypeptide" and an "ovarian cancer polynucleotide," include both naturally occurring or recombinant forms.

5 A "full length" ovarian cancer protein or nucleic acid refers to an ovarian cancer polypeptide or polynucleotide sequence, or a variant thereof, that contains all of the elements normally contained in one or more naturally occurring, wild type ovarian cancer polynucleotide or polypeptide sequences. The "full length" may be prior to, or after, various stages of post-translation processing or splicing, including alternative splicing.

10 "Biological sample" as used herein is a sample of biological tissue or fluid that contains nucleic acids or polypeptides, e.g., of an ovarian cancer protein, polynucleotide or transcript. Such samples include, but are not limited to, tissue isolated from primates, e.g., humans, or rodents, e.g., mice, and rats. Biological samples may also include sections of tissues such as biopsy and autopsy samples, frozen sections taken for histologic purposes, 15 blood, plasma, serum, sputum, stool, tears, mucus, hair, skin, etc. Biological samples also include explants and primary and/or transformed cell cultures derived from patient tissues. A biological sample is typically obtained from a eukaryotic organism, most preferably a mammal such as a primate e.g., chimpanzee or human; cow; dog; cat; a rodent, e.g., guinea pig, rat, mouse; rabbit; or a bird; reptile; or fish. Livestock and domestic animals are of 20 particular interest.

"Providing a biological sample" means to obtain a biological sample for use in methods described in this invention. Most often, this will be done by removing a sample of cells from an animal, but can also be accomplished by using previously isolated cells (e.g., isolated by another person, at another time, and/or for another purpose), or by performing the 25 methods of the invention in vivo. Archival tissues, having treatment or outcome history, will be particularly useful.

The terms "identical" or percent "identity," in the context of two or more nucleic acids or polypeptide sequences, refer to two or more sequences or subsequences that are the same or have a specified percentage of amino acid residues or nucleotides that are the same 30 (e.g., about 60% identity, preferably 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or higher identity over a specified region, when compared and aligned for maximum correspondence over a comparison window or designated region) as measured using a BLAST or BLAST 2.0 sequence comparison algorithms with default

parameters described below, or by manual alignment and visual inspection (see, e.g., NCBI web site <http://www.ncbi.nlm.nih.gov/BLAST/> or the like). Such sequences are then said to be "substantially identical." This definition also refers to, or may be applied to, the compliment of a test sequence. The definition also includes sequences that have deletions and/or additions, as well as those that have substitutions, as well as naturally occurring, e.g., polymorphic or allelic variants, and man-made variants. As described below, the preferred algorithms can account for gaps and the like. Preferably, identity exists over a region that is at least about 25 amino acids or nucleotides in length, or more preferably over a region that is 50-100 amino acids or nucleotides in length.

For sequence comparison, typically one sequence acts as a reference sequence, to which test sequences are compared. When using a sequence comparison algorithm, test and reference sequences are entered into a computer, subsequence coordinates are designated, if necessary, and sequence algorithm program parameters are designated. Preferably, default program parameters can be used, or alternative parameters can be designated. The sequence comparison algorithm then calculates the percent sequence identities for the test sequences relative to the reference sequence, based on the program parameters.

A "comparison window", as used herein, includes reference to a segment of one of the number of contiguous positions selected from the group consisting typically of from 20 to 600, usually about 50 to about 200, more usually about 100 to about 150 in which a sequence may be compared to a reference sequence of the same number of contiguous positions after the two sequences are optimally aligned. Methods of alignment of sequences for comparison are well-known in the art. Optimal alignment of sequences for comparison can be conducted, e.g., by the local homology algorithm of Smith and Waterman (1981) Adv. Appl. Math. 2:482-489, by the homology alignment algorithm of Needleman and Wunsch (1970) J. Mol. Biol. 48:443-453, by the search for similarity method of Pearson and Lipman (1988) Proc. Nat'l. Acad. Sci. USA 85:2444-2448, by computerized implementations of these algorithms (GAP, BESTFIT, FASTA, and TFASTA in the Wisconsin Genetics Software Package, Genetics Computer Group, 575 Science Dr., Madison, WI), or by manual alignment and visual inspection (see, e.g., Ausubel, et al. (eds. 1995 and supplements) Current Protocols in Molecular Biology Lippincott.

Preferred examples of algorithms that are suitable for determining percent sequence identity and sequence similarity include the BLAST and BLAST 2.0 algorithms, which are described in Altschul, et al. (1977) Nuc. Acids Res. 25:3389-3402 and Altschul, et al. (1990)

J. Mol. Biol. 215:403-410. BLAST and BLAST 2.0 are used, with the parameters described herein, to determine percent sequence identity for the nucleic acids and proteins of the invention. Software for performing BLAST analyses is publicly available through the National Center for Biotechnology Information (<http://www.ncbi.nlm.nih.gov/>). This

5 algorithm involves first identifying high scoring sequence pairs (HSPs) by identifying short words of length W in the query sequence, which either match or satisfy some positive-valued threshold score T when aligned with a word of the same length in a database sequence. T is referred to as the neighborhood word score threshold (Altschul, et al., supra). These initial neighborhood word hits act as seeds for initiating searches to find longer HSPs containing

10 them. The word hits are extended in both directions along each sequence for as far as the cumulative alignment score can be increased. Cumulative scores are calculated using, e.g., for nucleotide sequences, the parameters M (reward score for a pair of matching residues; always > 0) and N (penalty score for mismatching residues; always < 0). For amino acid sequences, a scoring matrix is used to calculate the cumulative score. Extension of the word

15 hits in each direction are halted when: the cumulative alignment score falls off by the quantity X from its maximum achieved value; the cumulative score goes to zero or below, due to the accumulation of one or more negative-scoring residue alignments; or the end of either sequence is reached. The BLAST algorithm parameters W, T, and X determine the sensitivity and speed of the alignment. The BLASTN program (for nucleotide sequences)

20 uses as defaults a wordlength (W) of 11, an expectation (E) of 10, M=5, N=-4 and a comparison of both strands. For amino acid sequences, the BLASTP program uses as defaults a word length of 3, and expectation (E) of 10, and the BLOSUM62 scoring matrix (see Henikoff and Henikoff (1989) Proc. Nat'l Acad. Sci. USA 89:10915-919) alignments (B) of 50, expectation (E) of 10, M=5, N=-4, and a comparison of both strands.

25 The BLAST algorithm also performs a statistical analysis of the similarity between two sequences (see, e.g., Karlin and Altschul (1993) Proc. Nat'l Acad. Sci. USA 90:5873-5887). One measure of similarity provided by the BLAST algorithm is the smallest sum probability (P(N)), which provides an indication of the probability by which a match between two nucleotide or amino acid sequences would occur by chance. For example, a nucleic acid

30 is considered similar to a reference sequence if the smallest sum probability in a comparison of the test nucleic acid to the reference nucleic acid is less than about 0.2, more preferably less than about 0.01, and most preferably less than about 0.001. Log values may be large negative numbers, e.g., 5, 10, 20, 30, 40, 40, 70, 90, 110, 150, 170, etc.

An indication that two nucleic acid sequences or polypeptides are substantially identical is that the polypeptide encoded by the first nucleic acid is immunologically cross reactive with the antibodies raised against the polypeptide encoded by the second nucleic acid, as described below. Thus, a polypeptide is typically substantially identical to a second polypeptide, e.g., where the two peptides differ only by conservative substitutions. Another indication that two nucleic acid sequences are substantially identical is that the two molecules or their complements hybridize to each other under stringent conditions, as described below. Yet another indication that two nucleic acid sequences are substantially identical is that the same primers can be used to amplify the sequences.

A "host cell" is a naturally occurring cell or a transformed cell that contains an expression vector and supports the replication or expression of the expression vector. Host cells may be cultured cells, explants, cells in vivo, and the like. Host cells may be prokaryotic cells such as *E. coli*, or eukaryotic cells such as yeast, insect, amphibian, or mammalian cells, such as CHO, HeLa, and the like (see, e.g., the American Type Culture Collection catalog or web site, www.atcc.org).

The terms "isolated," "purified," or "biologically pure" refer to material that is substantially or essentially free from components that normally accompany it as found in its native state. Purity and homogeneity are typically determined using analytical chemistry techniques such as polyacrylamide gel electrophoresis or high performance liquid chromatography. A protein or nucleic acid that is the predominant species present in a preparation is substantially purified. In particular, an isolated nucleic acid is separated from some open reading frames that naturally flank the gene and encode proteins other than protein encoded by the gene. The term "purified" in some embodiments denotes that a nucleic acid or protein gives rise to essentially one band in an electrophoretic gel. Preferably, it means that the nucleic acid or protein is at least 85% pure, more preferably at least 95% pure, and most preferably at least 99% pure. "Purify" or "purification" in other embodiments means removing at least one contaminant from the composition to be purified. In this sense, purification does not require that the purified compound be homogenous, e.g., 100% pure.

The terms "polypeptide," "peptide" and "protein" are used interchangeably herein to refer to a polymer of amino acid residues. The terms apply to amino acid polymers in which one or more amino acid residue is an artificial chemical mimetic of a corresponding naturally occurring amino acid, as well as to naturally occurring amino acid polymers, those containing modified residues, and non-naturally occurring amino acid polymers.

The term "amino acid" refers to naturally occurring and synthetic amino acids, as well as amino acid analogs and amino acid mimetics that function similarly to the naturally occurring amino acids. Naturally occurring amino acids are those encoded by the genetic code, as well as those amino acids that are later modified, e.g., hydroxyproline, γ -carboxyglutamate, and O-phosphoserine. Amino acid analogs refers to compounds that have the same basic chemical structure as a naturally occurring amino acid, e.g., an α carbon that is bound to a hydrogen, a carboxyl group, an amino group, and an R group, e.g., homoserine, norleucine, methionine sulfoxide, methionine methyl sulfonium. Such analogs may have modified R groups (e.g., norleucine) or modified peptide backbones, but retain the same basic chemical structure as a naturally occurring amino acid. Amino acid mimetics refers to chemical compounds that have a structure that is different from the general chemical structure of an amino acid, but that functions similarly to a naturally occurring amino acid.

Amino acids may be referred to herein by either their commonly known three letter symbols or by the one-letter symbols recommended by the IUPAC-IUB Biochemical Nomenclature Commission. Nucleotides, likewise, may be referred to by their commonly accepted single-letter codes.

"Conservatively modified variants" applies to both amino acid and nucleic acid sequences. With respect to particular nucleic acid sequences, conservatively modified variants refers to those nucleic acids which encode identical or essentially identical amino acid sequences, or where the nucleic acid does not encode an amino acid sequence, to essentially identical or associated, e.g., naturally contiguous, sequences. Because of the degeneracy of the genetic code, a large number of functionally identical nucleic acids encode most proteins. For instance, the codons GCA, GCC, GCG, and GCU all encode the amino acid alanine. Thus, at every position where an alanine is specified by a codon, the codon can be altered to another of the corresponding codons described without altering the encoded polypeptide. Such nucleic acid variations are "silent variations," which are one species of conservatively modified variations. Every nucleic acid sequence herein which encodes a polypeptide also describes silent variations of the nucleic acid. In certain contexts each codon in a nucleic acid (except AUG, which is ordinarily the only codon for methionine, and TGG, which is ordinarily the only codon for tryptophan) can be modified to yield a functionally identical molecule. Accordingly, a silent variation of a nucleic acid which encodes a polypeptide is implicit in a described sequence with respect to the expression product, but not necessarily with respect to actual probe sequences.

As to amino acid sequences, one of skill will recognize that individual substitutions, deletions, or additions to a nucleic acid, peptide, polypeptide, or protein sequence which alters, adds, or deletes a single amino acid or a small percentage of amino acids in the encoded sequence is a "conservatively modified variant" where the alteration results in the substitution of an amino acid with a chemically similar amino acid. Conservative substitution tables providing functionally similar amino acids are well known in the art. Such conservatively modified variants are in addition to and do not exclude polymorphic variants, interspecies homologs, and alleles of the invention. Typically conservative substitutions for one another: 1) Alanine (A), Glycine (G); 2) Aspartic acid (D), Glutamic acid (E); 3) Asparagine (N), Glutamine (Q); 4) Arginine (R), Lysine (K); 5) Isoleucine (I), Leucine (L), Methionine (M), Valine (V); 6) Phenylalanine (F), Tyrosine (Y), Tryptophan (W); 7) Serine (S), Threonine (T); and 8) Cysteine (C), Methionine (M) (see, e.g., Creighton (1984) Proteins Freeman).

Macromolecular structures such as polypeptide structures can be described in terms of various levels of organization. For a general discussion of this organization, see, e.g., Alberts, et al. (2001) Molecular Biology of the Cell (4th ed.) Garland Pub.; and Cantor and Schimmel (1980) Biophysical Chemistry Part I: The Conformation of Biological Macromolecules Freeman. "Primary structure" refers to the amino acid sequence of a particular peptide. "Secondary structure" refers to locally ordered, three dimensional structures within a polypeptide. These structures are commonly known as domains. Domains are portions of a polypeptide that often form a compact unit of the polypeptide and are typically 25 to approximately 500 amino acids long. Typical domains are made up of sections of lesser organization such as stretches of β -sheet and α -helices. "Tertiary structure" refers to the complete three dimensional structure of a polypeptide monomer. "Quaternary structure" refers to the three dimensional structure formed, usually by the non-covalent association of independent tertiary units. Anisotropic terms are also known as energy terms.

"Nucleic acid" or "oligonucleotide" or "polynucleotide" or grammatical equivalents used herein means at least two nucleotides covalently linked together. Oligonucleotides are typically from about 5, 6, 7, 8, 9, 10, 12, 15, 25, 30, 40, 50, or more nucleotides in length, up to about 100 nucleotides in length. Nucleic acids and polynucleotides are polymers of any length, including longer lengths, e.g., 200, 300, 500, 1000, 2000, 3000, 5000, 7000, 10,000, etc. A nucleic acid of the present invention will generally contain phosphodiester bonds,

although in some cases, nucleic acid analogs are included that may have at least one different linkage, e.g., phosphoramidate, phosphorothioate, phosphorodithioate, or O-methylphosphoroamidite linkages (see Eckstein (1992) Oligonucleotides and Analogues: A Practical Approach Oxford University Press); and peptide nucleic acid backbones and linkages. Other analog nucleic acids include those with positive backbones; non-ionic backbones, and non-ribose backbones, including those described in U.S. Patent Nos. 5,235,033 and 5,034,506, and Chapters 6 and 7 of Sanghvi and Cook (eds. 1994) Carbohydrate Modifications in Antisense Research ASC Symposium Series 580. Nucleic acids containing one or more carbocyclic sugars are also included within one definition of nucleic acids. Modifications of the ribose-phosphate backbone may be done for a variety of reasons, e.g., to increase the stability and half-life of such molecules in physiological environments or as probes on a biochip. Mixtures of naturally occurring nucleic acids and analogs can be made; alternatively, mixtures of different nucleic acid analogs, and mixtures of naturally occurring nucleic acids and analogs may be made.

A variety of references disclose such nucleic acid analogs, including, e.g., phosphoramidate (Beaucage, et al. (1993) Tetrahedron 49:1925-1963 and references therein; Letsinger (1970) J. Org. Chem. 35:3800-3803; Sprinzl, et al. (1977) Eur. J. Biochem. 81:579-589; Letsinger, et al. (1986) Nucl. Acids Res. 14:3487-499; Sawai, et al. (1984) Chem. Lett. 805; Letsinger, et al. (1988) J. Am. Chem. Soc. 110:4470-4471; and Pauwels, et al. (1986), Chemica Scripta 26:141-149), phosphorothioate (Mag, et al. (1991) Nucl. Acids Res. 19:1437-441; and U.S. Patent No. 5,644,048), phosphorodithioate (Brill, et al. (1989) J. Am. Chem. Soc. 111:2321-2322), O-methylphosphoroamidite linkages (see Eckstein (1992) Oligonucleotides and Analogues: A Practical Approach Oxford Univ. Press), and peptide nucleic acid backbones and linkages (see Egholm (1992) J. Am. Chem. Soc. 114:1895-897; Meier, et al. (1992) Angew. Chem. Int. Ed. Engl. 31:1008-1010; Nielsen (1993) Nature, 365:566-568; Carlsson, et al. (1996) Nature 380:207, each of which is incorporated by reference). Other analog nucleic acids include those with positive backbones (Denpcy, et al. (1995) Proc. Nat'l Acad. Sci. USA 92:6097-101; non-ionic backbones (U.S. Patent Nos. 5,386,023, 5,637,684, 5,602,240, 5,216,141 and 4,469,863; Kiedrowski, et al. (1991) Angew. Chem. Intl. Ed. English 30:423-426; Letsinger, et al. (1988) J. Am. Chem. Soc. 110:4470-4471; Jung, et al. (1994) Nucleoside and Nucleotide 13:1597; Chapters 2 and 3, in Sanghvi and Cook (eds. 1994) Carbohydrate Modifications in Antisense Research ASC Symposium Series 580; Mesmaeker, et al. (1994) Bioorganic and Medicinal Chem. Lett. 4:395-398; Jeffs,

et al. (1994) J. Biomolecular NMR 34:17-xx; Horn, et al. (1996) Tetrahedron Lett. 37:743-xxx) and non-ribose backbones, including those described in U.S. Patent Nos. 5,235,033 and 5,034,506, and Chapters 6 and 7, in Sanghvi and Cook (eds. 1994) Carbohydrate Modifications in Antisense Research ASC Symposium Series 580. Nucleic acids containing one or more carbocyclic sugars are also included within one definition of nucleic acids (see Jenkins, et al. (1995) Chem. Soc. Rev. pp 169-176). Several nucleic acid analogs are described in Rawls (p. 35 June 2, 1997) C&E News. Each of these references is hereby expressly incorporated by reference.

Particularly preferred are peptide nucleic acids (PNA) which includes peptide nucleic acid analogs. These backbones are substantially non-ionic under neutral conditions, in contrast to the highly charged phosphodiester backbone of naturally occurring nucleic acids. This results in two advantages. First, the PNA backbone exhibits improved hybridization kinetics. PNAs have larger changes in the melting temperature (T_m) for mismatched versus perfectly matched base pairs. DNA and RNA typically exhibit a 2-4° C drop in T_m for an internal mismatch. With the non-ionic PNA backbone, the drop is closer to 7-9° C. Similarly, due to their non-ionic nature, hybridization of the bases attached to these backbones is relatively insensitive to salt concentration. In addition, PNAs are not degraded by cellular enzymes, and thus can be more stable.

The nucleic acids may be single stranded or double stranded, as specified, or contain portions of both double stranded or single stranded sequence. As will be appreciated by those in the art, the depiction of a single strand also defines the sequence of the complementary strand; thus the sequences described herein also provide the complement of the sequence. The nucleic acid may be DNA, both genomic and cDNA, RNA, or a hybrid, where the nucleic acid may contain combinations of deoxyribo- and ribo-nucleotides, and combinations of bases, including uracil, adenine, thymine, cytosine, guanine, inosine, xanthine hypoxanthine, isocytosine, isoguanine, etc. "Transcript" typically refers to a naturally occurring RNA, e.g., a pre-mRNA, hnRNA, or mRNA. As used herein, the term "nucleoside" includes nucleotides and nucleoside and nucleotide analogs, and modified nucleosides such as amino modified nucleosides. In addition, "nucleoside" includes non-naturally occurring analog structures. Thus, e.g., the individual units of a peptide nucleic acid, each containing a base, are referred to herein as a nucleoside.

A "label" or a "detectable moiety" is a composition detectable by spectroscopic,

photochemical, biochemical, immunochemical, chemical, or other physical means. For example, useful labels include ^{32}P , fluorescent dyes, electron-dense reagents, enzymes (e.g., as commonly used in an ELISA), biotin, digoxigenin, or haptens and proteins or other entities which can be made detectable, e.g., by incorporating a radiolabel into the peptide or used to detect antibodies specifically reactive with the peptide. The labels may be incorporated into the ovarian cancer nucleic acids, proteins and antibodies at any position. Any method known in the art for conjugating the antibody to the label may be employed, including those methods described by Hunter, et al. (1962) Nature 144:945-xxx; David, et al. (1974) Biochemistry 13:1014-1021; Pain, et al. (1981) J. Immunol. Meth. 40:219-230; and Nygren (1982) J. Histochem. and Cytochem. 30:407-412.

An "effector" or "effector moiety" or "effector component" is a molecule that is bound (or linked, or conjugated), either covalently, through a linker or a chemical bond, or non-covalently, through ionic, van der Waals, electrostatic, or hydrogen bonds, to an antibody. The "effector" can be a variety of molecules including, e.g., detection moieties including radioactive compounds, fluorescent compounds, an enzyme or substrate, tags such as epitope tags, a toxin; activatable moieties, a chemotherapeutic agent; a lipase; an antibiotic; or a radioisotope emitting "hard" e.g., beta radiation.

A "labeled nucleic acid probe or oligonucleotide" is one that is bound, either covalently, through a linker or a chemical bond, or non-covalently, through ionic, van der Waals, electrostatic, or hydrogen bonds to a label such that the presence of the probe may be detected by detecting the presence of the label bound to the probe. Alternatively, method using high affinity interactions may achieve the same results where one of a pair of binding partners binds to the other, e.g., biotin, streptavidin.

As used herein a "nucleic acid probe or oligonucleotide" is a nucleic acid capable of binding to a target nucleic acid of complementary sequence through one or more types of chemical bonds, usually through complementary base pairing, usually through hydrogen bond formation. As used herein, a probe may include natural (e.g., A, G, C, or T) or modified bases (7-deazaguanosine, inosine, etc.). In addition, the bases in a probe may be joined by a linkage other than a phosphodiester bond, so long as it does not functionally interfere with hybridization. Thus, e.g., probes may be peptide nucleic acids in which the constituent bases are joined by peptide bonds rather than phosphodiester linkages. Probes may bind target sequences lacking complete complementarity with the probe sequence depending upon the

stringency of the hybridization conditions. The probes are preferably directly labeled, e.g., with isotopes, chromophores, lumiphores, chromogens, or indirectly labeled such as with biotin to which a streptavidin complex may later bind. By assaying for the presence or absence of the probe, one can detect the presence or absence of the select sequence or
5 subsequence. Diagnosis or prognosis may be based at the genomic level, or at the level of RNA or protein expression.

The term "recombinant" when used with reference, e.g., to a cell, or nucleic acid, protein, or vector, indicates that the cell, nucleic acid, protein or vector, has been modified by the introduction of a heterologous nucleic acid or protein or the alteration of a native nucleic
10 acid or protein, or that the cell is derived from a cell so modified. Thus, e.g., recombinant cells express genes that are not found within the native (non-recombinant) form of the cell or express native genes that are otherwise abnormally expressed, under expressed or not expressed at all. By the term "recombinant nucleic acid" herein is meant nucleic acid, originally formed in vitro, in general, by the manipulation of nucleic acid, e.g., using
15 polymerases and endonucleases, in a form not normally found in nature. In this manner, operably linkage of different sequences is achieved. Thus an isolated nucleic acid, in a linear form, or an expression vector formed in vitro by ligating DNA molecules that are not normally joined, are both considered recombinant for the purposes of this invention. It is understood that once a recombinant nucleic acid is made and reintroduced into a host cell or
20 organism, it will replicate non-recombinantly, e.g., using the in vivo cellular machinery of the host cell rather than in vitro manipulations; however, such nucleic acids, once produced recombinantly, although subsequently replicated non-recombinantly, are still considered recombinant for the purposes of the invention. Similarly, a "recombinant protein" is a protein made using recombinant techniques, e.g., through the expression of a recombinant nucleic
25 acid as depicted above.

The term "heterologous" when used with reference to portions of a nucleic acid indicates that the nucleic acid comprises two or more subsequences that are not normally found in the same relationship to each other in nature. For instance, the nucleic acid is typically recombinantly produced, having two or more sequences, e.g., from unrelated genes
30 arranged to make a new functional nucleic acid, e.g., a promoter from one source and a coding region from another source. Similarly, a heterologous protein will often refer to two or more subsequences that are not found in the same relationship to each other in nature (e.g., a fusion protein).

A "promoter" is defined as an array of nucleic acid control sequences that direct transcription of a nucleic acid. As used herein, a promoter includes necessary nucleic acid sequences near the start site of transcription, such as, in the case of a polymerase II type promoter, a TATA element. A promoter also optionally includes distal enhancer or repressor elements, which can be located as much as several thousand base pairs from the start site of transcription. A "constitutive" promoter is a promoter that is active under most environmental and developmental conditions. An "inducible" promoter is a promoter that is active under environmental or developmental regulation. The term "operably linked" refers to a functional linkage between a nucleic acid expression control sequence (such as a promoter, or array of transcription factor binding sites) and a second nucleic acid sequence, e.g., wherein the expression control sequence directs transcription of the nucleic acid corresponding to the second sequence.

An "expression vector" is a nucleic acid construct, generated recombinantly or synthetically, with a series of specified nucleic acid elements that permit transcription of a particular nucleic acid in a host cell. The expression vector can be part of a plasmid, virus, or nucleic acid fragment. Typically, the expression vector includes a nucleic acid to be transcribed operably linked to a promoter.

The phrase "selectively (or specifically) hybridizes to" refers to the binding, duplexing, or hybridizing of a molecule only to a particular nucleotide sequence under stringent hybridization conditions when that sequence is present in a complex mixture (e.g., total cellular or library DNA or RNA).

The phrase "stringent hybridization conditions" refers to conditions under which a probe will hybridize to its target subsequence, typically in a complex mixture of nucleic acids, but to no other sequences. Stringent conditions are sequence-dependent and will be different in different circumstances. Longer sequences hybridize specifically at higher temperatures. An extensive guide to the hybridization of nucleic acids is found in "Overview of principles of hybridization and the strategy of nucleic acid assays" in Tijssen (1993) Hybridization with Nucleic Probes (Laboratory Techniques in Biochemistry and Molecular Biology) (vol. 24) Elsevier. Generally, stringent conditions are selected to be about 5-10° C lower than the thermal melting point (T_m) for the specific sequence at a defined ionic strength pH. The T_m is the temperature (under defined ionic strength, pH, and nucleic concentration) at which 50% of the probes complementary to the target hybridize to the target

sequence at equilibrium (as the target sequences are present in excess, at T_m , 50% of the probes are occupied at equilibrium). Stringent conditions will be those in which the salt concentration is less than about 1.0 M sodium ion, typically about 0.01 to 1.0 M sodium ion concentration (or other salts) at pH 7.0 to 8.3 and the temperature is at least about 30° C for short probes (e.g., 10 to 50 nucleotides) and at least about 60° C for long probes (e.g., greater than 50 nucleotides). Stringent conditions may also be achieved with the addition of destabilizing agents such as formamide. For selective or specific hybridization, a positive signal is typically at least two times background, preferably 10 times background hybridization. Exemplary stringent hybridization conditions can be as following: 50% formamide, 5x SSC, and 1% SDS, incubating at 42° C, or, 5x SSC, 1% SDS, incubating at 65° C, with wash in 0.2x SSC, and 0.1% SDS at 65° C. For PCR, a temperature of about 36° C is typical for low stringency amplification, although annealing temperatures may vary between about 32-48° C depending on primer length. For high stringency PCR amplification, a temperature of about 62° C is typical, although high stringency annealing temperatures can range from about 50° C to about 65° C, depending on the primer length and specificity. Typical cycle conditions for both high and low stringency amplifications include a denaturation phase of 90-95° C for 30-120 sec, an annealing phase lasting 30-120 sec, and an extension phase of about 72° C for 1-2 min. Protocols and guidelines for low and high stringency amplification reactions are available, e.g., in Innis, et al. (1990) PCR Protocols: A Guide to Methods and Applications Academic Press, N.Y.

Nucleic acids that do not hybridize to each other under stringent conditions are still substantially identical if the polypeptides which they encode are substantially identical. This occurs, e.g., when a copy of a nucleic acid is created using the maximum codon degeneracy permitted by the genetic code. In such cases, the nucleic acids typically hybridize under moderately stringent hybridization conditions. Exemplary "moderately stringent hybridization conditions" include a hybridization in a buffer of 40% formamide, 1 M NaCl, 1% SDS at 37° C, and a wash in 1X SSC at 45° C. A positive hybridization is at least twice background. Alternative hybridization and wash conditions can be utilized to provide conditions of similar stringency. Additional guidelines for determining hybridization parameters are provided, e.g., Ausubel, et al. (ed. 1991 and supplements) Current Protocols in Molecular Biology Lippincott.

The phrase "functional effects" in the context of assays for testing compounds that

modulate activity of an ovarian cancer protein includes the determination of a parameter that is indirectly or directly under the influence of the ovarian cancer protein or nucleic acid, e.g., a functional, physical, physiological, or chemical effect, such as the ability to decrease ovarian cancer. It includes ligand binding activity; cell growth on soft agar; anchorage
5 dependence; contact inhibition and density limitation of growth; cellular proliferation; cellular transformation; growth factor or serum dependence; tumor specific marker levels; invasiveness into Matrigel; tumor growth and metastasis in vivo; mRNA and protein expression in cells undergoing metastasis, and other characteristics of ovarian cancer cells. "Functional effects" include in vitro, in vivo, and ex vivo activities.

10 By "determining the functional effect" is meant assaying for a compound that increases or decreases a parameter that is indirectly or directly under the influence of an ovarian cancer protein sequence, e.g., functional, enzymatic, physical, physiological, and chemical effects. Such functional effects can be measured by any means known to those skilled in the art, e.g., changes in spectroscopic characteristics (e.g., fluorescence,
15 absorbance, refractive index), hydrodynamic (e.g., shape), chromatographic, or solubility properties for the protein, measuring inducible markers or transcriptional activation of the ovarian cancer protein; measuring binding activity or binding assays, e.g., binding to antibodies or other ligands, and measuring cellular proliferation. Determination of the functional effect of a compound on ovarian cancer can also be performed using ovarian
20 cancer assays known to those of skill in the art such as an in vitro assays, e.g., cell growth on soft agar; anchorage dependence; contact inhibition and density limitation of growth; cellular proliferation; cellular transformation; growth factor or serum dependence; tumor specific marker levels; invasiveness into Matrigel; tumor growth and metastasis in vivo; mRNA and protein expression in cells undergoing metastasis, and other characteristics of ovarian cancer
25 cells. The functional effects can be evaluated by means known to those skilled in the art, e.g., microscopy for quantitative or qualitative measures of alterations in morphological features, measurement of changes in RNA or protein levels for ovarian cancer-associated sequences, measurement of RNA stability, or identification of downstream or reporter gene expression (CAT, luciferase, β -gal, GFP, and the like), e.g., via chemiluminescence, fluorescence,
30 colorimetric reactions, antibody binding, inducible markers, and ligand binding assays.

"Inhibitors", "activators", and "modulators" of ovarian cancer polynucleotide and polypeptide sequences are used to refer to activating, inhibitory, or modulating molecules or compounds identified using in vitro and in vivo assays of ovarian cancer polynucleotide and

polypeptide sequences. Inhibitors are compounds that, e.g., bind to, partially or totally block activity, decrease, prevent, delay activation, inactivate, desensitize, or down regulate the activity or expression of ovarian cancer proteins, e.g., antagonists. Antisense or inhibitory nucleic acids may inhibit expression and subsequent function of the protein. "Activators" are compounds that increase, open, activate, facilitate, enhance activation, sensitize, agonize, or up regulate ovarian cancer protein activity. Inhibitors, activators, or modulators also include genetically modified versions of ovarian cancer proteins, e.g., versions with altered activity, as well as naturally occurring and synthetic ligands, antagonists, agonists, antibodies, small chemical molecules, and the like. Assays for inhibitors and activators include, e.g., expressing the ovarian cancer protein in vitro, in cells, or cell membranes, applying putative modulator compounds, and then determining the functional effects on activity, as described above. Activators and inhibitors of ovarian cancer can also be identified by incubating ovarian cancer cells with the test compound and determining increases or decreases in the expression of one or more ovarian cancer proteins, e.g., 1, 2, 3, 4, 5, 10, 15, 20, 25, 30, 40, 50, or more ovarian cancer proteins, such as ovarian cancer proteins encoded by the sequences set out in Tables 1-26.

Samples or assays comprising ovarian cancer proteins that are treated with a potential activator, inhibitor, or modulator are compared to control samples without the inhibitor, activator, or modulator to examine the extent of inhibition. Control samples (untreated with inhibitors) are assigned a relative protein activity value of 100%. Inhibition of a polypeptide is achieved when the activity value relative to the control is about 80%, preferably 50%, more preferably 25% or less. Activation of an ovarian cancer polypeptide is achieved when the activity value relative to the control (untreated with activators) is 110%, more preferably 150%, more preferably 200-500% (e.g., 2-5 fold higher relative to the control), more preferably 1000-3000% higher.

The phrase "changes in cell growth" refers to a change in cell growth and proliferation characteristics in vitro or in vivo, e.g., cell viability, formation of foci, anchorage independence, semi-solid or soft agar growth, change in contact inhibition or density limitation of growth, loss of growth factor or serum requirements, change in cell morphology, gain or loss of immortalization, gain or loss of tumor specific markers, ability to form or suppress tumors when injected into suitable animal hosts, and/or immortalization of the cell. See, e.g., pp. 231-241 in Freshney (1994) Culture of Animal Cells: A Manual of Basic Technique (3d ed.) Wiley-Liss.

“Tumor cell” refers to pre-cancerous, cancerous, and normal cells in a tumor.

“Cancer cells,” “transformed” cells or “transformation” in tissue culture, refers to spontaneous or induced phenotypic changes that do not necessarily involve the uptake of new genetic material. Although transformation can arise from infection with a transforming virus and incorporation of new genomic DNA, or uptake of exogenous DNA, it can also arise spontaneously or following exposure to a carcinogen, thereby mutating an endogenous gene. Transformation is typically associated with phenotypic changes, such as immortalization of cells, aberrant growth control, non-morphological changes, and/or malignancy. See, Freshney (1994) Culture of Animal Cells.

“Antibody” refers to a polypeptide comprising a framework region from an immunoglobulin gene or fragments thereof that specifically binds and recognizes an antigen. The recognized immunoglobulin genes include the kappa, lambda, alpha, gamma, delta, epsilon, and mu constant region genes, as well as the myriad immunoglobulin variable region genes. Light chains are classified as either kappa or lambda. Heavy chains are classified as gamma, mu, alpha, delta, or epsilon, which in turn define the immunoglobulin classes, IgG, IgM, IgA, IgD, and IgE, respectively. Typically, the antigen-binding region of an antibody or its functional equivalent will be most critical in specificity and affinity of binding. See, e.g., Paul (ed. 1999) Fundamental Immunology (4th ed.) Raven.

An exemplary immunoglobulin (antibody) structural unit comprises a tetramer. Each tetramer is composed of two identical pairs of polypeptide chains, each pair having one “light” (about 25 kD) and one “heavy” chain (about 50-70 kD). The N-terminus of each chain defines a variable region of about 100 to 110 or more amino acids primarily responsible for antigen recognition. The terms variable light chain (V_L) and variable heavy chain (V_H) refer to these light and heavy chains respectively.

Antibodies exist, e.g., as intact immunoglobulins or as a number of well-characterized fragments produced by digestion with various peptidases. Thus, e.g., pepsin digests an antibody below the disulfide linkages in the hinge region to produce $F(ab)'_2$, a dimer of Fab which itself is a light chain joined to V_H -C_H1 by a disulfide bond. The $F(ab)'_2$ may be reduced under mild conditions to break the disulfide linkage in the hinge region, thereby converting the $F(ab)'_2$ dimer into an Fab' monomer. The Fab' monomer is essentially Fab with part of the hinge region. See Paul (ed. 1999) Fundamental Immunology (4th ed.) Raven. While various antibody fragments are defined in terms of the digestion of an intact antibody,

one of skill will appreciate that such fragments may be synthesized de novo either chemically or by using recombinant DNA methodology. Thus, the term antibody, as used herein, also includes antibody fragments either produced by the modification of whole antibodies, or those synthesized de novo using recombinant DNA methodologies (e.g., single chain Fv) or those identified using phage display libraries. See, e.g., McCafferty, et al. (1990) Nature 348:552-554.

For preparation of antibodies, e.g., recombinant, monoclonal, or polyclonal antibodies, many techniques known in the art can be used (see, e.g., Kohler and Milstein (1975) Nature 256:495-497; Kozbor, et al. (1983) Immunology Today 4:72; Cole, et al., pp. 77-96 in Reisfeld and Sell (1985) Monoclonal Antibodies and Cancer Therapy Liss; Coligan (1991) Current Protocols in Immunology Lippincott; Harlow and Lane (1988) Antibodies: A Laboratory Manual CSH Press; and Goding (1986) Monoclonal Antibodies: Principles and Practice (2d ed.) Academic Press. Techniques for the production of single chain antibodies (U.S. Patent 4,946,778) can be adapted to produce antibodies to polypeptides of this invention. Transgenic mice, or other organisms, e.g., other mammals, may be used to express humanized antibodies. Alternatively, phage display technology can be used to identify antibodies and heteromeric Fab fragments that specifically bind to selected antigens. See, e.g., McCafferty, et al. (1990) Nature 348:552-554; and Marks, et al. (1992) Biotechnology 10:779-783.

A "chimeric antibody" is an antibody molecule in which (a) the constant region, or a portion thereof, is altered, replaced or exchanged so that the antigen binding site (variable region) is linked to a constant region of a different or altered class, effector function and/or species, or an entirely different molecule which confers new properties to the chimeric antibody, e.g., an enzyme, toxin, hormone, growth factor, drug, etc.; or (b) the variable region, or a portion thereof, is altered, replaced or exchanged with a variable region having a different or altered antigen specificity.

Identification of ovarian cancer-associated sequences

In one aspect, the expression levels of genes are determined in different patient samples for which diagnosis information is desired, to provide expression profiles. An expression profile of a particular sample is essentially a "fingerprint" of the state of the sample; while two states may have any particular gene similarly expressed, the evaluation of a number of genes simultaneously allows the generation of a gene expression profile that is

characteristic of the state of the cell. That is, normal tissue (e.g., normal ovarian or other tissue) may be distinguished from cancerous or metastatic cancerous tissue of the ovarian, or ovarian cancer tissue or metastatic ovarian cancerous tissue can be compared with tissue samples of ovarian and other tissues from surviving cancer patients. By comparing
5 expression profiles of tissue in known different ovarian cancer states, information regarding which genes are important (including both up- and down-regulation of genes) in each of these states is obtained. Molecular profiling may distinguish subtypes of a currently collective disease designation, e.g., different forms of a cancer.

The identification of sequences that are differentially expressed in ovarian cancer
10 versus non-ovarian cancer tissue allows the use of this information in a number of ways. For example, a particular treatment regime may be evaluated: does a chemotherapeutic drug act to down-regulate ovarian cancer, and thus tumor growth or recurrence, in a particular patient. Alternatively, does existing treatment induce expression of a target. Similarly, diagnosis and treatment outcomes may be done or confirmed by comparing patient samples with the known
15 expression profiles. Metastatic tissue can also be analyzed to determine the stage of ovarian cancer in the tissue or origin of the primary tumor. Furthermore, these gene expression profiles (or individual genes) allow screening of drug candidates with an eye to mimicking or altering a particular expression profile; e.g., screening can be done for drugs that suppress the ovarian cancer expression profile. This may be done by making biochips comprising sets of
20 the important ovarian cancer genes, which can then be used in these screens. These methods can also be based on evaluating protein expression; that is, protein expression levels of the ovarian cancer proteins can be evaluated for diagnostic purposes or to screen candidate agents. In addition, the ovarian cancer nucleic acid sequences can be administered for gene therapy purposes, including the administration of antisense or RNAi nucleic acids, or the
25 ovarian cancer proteins (including antibodies and other modulators thereof) administered as therapeutic drugs.

Thus the present invention provides nucleic acid and protein sequences that are differentially expressed in ovarian cancer relative to normal tissues and/or non-malignant tissues, herein termed "ovarian cancer sequences." As outlined below, ovarian cancer
30 sequences include those that are up-regulated (e.g., expressed at a higher level) in ovarian cancer, as well as those that are down-regulated (e.g., expressed at a lower level). In a preferred embodiment, the ovarian cancer sequences are from humans; however, as will be appreciated by those in the art, ovarian cancer sequences from other organisms may be useful

in animal models of disease and drug evaluation; thus, other ovarian cancer sequences are provided, from vertebrates, including mammals, including rodents (rats, mice, hamsters, guinea pigs, etc.), primates, farm animals (including sheep, goats, pigs, cows, horses, etc.) and pets (e.g., dogs, cats, etc.). Ovarian cancer sequences, e.g., counterpart genes, from other organisms may be obtained using the techniques outlined below.

Ovarian cancer sequences can include both nucleic acid and amino acid sequences. Ovarian cancer nucleic acid sequences are useful in a variety of applications, including diagnostic applications, which will detect naturally occurring nucleic acids. Screening applications; e.g., biochips comprising nucleic acid probes or PCR microtiter plates with selected probes to the ovarian cancer sequences, are also provided.

An ovarian cancer sequence can be initially identified by substantial nucleic acid and/or amino acid sequence homology to the ovarian cancer sequences outlined herein. Such homology can be based upon the overall nucleic acid or amino acid sequence, and is generally determined as outlined below, using either homology programs or hybridization conditions.

For identifying ovarian cancer-associated sequences, the ovarian cancer screen typically includes comparing genes identified in different tissues, e.g., normal and cancerous tissues, or tumor tissue samples from patients who have metastatic disease vs. non metastatic tissue. Other suitable tissue comparisons include comparing ovarian cancer samples with metastatic cancer samples from other cancers, such as lung, ovarian, gastrointestinal cancers, etc. Samples of different stages of ovarian cancer, e.g., survivor tissue, drug resistant states, and tissue undergoing metastasis, are applied to biochips comprising nucleic acid probes. The samples are first microdissected, if applicable, and treated for the preparation of mRNA. Suitable biochips are commercially available, e.g., from Affymetrix. Gene expression profiles as described herein are generated and the data analyzed.

In one embodiment, the genes showing changes in expression as between normal and disease states are compared to genes expressed in other normal tissues, preferably normal ovarian, but also including, and not limited to, lung, heart, brain, liver, ovarian, kidney, muscle, colon, small intestine, large intestine, spleen, bone, and/or placenta. In a preferred embodiment, those genes identified during the ovarian cancer screen that are expressed in any significant amount in other tissues are removed from the profile, although in some embodiments, expression in non-essential tissues may be tolerated. That is, when screening for drugs, it is usually preferable that the target be disease specific, to minimize possible side

effects by interaction with target present in other organs.

In a preferred embodiment, ovarian cancer sequences are those that are up-regulated in ovarian cancer; that is, the expression of these genes is higher in the ovarian cancer tissue as compared to non-cancerous tissue. "Up-regulation" as used herein often means at least
5 about a two-fold change, preferably at least about a three fold change, with at least about five-fold or higher being preferred. Other embodiments are directed to sequences up regulated in non-malignant conditions relative to normal.

Unigene cluster identification numbers and accession numbers herein refer to the GenBank sequence database and the sequences of the accession numbers are hereby
10 expressly incorporated by reference. GenBank is known in the art, see, e.g., Benson, et al. (1998) Nucl. Acids Res. 26:1-7; and <http://www.ncbi.nlm.nih.gov/>. Sequences are also available in other databases, e.g., European Molecular Biology Laboratory (EMBL) and DNA Database of Japan (DDBJ). In some situations, the sequences may be derived from assembly of available sequences or be predicted from genomic DNA using exon prediction
15 algorithms, e.g., FGENESH. See Salamov and Solovyev (2000) Genome Res. 10:516-522. In other situations, sequences have been derived from cloning and sequencing of isolated nucleic acids.

In another preferred embodiment, ovarian cancer sequences are those that are down-regulated in ovarian cancer; that is, the expression of these genes is lower in ovarian cancer
20 tissue as compared to non-cancerous tissue. "Down-regulation" as used herein often means at least about a two-fold change, preferably at least about a three-fold change, with at least about five-fold or higher being preferred.

Informatics

The ability to identify genes that are over or under expressed in ovarian cancer can additionally provide high-resolution, high-sensitivity datasets which can be used in the areas of diagnostics, therapeutics, drug development, pharmacogenetics, protein structure, biosensor development, and other related areas. Expression profiles can be used in diagnostic or prognostic evaluation of patients with ovarian cancer. Subcellular toxicological
25 information can be generated to better direct drug structure and activity correlation (see Anderson (June 11-12, 1998) Pharmaceutical Proteomics: Targets, Mechanism, and Function, paper presented at the IBC Proteomics conference, Coronado, CA) or in a biological sensor device to predict the likely toxicological effect of chemical exposures and likely tolerable
30

exposure thresholds (see U.S. Patent No. 5,811,231). Similar advantages accrue from datasets relevant to other biomolecules and bioactive agents (e.g., nucleic acids, saccharides, lipids, drugs, and the like).

Thus, in another embodiment, the present invention provides a database that includes at least one set of assay data. The data contained in the database is acquired, e.g., using array analysis either singly or in a library format. The database can be in a form in which data can be maintained and transmitted, but is preferably an electronic database, and can be maintained on any electronic device allowing for the storage of and access to the database, such as a personal computer, but is preferably distributed on a wide area network, such as the World Wide Web.

The focus of the present section on databases that include peptide sequence data is for clarity of illustration only. It will be apparent to those of skill in the art that similar databases can be assembled for any assay data acquired using an assay of the invention.

The compositions and methods for identifying and/or quantitating the relative and/or absolute abundance of a variety of molecular and macromolecular species from a biological sample undergoing ovarian cancer, e.g., the identification of ovarian cancer-associated sequences described herein, provide an abundance of information which can be correlated with pathological conditions, predisposition to disease, drug testing, therapeutic monitoring, gene-disease causal linkages, identification of correlates of immunity and physiological status, and outcome data, among others. Although data generated from the assays of the invention is suited for manual review and analysis, in a preferred embodiment, data processing using high-speed computers is utilized.

An array of methods for indexing and retrieving biomolecular information is known in the art. For example, U.S. Patents 6,023,659 and 5,966,712 disclose a relational database system for storing biomolecular sequence information in a manner that allows sequences to be catalogued and searched according to one or more protein function hierarchies. U.S. Patent 5,953,727 discloses a relational database having sequence records containing information in a format that allows a collection of partial-length DNA sequences to be catalogued and searched according to association with one or more sequencing projects for obtaining full-length sequences from the collection of partial length sequences. U.S. Patent 5,706,498 discloses a gene database retrieval system for making a retrieval of a gene sequence similar to a sequence data item in a gene database based on the degree of similarity between a key sequence and a target sequence. U.S. Patent 5,538,897 discloses a method

using mass spectroscopy fragmentation patterns of peptides to identify amino acid sequences in computer databases by comparison of predicted mass spectra with experimentally-derived mass spectra using a closeness-of-fit measure. U.S. Patent 5,926,818 discloses a multi-dimensional database comprising a functionality for multi-dimensional data analysis described as on-line analytical processing (OLAP), which entails the consolidation of projected and actual data according to more than one consolidation path or dimension. U.S. Patent 5,295,261 reports a hybrid database structure in which the fields of each database record are divided into two classes, navigational and informational data, with navigational fields stored in a hierarchical topological map which can be viewed as a tree structure or as the merger of two or more such tree structures.

Fundamentals of bioinformatics are provided, e.g., in Mount, et al. (2001) Bioinformatics: Sequence and Genome Analysis CSH Press, NY; Durbin, et al. (eds. 1999) Biological Sequence Analysis: Probabilistic Models of Proteins and Nucleic Acids Cambridge Univ. Press; Baxeavanis and Ouellette (eds. 1998) Bioinformatics: A Practical Guide to the Analysis of Genes and Proteins (2d ed.) Wiley-Liss; Rashidi and Buehler (1999) Bioinformatics: Basic Applications in Biological Science and Medicine CRC Press; Setubal, et al. (eds 1997) Introduction to Computational Molecular Biology Brooks/Cole; Misener and Krawetz (eds. 2000) Bioinformatics: Methods and Protocols Humana Press; Higgins and Taylor (eds. 2000) Bioinformatics: Sequence, Structure, and Databanks: A Practical Approach Oxford Univ. Press; Brown (2001) Bioinformatics: A Biologist's Guide to Biocomputing and the Internet Eaton Pub.; Han and Kamber (2000) Data Mining: Concepts and Techniques Kaufmann Pub.; and Waterman (1995) Introduction to Computational Biology: Maps, Sequences, and Genomes Chap and Hall.

The present invention provides a computer database comprising a computer and software for storing in computer-retrievable form assay data records cross-tabulated, e.g., with data specifying the source of the target-containing sample from which each sequence specificity record was obtained.

In an exemplary embodiment, at least one of the sources of target-containing sample is from a control tissue sample known to be free of pathological disorders. In a variation, at least one of the sources is a known pathological tissue specimen, e.g., a neoplastic lesion or another tissue specimen to be analyzed for ovarian cancer. In another variation, assay records cross-tabulate one or more of the following parameters for a target species in a sample: (1) a unique identification code, which can include, e.g., a target molecular structure and/or

characteristic separation coordinate (e.g., electrophoretic or genomic position coordinates); (2) sample source; and (3) absolute and/or relative quantity of target species present in the sample.

The invention also provides for the storage and retrieval of a collection of target data in a computer data storage apparatus, which can include magnetic disks, optical disks, magneto-optical disks, DRAM, SRAM, SGRAM, SDRAM, RDRAM, DDR RAM, magnetic bubble memory devices, and other data storage devices, including CPU registers and on-CPU data storage arrays. Typically, the target data records are stored as a bit pattern in an array of magnetic domains on a magnetizable medium or as an array of charge states or transistor gate states, such as an array of cells in a DRAM device (e.g., each cell comprised of a transistor and a charge storage area, which may be on the transistor). In one embodiment, the invention provides such storage devices, and computer systems built therewith, comprising a bit pattern encoding a protein expression fingerprint record comprising unique identifiers for at least 10 target data records cross-tabulated with target source.

When the target is a peptide or nucleic acid, the invention preferably provides a method for identifying related peptide or nucleic acid sequences, comprising performing a computerized comparison between a peptide or nucleic acid sequence assay record stored in or retrieved from a computer storage device or database and at least one other sequence. The comparison can include a sequence analysis or comparison algorithm or computer program embodiment thereof (e.g., FASTA, TFASTA, GAP, BESTFIT) and/or the comparison may be of the relative amount of a peptide or nucleic acid sequence in a pool of sequences determined from a polypeptide or nucleic acid sample of a specimen.

The invention also preferably provides a magnetic disk, such as an IBM-compatible (DOS, Windows, Windows95/98/2000, Windows NT, OS/2) or other format (e.g., Linux, SunOS, Solaris, AIX, SCO Unix, VMS, MV, Macintosh, etc.) floppy diskette or hard (fixed, Winchester) disk drive, comprising a bit pattern encoding data from an assay of the invention in a file format suitable for retrieval and processing in a computerized sequence analysis, comparison, or relative quantitation method.

The invention also provides a network, comprising a plurality of computing devices linked via a data link, such as an Ethernet cable (coax or 10BaseT), telephone line, ISDN line, wireless network, optical fiber, or other suitable signal transmission medium, whereby at least one network device (e.g., computer, disk array, etc.) comprises a pattern of magnetic domains (e.g., magnetic disk) and/or charge domains (e.g., an array of DRAM cells)

composing a bit pattern encoding data acquired from an assay of the invention.

The invention also provides a method for transmitting assay data that includes generating an electronic signal on an electronic communications device, such as a modem, ISDN terminal adapter, DSL, cable modem, ATM switch, or the like, wherein the signal
5 includes (in native or encrypted format) a bit pattern encoding data from an assay or a database comprising a plurality of assay results obtained by the method of the invention.

In a preferred embodiment, the invention provides a computer system for comparing a query target to a database containing an array of data structures, such as an assay result obtained by the method of the invention, and ranking database targets based on the degree of
10 identity and gap weight to the target data. A central processor is preferably initialized to load and execute the computer program for alignment and/or comparison of the assay results. Data for a query target is entered into the central processor via an I/O device. Execution of the computer program results in the central processor retrieving the assay data from the data file, which comprises a binary description of an assay result.

The target data or record and the computer program can be transferred to secondary
15 memory, which is typically random access memory (e.g., DRAM, SRAM, SGRAM, or SDRAM). Targets are ranked according to the degree of correspondence between a selected assay characteristic (e.g., binding to a selected affinity moiety) and the same characteristic of the query target and results are output via an I/O device. For example, a central processor
20 can be a conventional computer (e.g., Intel Pentium, PowerPC, Alpha, PA-8000, SPARC, MIPS 4400, MIPS 10000, VAX, etc.); a program can be a commercial or public domain molecular biology software package (e.g., UWGCG Sequence Analysis Software, Darwin); a data file can be an optical or magnetic disk, a data server, a memory device (e.g., DRAM, SRAM, SGRAM, SDRAM, EPROM, bubble memory, flash memory, etc.); an I/O device can
25 be a terminal comprising a video display and a keyboard, a modem, an ISDN terminal adapter, an Ethernet port, a punched card reader, a magnetic strip reader, or other suitable I/O device.

The invention also preferably provides the use of a computer system, e.g., which typically comprises one or more of: (1) a computer; (2) a stored bit pattern encoding a
30 collection of peptide sequence specificity records obtained by methods of the inventions, which may be stored in the computer; (3) a comparison target, such as a query target; and (4) a program for alignment and comparison, typically with rank-ordering of comparison results on the basis of computed similarity values.

Characteristics of ovarian cancer-associated proteins

Ovarian cancer proteins of the present invention may be categorized as secreted proteins, transmembrane proteins, or intracellular proteins. In one embodiment, the ovarian cancer protein is an intracellular protein. Intracellular proteins may be found in the cytoplasm and/or in the nucleus. Intracellular proteins are involved in all aspects of cellular function and replication (including, e.g., signaling pathways); aberrant expression of such proteins often results in unregulated or dysregulated cellular processes. See, e.g., Alberts, et al. (eds. 1994) Molecular Biology of the Cell (3d ed.) Garland. For example, many intracellular proteins have enzymatic activity such as protein kinase activity, protein phosphatase activity, protease activity, nucleotide cyclase activity, polymerase activity, and the like. Intracellular proteins can also serve as docking proteins that are involved in organizing complexes of proteins, or targeting proteins to various subcellular localizations, and are often involved in maintaining the structural integrity of organelles.

An increasingly appreciated concept in characterizing proteins is the presence in the proteins of one or more structural motifs for which defined functions have been attributed. In addition to the highly conserved sequences found in the enzymatic domain of proteins, highly conserved sequences have been identified in proteins that are involved in protein-protein interaction. For example, Src-homology-2 (SH2) domains bind tyrosine-phosphorylated targets in a sequence dependent manner. PTB domains, which are distinct from SH2 domains, also bind tyrosine phosphorylated targets. SH3 domains bind to proline-rich targets. In addition, PH domains, tetratricopeptide repeats and WD domains to name only a few, have been shown to mediate protein-protein interactions. Some of these may also be involved in binding to phospholipids or other second messengers. As will be appreciated by one of ordinary skill in the art, these motifs can be identified on the basis of amino acid sequence; thus, an analysis of the sequence of proteins may provide insight into both the enzymatic potential of the molecule and/or molecules with which the protein may associate. One useful database is Pfam (protein families), which is a large collection of multiple sequence alignments and hidden Markov models covering many common protein domains. Versions are available via the internet from Washington University in St. Louis, the Sanger Center in England, and the Karolinska Institute in Sweden. See, e.g., Bateman, et al. (2000) Nuc. Acids Res. 28:263-266; Sonnhammer, et al. (1997) Proteins 28:405-420; Bateman, et al. (1999) Nuc. Acids Res. 27:260-262; and Sonnhammer, et al. (1998) Nuc. Acids Res. 26:320-

322.

In another preferred embodiment, the ovarian cancer sequences are transmembrane proteins. Transmembrane proteins are molecules that span a phospholipid bilayer of a cell. They may have an intracellular domain, an extracellular domain, or both. The intracellular domains of such proteins may have a number of functions including those already described for intracellular proteins. For example, the intracellular domain may have enzymatic activity and/or may serve as a binding site for additional proteins. Frequently the intracellular domain of transmembrane proteins serves both roles. For example certain receptor tyrosine kinases have both protein kinase activity and SH2 domains. In addition, autophosphorylation of tyrosines on the receptor molecule itself, creates binding sites for additional SH2 domain containing proteins.

Transmembrane proteins may contain from one to many transmembrane domains. For example, receptor tyrosine kinases, certain cytokine receptors, receptor guanylyl cyclases and receptor serine/threonine protein kinases contain a single transmembrane domain. However, various other proteins including channels and adenylyl cyclases contain numerous transmembrane domains. Many important cell surface receptors such as G protein coupled receptors (GPCRs) are classified as "seven transmembrane domain" proteins, as they contain 7 membrane spanning regions. Characteristics of transmembrane domains include approximately 17 consecutive hydrophobic amino acids that may be followed by charged amino acids. Therefore, upon analysis of the amino acid sequence of a particular protein, the localization and number of transmembrane domains within the protein may be predicted (see, e.g., PSORT web site <http://psort.nibb.ac.jp/>). Important transmembrane protein receptors include, but are not limited to the insulin receptor, insulin-like growth factor receptor, human growth hormone receptor, glucose transporters, transferrin receptor, epidermal growth factor receptor, low density lipoprotein receptor, epidermal growth factor receptor, leptin receptor, interleukin receptors, e.g., IL-1 receptor, IL-2 receptor, etc.

The extracellular domains of transmembrane proteins are diverse; however, conserved motifs are found repeatedly among various extracellular domains. Conserved structure and/or functions have been ascribed to different extracellular motifs. Many extracellular domains are involved in binding to other molecules. In one aspect, extracellular domains are found on receptors. Factors that bind the receptor domain include circulating ligands, which may be peptides, proteins, or small molecules such as adenosine and the like. For example, growth factors such as EGF, FGF, and PDGF are circulating growth factors that bind to their

cognate receptors to initiate a variety of cellular responses. Other factors include cytokines, mitogenic factors, neurotrophic factors and the like. Extracellular domains also bind to cell-associated molecules, or may be processed or shed to the blood stream. In this respect, they can mediate cell-cell interactions. Cell-associated ligands can be tethered to the cell, e.g., via a glycosylphosphatidylinositol (GPI) anchor, or may themselves be transmembrane proteins. Extracellular domains also associate with the extracellular matrix and contribute to the maintenance of the cell structure.

Ovarian cancer proteins that are transmembrane are particularly preferred in the present invention as they are readily accessible targets for immunotherapeutics, as are described herein. In addition, as outlined below, transmembrane proteins can be also useful in imaging modalities. Antibodies may be used to label such readily accessible proteins in situ. Alternatively, antibodies can also label intracellular proteins, in which case samples are typically permeabilized to provide access to intracellular proteins. In addition, some membrane proteins can be processed to release a soluble protein, or to expose a residual fragment. Released soluble proteins may be useful diagnostic markers, processed residual protein fragments may be useful ovarian markers of disease.

It will also be appreciated by those in the art that a transmembrane protein can be made soluble by removing transmembrane sequences, e.g., through recombinant methods. Furthermore, transmembrane proteins that have been made soluble can be made to be secreted through recombinant means by adding an appropriate signal sequence.

In another embodiment, the ovarian cancer proteins are secreted proteins; the secretion of which can be either constitutive or regulated. These proteins may have a signal peptide or signal sequence that targets the molecule to the secretory pathway. Secreted proteins are involved in numerous physiological events; e.g., if circulating, they often serve to transmit signals to various other cell types. The secreted protein may function in an autocrine manner (acting on the cell that secreted the factor), a paracrine manner (acting on cells in close proximity to the cell that secreted the factor), an endocrine manner (acting on cells at a distance, e.g., secretion into the blood stream), or exocrine (secretion, e.g., through a duct or to an adjacent epithelial surface as sweat glands, sebaceous glands, pancreatic ducts, lacrimal glands, mammary glands, wax producing glands of the ear, etc.). Thus, secreted molecules often find use in modulating or altering numerous aspects of physiology. Ovarian cancer proteins that are secreted proteins are particularly preferred as good diagnostic markers, e.g., for blood, plasma, serum, or stool tests. Those which are enzymes may be

antibody or small molecule therapeutic targets. Others may be useful as vaccine targets, e.g., via CTL mechanisms, as protein or DNA vaccines.

Use of ovarian cancer nucleic acids

5 As described above, ovarian cancer sequence is initially identified by substantial nucleic acid and/or amino acid sequence homology or linkage to the ovarian cancer sequences outlined herein. Such homology can be based upon the overall nucleic acid or amino acid sequence, and is generally determined as outlined below, using either homology programs or hybridization conditions. Typically, linked sequences on a mRNA are found on
10 the same molecule.

The ovarian cancer nucleic acid sequences of the invention, e.g., in Table 1-26, can be fragments of larger genes, e.g., they are nucleic acid segments. "Genes" in this context includes coding regions, non-coding regions, and mixtures of coding and non-coding regions. Accordingly, as will be appreciated by those in the art, using the sequences provided herein,
15 extended sequences, in either direction, of the ovarian cancer genes can be obtained, using techniques well known in the art for cloning either longer sequences or the full length sequences; see Ausubel, et al., supra. Much can be done by informatics and many sequences can be clustered to include multiple sequences corresponding to a single gene, e.g., systems such as UniGene (see, <http://www.ncbi.nlm.nih.gov/UniGene/>).

20 Once the ovarian cancer nucleic acid is identified, it can be cloned and, if necessary, its constituent parts recombined to form the entire ovarian cancer nucleic acid coding regions or the entire mRNA sequence. Once isolated from its natural source, e.g., contained within a plasmid or other vector or excised as a linear nucleic acid segment, the recombinant ovarian cancer nucleic acid can be further-used as a probe to identify and isolate other ovarian cancer
25 nucleic acids, e.g., extended coding regions. It can also be used as a "precursor" nucleic acid to make modified or variant ovarian cancer nucleic acids and proteins.

The ovarian cancer nucleic acids of the present invention are useful in several ways. In a first embodiment, nucleic acid probes to the ovarian cancer nucleic acids are made and attached to biochips to be used in screening and diagnostic methods, as outlined below, or for
30 administration, e.g., for gene therapy, vaccine, RNAi, and/or antisense applications. Alternatively, the ovarian cancer nucleic acids that include coding regions of ovarian cancer proteins can be put into expression vectors for the expression of ovarian cancer proteins, again for screening purposes or for administration to a patient.

In a preferred embodiment, nucleic acid probes to ovarian cancer nucleic acids (both the nucleic acid sequences outlined in the figures and/or the complements thereof) are made. The nucleic acid probes attached to the biochip are designed to be substantially complementary to the ovarian cancer nucleic acids, e.g., the target sequence (either the target
5 sequence of the sample or to other probe sequences, e.g., in sandwich assays), such that hybridization of the target sequence and the probes of the present invention occurs. As outlined below, this complementarity need not be perfect; there may be any number of base pair mismatches which will interfere with hybridization between the target sequence and the single stranded nucleic acids of the present invention. However, if the number of mutations
10 is so great that no hybridization can occur under even the least stringent of hybridization conditions, the sequence is not a complementary target sequence. Thus, by "substantially complementary" herein is meant that the probes are sufficiently complementary to the target sequences to hybridize under normal reaction conditions, particularly high stringency conditions, as outlined herein.

A nucleic acid probe is generally single stranded but can be partially single and partially double stranded. The strandedness of the probe is dictated by the structure, composition, and properties of the target sequence. In general, the nucleic acid probes range from about 8 to about 100 bases long, with from about 10 to about 80 bases being preferred, and from about 30 to about 50 bases being particularly preferred. That is, generally whole
20 genes are not used. In some embodiments, much longer nucleic acids can be used, up to hundreds of bases.

In a preferred embodiment, more than one probe per sequence is used, with either overlapping probes or probes to different sections of the target being used. That is, two, three, four or more probes, with three being preferred, are used to build in a redundancy for a
25 particular target. The probes can be overlapping (e.g., have some sequence in common), or separate. In some cases, PCR primers may be used to amplify signal for higher sensitivity.

As will be appreciated by those in the art, nucleic acids can be attached or immobilized to a solid support in a wide variety of ways. By "immobilized" and grammatical equivalents herein is meant the association or binding between the nucleic acid probe and the
30 solid support is sufficient to be stable under the conditions of binding, washing, analysis, and removal as outlined below. The binding can typically be covalent or non-covalent. By "non-covalent binding" and grammatical equivalents herein is meant one or more of electrostatic, hydrophilic, and hydrophobic interactions. Included in non-covalent binding is the covalent

attachment of a molecule, such as, streptavidin to the support and the non-covalent binding of the biotinylated probe to the streptavidin. By "covalent binding" and grammatical equivalents herein is meant that the two moieties, the solid support and the probe, are attached by at least one bond, including sigma bonds, pi bonds and coordination bonds.

- 5 Covalent bonds can be formed directly between the probe and the solid support or can be formed by a cross linker or by inclusion of a specific reactive group on either the solid support or the probe or both molecules. Immobilization may also involve a combination of covalent and non-covalent interactions.

- 10 In general, the probes are attached to the biochip in a wide variety of ways, as will be appreciated by those in the art. As described herein, the nucleic acids can either be synthesized first, with subsequent attachment to the biochip, or can be directly synthesized on the biochip.

- The biochip comprises a suitable solid substrate. By "substrate" or "solid support" or other grammatical equivalents herein is meant a material that can be modified to contain discrete individual sites appropriate for the attachment or association of the nucleic acid probes and is amenable to at least one detection method. As will be appreciated by those in the art, the number of possible substrates are very large, and include, but are not limited to, glass and modified or functionalized glass, plastics (including acrylics, polystyrene and copolymers of styrene and other materials, polypropylene, polyethylene, polybutylene, polyurethanes, Teflon, etc.), polysaccharides, nylon or nitrocellulose, resins, silica or silica-based materials including silicon and modified silicon, carbon, metals, inorganic glasses, plastics, etc. In general, the substrates allow optical detection and do not appreciably fluoresce. See, e.g., WO0055627 Reusable Low Fluorescent Plastic Biochip.
- 20

- Generally the substrate is planar, although as will be appreciated by those in the art, other configurations of substrates may be used as well. For example, the probes may be placed on the inside surface of a tube, for flow-through sample analysis to minimize sample volume. Similarly, the substrate may be flexible, such as a flexible foam, including closed cell foams made of particular plastics.
- 25

- In a preferred embodiment, the surface of the biochip and the probe may be derivatized with chemical functional groups for subsequent attachment of the two. Thus, e.g., the biochip is derivatized with a chemical functional group including, but not limited to, amino groups, carboxyl groups, oxo groups and thiol groups, with amino groups being particularly preferred. Using these functional groups, the probes can be attached using
- 30

functional groups on the probes. For example, nucleic acids containing amino groups can be attached to surfaces comprising amino groups, e.g., using linkers as are known in the art; e.g., homo- or hetero-bifunctional linkers as are well known (see 1994 Pierce Chemical Company catalog, technical section on cross-linkers, pages 155-200). In addition, in some cases, additional linkers, such as alkyl groups (including substituted and heteroalkyl groups) may be used.

In this embodiment, oligonucleotides are synthesized as is known in the art, and then attached to the surface of the solid support. As will be appreciated by those skilled in the art, either the 5' or 3' terminus may be attached to the solid support, or attachment may be via an internal nucleoside.

In another embodiment, the immobilization to the solid support may be very strong, yet non-covalent. For example, biotinylated oligonucleotides can be made, which bind to surfaces covalently coated with streptavidin, resulting in attachment.

Alternatively, the oligonucleotides may be synthesized on the surface, as is known in the art. For example, photoactivation techniques utilizing photopolymerization compounds and techniques are used. In a preferred embodiment, the nucleic acids can be synthesized in situ, using well known photolithographic techniques, such as those described in WO 95/25116; WO 95/35505; U.S. Patent Nos. 5,700,637 and 5,445,934; and references cited within, all of which are expressly incorporated by reference; these methods of attachment form the basis of the Affymetrix GeneChip™ technology.

Often, amplification-based assays are performed to measure the expression level of ovarian cancer-associated sequences. These assays are typically performed in conjunction with reverse transcription. In such assays, an ovarian cancer-associated nucleic acid sequence acts as a template in an amplification reaction (e.g., Polymerase Chain Reaction, or PCR). In a quantitative amplification, the amount of amplification product will be proportional to the amount of template in the original sample. Comparison to appropriate controls provides a measure of the amount of ovarian cancer-associated RNA. Methods of quantitative amplification are well known to those of skill in the art. Detailed protocols for quantitative PCR are available. See, e.g., Innis, et al. (1990) PCR Protocols: A Guide to Methods and Applications Academic Press.

In some embodiments, a TaqMan based assay is used to measure expression. TaqMan based assays use a fluorogenic oligonucleotide probe that contains a 5' fluorescent dye and a 3' quenching agent. The probe hybridizes to a PCR product, but cannot itself be

extended due to a blocking agent at the 3' end. When the PCR product is amplified in subsequent cycles, the 5' nuclease activity of the polymerase, e.g., AmpliTaq, results in the cleavage of the TaqMan probe. This cleavage separates the 5' fluorescent dye and the 3' quenching agent, thereby resulting in an increase in fluorescence as a function of

5 amplification (see, e.g., literature provided by Perkin-Elmer, e.g., www2.perkin-elmer.com).

Other suitable amplification methods include, but are not limited to, ligase chain reaction (LCR; see Wu and Wallace (1989) Genomics 4:560-569; Landegren, et al. (1988) Science 241:1077-1980; and Barringer, et al. (1990) Gene 89:117-122), transcription amplification (Kwoh, et al. (1989) Proc. Nat'l Acad. Sci. USA 86:1173-1177), self-sustained

10 sequence replication (Guatelli, et al. (1990) Proc. Nat'l Acad. Sci. USA 87:1874-1878), dot PCR, linker adapter PCR, etc.

Expression of ovarian cancer proteins from nucleic acids

In a preferred embodiment, ovarian cancer nucleic acids, e.g., encoding ovarian

15 cancer proteins are used to make a variety of expression vectors to express ovarian cancer proteins which can then be used in screening assays, as described below. Expression vectors and recombinant DNA technology are well known and are used to express proteins. See, e.g., Ausubel, supra; and Fernandez and Hoeffler (eds. 1999) Gene Expression Systems Academic Press. The expression vectors may be either self-replicating extrachromosomal vectors or

20 vectors which integrate into a host genome. Generally, these expression vectors include transcriptional and translational regulatory nucleic acid operably linked to the nucleic acid encoding the ovarian cancer protein. The term "control sequences" refers to DNA sequences used for the expression of an operably linked coding sequence in a particular host organism. Control sequences that are suitable for prokaryotes, e.g., include a promoter, optionally an

25 operator sequence, and a ribosome binding site. Eukaryotic cells are known to utilize promoters, polyadenylation signals, and enhancers.

Nucleic acid is "operably linked" when it is placed into a functional relationship with another nucleic acid sequence. For example, DNA for a pre-sequence or secretory leader is operably linked to DNA for a polypeptide if it is expressed as a pre-protein that participates

30 in the secretion of the polypeptide; a promoter or enhancer is operably linked to a coding sequence if it affects the transcription of the sequence; a ribosome binding site is operably linked to a coding sequence if it is positioned so as to facilitate translation; and two sequences may be operably linked when they are physically part of the same polymer. Generally,

"operably linked" means that the DNA sequences being linked are contiguous, and, in the case of a secretory leader, contiguous and in reading phase. However, enhancers do not have to be contiguous. Linking is typically accomplished by ligation at convenient restriction sites. If such sites do not exist, synthetic oligonucleotide adaptors or linkers are used in accordance with conventional practice. Transcriptional and translational regulatory nucleic acid will generally be appropriate to the host cell used to express the ovarian cancer protein. Numerous types of appropriate expression vectors, and suitable regulatory sequences are known in the art for a variety of host cells.

In general, transcriptional and translational regulatory sequences may include, but are not limited to, promoter sequences, ribosomal binding sites, transcriptional start and stop sequences, translational start and stop sequences, and enhancer or activator sequences. In a preferred embodiment, the regulatory sequences include a promoter and transcriptional start and stop sequences.

Promoter sequences typically encode constitutive or inducible promoters. The promoters may be naturally occurring promoters or hybrid promoters. Hybrid promoters, which combine elements of more than one promoter, are also known in the art, and are useful in the present invention.

In addition, an expression vector may comprise additional elements. For example, the expression vector may have two replication systems, thus allowing it to be maintained in two organisms, e.g., in mammalian or insect cells for expression and in a procaryotic host for cloning and amplification. Furthermore, for integrating expression vectors, the expression vector contains at least one sequence homologous to the host cell genome, and preferably two homologous sequences which flank the expression construct. The integrating vector may be directed to a specific locus in the host cell by selecting the appropriate homologous sequence for inclusion in the vector. Constructs for integrating vectors are available. See, e.g., Fernandez and Hoeffler, supra.

In addition, in a preferred embodiment, the expression vector contains a selectable marker gene to allow the selection of transformed host cells. Selection genes are well known in the art and will vary with the host cell used.

The ovarian cancer proteins of the present invention are produced by culturing a host cell transformed with an expression vector containing nucleic acid encoding an ovarian cancer protein, under the appropriate conditions to induce or cause expression of the ovarian cancer protein. Conditions appropriate for ovarian cancer protein expression will vary with

the choice of the expression vector and the host cell, and will be easily ascertained by one skilled in the art through routine experimentation or optimization. For example, the use of constitutive promoters in the expression vector will require optimizing the growth and proliferation of the host cell, while the use of an inducible promoter requires the appropriate growth conditions for induction. In addition, in some embodiments, the timing of the harvest is important. For example, the baculovirus systems used in insect cell expression are lytic viruses, and thus harvest time selection can be crucial for product yield.

Appropriate host cells include yeast, bacteria, archaeobacteria, fungi, and insect and animal cells, including mammalian cells. Of particular interest are *Saccharomyces cerevisiae* and other yeasts, *E. coli*, *Bacillus subtilis*, Sf9 cells, C129 cells, 293 cells, *Neurospora*, BHK, CHO, COS, HeLa cells, HUVEC (human umbilical vein endothelial cells), THP1 cells (a macrophage cell line) and various other human cells and cell lines.

In a preferred embodiment, the ovarian cancer proteins are expressed in mammalian cells. Mammalian expression systems are also known in the art, and include retroviral and adenoviral systems. One expression vector system is a retroviral vector system such as is generally described in PCT/US97/01019 and PCT/US97/01048, both of which are hereby expressly incorporated by reference. Of particular use as mammalian promoters are the promoters from mammalian viral genes, since the viral genes are often highly expressed and have a broad host range. Examples include the SV40 early promoter, mouse mammary tumor virus LTR promoter, adenovirus major late promoter, herpes simplex virus promoter, and the CMV promoter. See, e.g., Fernandez and Hoeffler, *supra*. Typically, transcription termination and polyadenylation sequences recognized by mammalian cells are regulatory regions located 3' to the translation stop codon and thus, together with the promoter elements, flank the coding sequence. Examples of transcription terminator and polyadenylation signals include those derived from SV40.

The methods of introducing exogenous nucleic acid into mammalian hosts, as well as other hosts, is well known in the art, and will vary with the host cell used. Techniques include dextran-mediated transfection, calcium phosphate precipitation, polybrene mediated transfection, protoplast fusion, electroporation, viral infection, encapsulation of the polynucleotide(s) in liposomes, and direct microinjection of the DNA into nuclei.

In a preferred embodiment, ovarian cancer proteins are expressed in bacterial systems. Bacterial expression systems are well known in the art. Promoters from bacteriophage may also be used and are known in the art. In addition, synthetic promoters and hybrid promoters

are also useful; e.g., the *tac* promoter is a hybrid of the *trp* and *lac* promoter sequences. Furthermore, a bacterial promoter can include naturally occurring promoters of non-bacterial origin that have the ability to bind bacterial RNA polymerase and initiate transcription. In addition to a functioning promoter sequence, an efficient ribosome binding site is desirable.

5 The expression vector may also include a signal peptide sequence that provides for secretion of the ovarian cancer protein in bacteria. The protein is either secreted into the growth media (gram-positive bacteria) or into the periplasmic space, located between the inner and outer membrane of the cell (gram-negative bacteria). The bacterial expression vector may also include a selectable marker gene to allow for the selection of bacterial strains that have been
10 transformed. Suitable selection genes include genes which render the bacteria resistant to drugs such as ampicillin, chloramphenicol, erythromycin, kanamycin, neomycin, and tetracycline. Selectable markers also include biosynthetic genes, such as those in the histidine, tryptophan, and leucine biosynthetic pathways. These components are assembled into expression vectors. Expression vectors for bacteria are well known in the art, and
15 include vectors for *Bacillus subtilis*, *E. coli*, *Streptococcus cremoris*, and *Streptococcus lividans*, among others. See Fernandez and Hoeffler, *supra*. The bacterial expression vectors are transformed into bacterial host cells using techniques well known in the art, such as calcium chloride treatment, electroporation, and others.

In one embodiment, ovarian cancer proteins are produced in insect cells. Expression
20 vectors for the transformation of insect cells, and in particular, baculovirus-based expression vectors, are well known in the art.

In a preferred embodiment, an ovarian cancer protein is produced in yeast cells. Yeast expression systems are well known in the art, and include expression vectors for *Saccharomyces cerevisiae*, *Candida albicans* and *C. maltosa*, *Hansenula polymorpha*,
25 *Kluyveromyces fragilis* and *K. lactis*, *Pichia guilliermondii* and *P. pastoris*, *Schizosaccharomyces pombe*, and *Yarrowia lipolytica*.

The ovarian cancer protein may also be made as a fusion protein, using techniques well known in the art. Thus, e.g., for the creation of monoclonal antibodies, if the desired epitope is small, the ovarian cancer protein may be fused to a carrier protein to form an
30 immunogen. Alternatively, the ovarian cancer protein may be made as a fusion protein to increase expression, or for other reasons. For example, when the ovarian cancer protein is an ovarian cancer peptide, the nucleic acid encoding the peptide may be linked to other nucleic acid for expression purposes.

In a preferred embodiment, the ovarian cancer protein is purified or isolated after expression. Ovarian cancer proteins may be isolated or purified in a variety of ways known to those skilled in the art depending on what other components are present in the sample. Standard purification methods include electrophoretic, molecular, immunological and chromatographic techniques, including ion exchange, hydrophobic, affinity, and reverse-phase HPLC chromatography, and chromatofocusing. For example, the ovarian cancer protein may be purified using a standard anti-ovarian cancer protein antibody column. Ultrafiltration and diafiltration techniques, in conjunction with protein concentration, are also useful. For general guidance in suitable purification techniques, see Scopes (1982) Protein Purification Springer-Verlag. The degree of purification necessary will vary depending on the use of the ovarian cancer protein. In some instances no purification will be necessary.

Once expressed and purified if necessary, the ovarian cancer proteins and nucleic acids are useful in a number of applications. They may be used as immunoselection reagents, as vaccine reagents, as screening agents, etc.

Variants of ovarian cancer proteins

In one embodiment, the ovarian cancer proteins are derivative or variant ovarian cancer proteins as compared to the wild-type sequence. That is, as outlined more fully below, the derivative ovarian cancer peptide will often contain at least one amino acid substitution, deletion or insertion, with amino acid substitutions being particularly preferred. The amino acid substitution, insertion, or deletion may occur at most any residue within the ovarian cancer peptide.

Also included within one embodiment of ovarian cancer proteins of the present invention are amino acid sequence variants. These variants typically fall into one or more of three classes: substitutional, insertional or deletional variants. These variants ordinarily are prepared by site specific mutagenesis of nucleotides in the DNA encoding the ovarian cancer protein, using cassette or PCR mutagenesis or other techniques well known in the art, to produce DNA encoding the variant, and thereafter expressing the DNA in recombinant cell culture as outlined above. However, variant ovarian cancer protein fragments having up to about 100-150 residues may be prepared by in vitro synthesis using established techniques. Amino acid sequence variants are characterized by the predetermined nature of the variation, a feature that sets them apart from naturally occurring allelic or interspecies variation of the ovarian cancer protein amino acid sequence. The variants typically exhibit the same

qualitative biological activity as the naturally occurring analogue, although variants can also be selected which have modified characteristics as will be more fully outlined below.

While the site or region for introducing an amino acid sequence variation is predetermined, the mutation per se need not be predetermined. For example, in order to optimize the performance of a mutation at a given site, random mutagenesis may be conducted at the target codon or region and the expressed ovarian cancer variants screened for the optimal combination of desired activity. Techniques for making substitution mutations at predetermined sites in DNA having a known sequence are well known, e.g., M13 primer mutagenesis and PCR mutagenesis. Screening of the mutants is done using assays of ovarian cancer protein activities.

Amino acid substitutions are typically of single residues; insertions usually will be on the order of from about 1 to 20 amino acids, although considerably larger insertions may be tolerated. Deletions range from about 1 to about 20 residues, although in some cases deletions may be much larger.

Substitutions, deletions, insertions or any combination thereof may be used to arrive at a final derivative. Generally these changes are done on a few amino acids to minimize the alteration of the molecule. However, larger changes may be tolerated in certain circumstances. When small alterations in the characteristics of the ovarian cancer protein are desired, substitutions are generally made in accordance with the amino acid substitution relationships provided in the definition section.

The variants typically exhibit the same qualitative biological activity and will elicit the same immune response as the naturally-occurring analog, although variants also are selected to modify the characteristics of the ovarian cancer proteins as needed. Alternatively, the variant may be designed such that the biological activity of the ovarian cancer protein is altered. For example, glycosylation sites may be altered or removed.

Substantial changes in function or immunological identity are made by selecting substitutions that are less conservative than those described above. For example, substitutions may be made which more significantly affect: the structure of the polypeptide backbone in the area of the alteration, for example the alpha-helical or beta-sheet structure; the charge or hydrophobicity of the molecule at the target site; or the bulk of the side chain. The substitutions which in general are expected to produce the greatest changes in the polypeptide's properties are those in which (a) a hydrophilic residue, e.g., serine or threonine is substituted for (or by) a hydrophobic residue, e.g., leucine, isoleucine, phenylalanine,

valine, or alanine; (b) a cysteine or proline is substituted for (or by) any other residue; (c) a residue having an electropositive side chain, e.g., lysine, arginine, or histidine, is substituted for (or by) an electronegative residue, e.g., glutamic or aspartic acid; (d) a residue having a bulky side chain, e.g., phenylalanine, is substituted for (or by) one not having a side chain, e.g., glycine; or (e) a proline residue is incorporated or substituted, which changes the degree of rotational freedom of the peptidyl bond.

Covalent modifications of ovarian cancer polypeptides are included within the scope of this invention. One type of covalent modification includes reacting targeted amino acid residues of an ovarian cancer polypeptide with an organic derivatizing agent that is capable of reacting with selected side chains or the N-or C-terminal residues of an ovarian cancer polypeptide. Derivatization with bifunctional agents is useful, for instance, for crosslinking ovarian cancer polypeptides to a water-insoluble support matrix or surface for use in the method for purifying anti-ovarian cancer polypeptide antibodies or screening assays, as is more fully described below. Commonly used crosslinking agents include, e.g., 1,1-bis(diazoacetyl)-2-phenylethane, glutaraldehyde, N-hydroxysuccinimide esters, e.g., esters with 4-azidosalicylic acid, homobifunctional imidoesters, including disuccinimidyl esters such as 3,3'-dithiobis(succinimidylpropionate), bifunctional maleimides such as bis-N-maleimido-1,8-octane and agents such as methyl-3-((p-azidophenyl)dithio)propioimide.

Other modifications include deamidation of glutamine and asparagine residues to the corresponding glutamic and aspartic acid residues, respectively, hydroxylation of proline and lysine, phosphorylation of hydroxyl groups of serine, threonine, or tyrosine residues, methylation of the amino groups of the lysine, arginine, and histidine side chains (e.g., pp. 79-86, Creighton (1983) Proteins: Structure and Molecular Properties Freeman), acetylation of the N-terminal amine, and amidation of a C-terminal carboxyl group.

Another type of covalent modification of the ovarian cancer polypeptide included within the scope of this invention comprises altering the native glycosylation pattern of the polypeptide. "Altering the native glycosylation pattern" is intended for purposes herein to mean deleting one or more carbohydrate moieties found in native sequence ovarian cancer polypeptide, and/or adding one or more glycosylation sites that are not present in the native sequence ovarian cancer polypeptide. Glycosylation patterns can be altered in many ways. For example the use of different cell types to express ovarian cancer-associated sequences can result in different glycosylation patterns.

Addition of glycosylation sites to ovarian cancer polypeptides may also be

accomplished by altering the amino acid sequence thereof. The alteration may be made, e.g., by the addition of, or substitution by, one or more serine or threonine residues to the native sequence ovarian cancer polypeptide (for O-linked glycosylation sites). The ovarian cancer amino acid sequence may optionally be altered through changes at the DNA level, particularly by mutating the DNA encoding the ovarian cancer polypeptide at pre-selected bases such that codons are generated that will translate into the desired amino acids.

Another means of increasing the number of carbohydrate moieties on the ovarian cancer polypeptide is by chemical or enzymatic coupling of glycosides to the polypeptide. See, e.g., WO 87/05330, and pp. 259-306 in Aplin and Wriston (1981) CRC Crit. Rev. Biochem. CRC Press.

Removal of carbohydrate moieties present on the ovarian cancer polypeptide may be accomplished chemically or enzymatically or by mutational substitution of codons encoding for amino acid residues that serve as targets for glycosylation. Chemical deglycosylation techniques are applicable. See, e.g., Sojar and Bahl (1987) Arch. Biochem. Biophys. 259:52-57; and Edge, et al. (1981) Anal. Biochem. 118:131-137. Enzymatic cleavage of carbohydrate moieties on polypeptides can be achieved by the use of a variety of endo- and exo-glycosidases. See, e.g., Thotakura, et al. (1987) Meth. Enzymol., 138:350-359.

Another type of covalent modification of ovarian cancer comprises linking the ovarian cancer polypeptide to one of a variety of non-proteinaceous polymers, e.g., polyethylene glycol, polypropylene glycol, or polyoxyalkylene. See, e.g., U.S. Patent Nos. 4,640,835; 4,496,689; 4,301,144; 4,670,417; 4,791,192; or 4,179,337.

Ovarian cancer polypeptides of the present invention may also be modified in a way to form chimeric molecules, e.g., comprising an ovarian cancer polypeptide fused to another heterologous polypeptide or amino acid sequence. In one embodiment, such a chimeric molecule comprises a fusion of an ovarian cancer polypeptide with a tag polypeptide which provides an epitope to which an anti-tag antibody can selectively bind. The epitope tag is generally placed at the amino- or carboxyl-terminus of the ovarian cancer polypeptide. The presence of such epitope-tagged forms of an ovarian cancer polypeptide can be detected using an antibody against the tag polypeptide. Also, provision of the epitope tag enables the ovarian cancer polypeptide to be readily purified by affinity purification using an anti-tag antibody or another type of affinity matrix that binds to the epitope tag. In an alternative embodiment, the chimeric molecule may comprise a fusion of an ovarian cancer polypeptide with an immunoglobulin or a particular region of an immunoglobulin. For a bivalent form of

the chimeric molecule, such a fusion could be to the Fc region of an IgG molecule.

Various tag polypeptides and their respective antibodies are well known in the art. Examples include poly-histidine (poly-his) or poly-histidine-glycine (poly-his-gly) tags; His6 and metal chelation tags, the flu HA tag polypeptide and its antibody 12CA5 (Field, et al. (1988) Mol. Cell. Biol. 8:2159-2165); the c-myc tag and the 8F9, 3C7, 6E10, G4, B7, and 9E10 antibodies thereto (Evan, et al. (1985) Mol. Cell. Biol. 5:3610-3616); and the Herpes Simplex virus glycoprotein D (gD) tag and its antibody (Paborsky, et al. (1990) Protein Engineering 3:547-553). Other tag polypeptides include, e.g., the Flag-peptide (Hopp, et al. (1988) BioTechnology 6:1204-1210); the KT3 epitope peptide (Martin, et al. (1992) Science 255:192-194); tubulin epitope peptide (Skinner, et al. (1991) J. Biol. Chem. 266:15163-15166); and the T7 gene 10 protein peptide tag (Lutz-Freyermuth et al. (1990) Proc. Nat'l Acad. Sci. USA 87:6393-6397).

Also included are other ovarian cancer proteins of the ovarian cancer family, and ovarian cancer proteins from other organisms, which are cloned and expressed as outlined below. Thus, probe or degenerate polymerase chain reaction (PCR) primer sequences may be used to find other related ovarian cancer proteins from humans or other organisms. As will be appreciated by those in the art, particularly useful probe and/or PCR primer sequences include the unique areas of the ovarian cancer nucleic acid sequence. As is generally known in the art, preferred PCR primers are from about 15 to about 35 nucleotides in length, with from about 20 to about 30 being preferred, and may contain inosine as needed. The conditions for the PCR reaction are well known in the art (e.g., Innis, PCR Protocols, supra).

Antibodies to ovarian cancer proteins

In a preferred embodiment, when the ovarian cancer protein is to be used to generate antibodies, e.g., for immunotherapy or immunodiagnosis, the ovarian cancer protein should share at least one epitope or determinant with the full length protein. By "epitope" or "determinant" herein is typically meant a portion of a protein which will generate and/or bind an antibody or T-cell receptor in the context of MHC. Thus, in most instances, antibodies made to a smaller ovarian cancer protein will be able to bind to the full-length protein, particularly linear epitopes. In a preferred embodiment, the epitope is unique; that is, antibodies generated to a unique epitope show little or no cross-reactivity.

Methods of preparing polyclonal antibodies are known to the skilled artisan (e.g., Coligan, supra; and Harlow and Lane, supra). Polyclonal antibodies can be raised in a

mammal, e.g., by one or more injections of an immunizing agent and, if desired, an adjuvant. Typically, the immunizing agent and/or adjuvant will be injected in the mammal by multiple subcutaneous or intraperitoneal injections. The immunizing agent may include a protein encoded by a nucleic acid of the figures or fragment thereof or a fusion protein thereof. It may be useful to conjugate the immunizing agent to a protein known to be immunogenic in the mammal being immunized. Examples of such immunogenic proteins include but are not limited to keyhole limpet hemocyanin, serum albumin, bovine thyroglobulin, and soybean trypsin inhibitor. Examples of adjuvants which may be employed include Freund's complete adjuvant and MPL-TDM adjuvant (monophosphoryl Lipid A, synthetic trehalose dicorynomycolate). The immunization protocol may be selected by one skilled in the art without undue experimentation.

The antibodies may, alternatively, be monoclonal antibodies. Monoclonal antibodies may be prepared using hybridoma methods, such as those described by Kohler and Milstein (1975) Nature 256:495-497. In a hybridoma method, a mouse, hamster, or other appropriate host animal, is typically immunized with an immunizing agent to elicit lymphocytes that produce or are capable of producing antibodies that will specifically bind to the immunizing agent. Alternatively, the lymphocytes may be immunized in vitro. The immunizing agent will typically include a polypeptide encoded by a nucleic acid of Tables 1-26 or fragment thereof, or a fusion protein thereof. Generally, either peripheral blood lymphocytes ("PBLs") are used if cells of human origin are desired, or spleen cells or lymph node cells are used if non-human mammalian sources are desired. The lymphocytes are then fused with an immortalized cell line using a suitable fusing agent, such as polyethylene glycol, to form a hybridoma cell (e.g., pp. 59-103 in Goding (1986) Monoclonal Antibodies: Principles and Practice Academic Press). Immortalized cell lines are usually transformed mammalian cells, particularly myeloma cells of rodent, bovine and human origin. Usually, rat or mouse myeloma cell lines are employed. The hybridoma cells may be cultured in a suitable culture medium that preferably contains one or more substances that inhibit the growth or survival of the unfused, immortalized cells. For example, if the parental cells lack the enzyme hypoxanthine guanine phosphoribosyl transferase (HGPRT or HPRT), the culture medium for the hybridomas typically will include hypoxanthine, aminopterin, and thymidine ("HAT medium"), which substances prevent the growth of HGPRT-deficient cells.

In one embodiment, the antibodies are bispecific antibodies. Bispecific antibodies are monoclonal, preferably human or humanized, antibodies that have binding specificities for at

least two different antigens or that have binding specificities for two epitopes on the same antigen. In one embodiment, one of the binding specificities is for a protein encoded by a nucleic acid Table 1-26 or a fragment thereof, the other one is for any other antigen, and preferably for a cell-surface protein or receptor or receptor subunit, preferably one that is tumor specific. Alternatively, tetramer-type technology may create multivalent reagents.

In a preferred embodiment, the antibodies to ovarian cancer protein are capable of reducing or eliminating a biological function of an ovarian cancer protein, as is described below. That is, the addition of anti-ovarian cancer protein antibodies (either polyclonal or preferably monoclonal) to ovarian cancer tissue (or cells containing ovarian cancer) may reduce or eliminate the ovarian cancer. Generally, at least a 25% decrease in activity, growth, size or the like is preferred, with at least about 50% being particularly preferred and about a 95-100% decrease being especially preferred.

In a preferred embodiment the antibodies to the ovarian cancer proteins are humanized antibodies (e.g., Xenerex Biosciences; Medarex, Inc.; Abgenix, Inc.; Protein Design Labs, Inc.) Humanized forms of non-human (e.g., murine) antibodies are chimeric molecules of immunoglobulins, immunoglobulin chains or fragments thereof (such as Fv, Fab, Fab', F(ab')₂ or other antigen-binding subsequences of antibodies) which contain minimal sequence derived from non-human immunoglobulin. Humanized antibodies include human immunoglobulins (recipient antibody) in which residues from a complementary determining region (CDR) of the recipient are replaced by residues from a CDR of a non-human species (donor antibody) such as mouse, rat or rabbit having the desired specificity, affinity and capacity. In some instances, Fv framework residues of the human immunoglobulin are replaced by corresponding non-human residues. Humanized antibodies may also comprise residues which are found neither in the recipient antibody nor in the imported CDR or framework sequences. In general, a humanized antibody will comprise substantially all of at least one, and typically two, variable domains, in which all or substantially all of the CDR regions correspond to those of a non-human immunoglobulin and all or substantially all of the framework (FR) regions are those of a human immunoglobulin consensus sequence. The humanized antibody optimally also will comprise at least a portion of an immunoglobulin constant region (Fc), typically that of a human immunoglobulin. Humanization can be essentially performed following the method of Winter and co-workers, e.g., by substituting rodent CDRs or CDR sequences for the

corresponding sequences of a human antibody. See, e.g., Jones, et al. (1986) Nature 321:522-525; Riechmann, et al. (1988) Nature 332:323-329; Presta (1992) Curr. Op. Struct. Biol. 2:593-596; and Verhoeyen, et al. (1988) Science 239:1534-1536). Accordingly, such humanized antibodies are chimeric antibodies (U.S. Patent No. 4,816,567), wherein
5 substantially less than an intact human variable domain has been substituted by the corresponding sequence from a non-human species.

Human antibodies can also be produced using various techniques known in the art, including phage display libraries (see, e.g., Hoogenboom and Winter (1991) J. Mol. Biol. 227:381-388; and Marks, et al. (1991) J. Mol. Biol. 222:581-597) or human monoclonal
10 antibodies (see, e.g., p. 77, Cöle, et al. in Reisfeld and Sell (1985) Monoclonal Antibodies and Cancer Therapy Liss; and Boerner, et al. (1991) J. Immunol. 147:86-95). Similarly, human antibodies can be made by introducing of human immunoglobulin loci into transgenic animals, e.g., mice in which the endogenous immunoglobulin genes have been partially or completely inactivated. Upon challenge, human antibody production is observed, which
15 closely resembles that seen in humans in all respects, including gene rearrangement, assembly, and antibody repertoire. See, e.g., U.S. Patent Nos. 5,545,807; 5,545,806; 5,569,825; 5,625,126; 5,633,425; 5,661,016; Marks, et al. (1992) Bio/Technology 10:779-783; Lonberg, et al. (1994) Nature 368:856-859; Morrison (1994) Nature 368:812-13; Neuberger (1996) Nature Biotechnology 14:826 commenting on Fishwild, et al. (1996)
20 Nature Biotechnology 14:845-51; and Lonberg and Huszar (1995) Intern. Rev. Immunol. 13:65-93.

By immunotherapy is meant treatment of ovarian cancer, e.g., with an antibody raised against ovarian cancer proteins. As used herein, immunotherapy can be passive or active. Passive immunotherapy as defined herein is the passive transfer of antibody to a recipient
25 (patient). Active immunization is the induction of antibody and/or T-cell responses in a recipient (patient). Induction of an immune response is the result of providing the recipient with an antigen to which antibodies are raised. The antigen may be provided by injecting a polypeptide against which antibodies are desired to be raised into a recipient, or contacting the recipient with a nucleic acid capable of expressing the antigen and under conditions for
30 expression of the antigen, leading to an immune response.

In a preferred embodiment the ovarian cancer proteins against which antibodies are raised are secreted proteins as described above. Without being bound by theory, antibodies used for treatment, bind and prevent the secreted protein from binding to its receptor, thereby

inactivating the secreted ovarian cancer protein.

In another preferred embodiment, the ovarian cancer protein to which antibodies are raised is a transmembrane protein. Without being bound by theory, antibodies used for treatment, bind the extracellular domain of the ovarian cancer protein and prevent it from binding to other proteins, such as circulating ligands or cell-associated molecules. The antibody may cause down-regulation of the transmembrane ovarian cancer protein. As will be appreciated by one of ordinary skill in the art, the antibody may be a competitive, non-competitive or uncompetitive inhibitor of protein binding to the extracellular domain of the ovarian cancer protein. The antibody is also an antagonist of the ovarian cancer protein. Further, the antibody prevents activation of the transmembrane ovarian cancer protein. In one aspect, when the antibody prevents the binding of other molecules to the ovarian cancer protein, the antibody prevents growth of the cell. The antibody may also be used to target or sensitize the cell to cytotoxic agents, including, but not limited to TNF- α , TNF- β , IL-1, INF- γ , and IL-2, or chemotherapeutic agents including 5FU, vinblastine, actinomycin D, cisplatin, methotrexate, and the like. In some instances the antibody belongs to a sub-type that activates serum complement when complexed with the transmembrane protein thereby mediating cytotoxicity or antigen-dependent cytotoxicity (ADCC). Thus, ovarian cancer is treated by administering to a patient antibodies directed against the transmembrane ovarian cancer protein. Antibody-labeling may activate a co-toxin, localize a toxin payload, or otherwise provide means to locally ablate cells.

In another preferred embodiment, the antibody is conjugated to an effector moiety. The effector moiety can be any number of molecules, including labeling moieties such as radioactive labels or fluorescent labels, or can be a therapeutic moiety. In one aspect the therapeutic moiety is a small molecule that modulates the activity of the ovarian cancer protein. In another aspect the therapeutic moiety modulates the activity of molecules associated with or in close proximity to the ovarian cancer protein. The therapeutic moiety may inhibit enzymatic activity such as protease or collagenase or protein kinase activity associated with ovarian cancer.

In a preferred embodiment, the therapeutic moiety can also be a cytotoxic agent. In this method, targeting the cytotoxic agent to ovarian cancer tissue or cells, results in a reduction in the number of afflicted cells, thereby reducing symptoms associated with ovarian cancer. Cytotoxic agents are numerous and varied and include, but are not limited to,

cytotoxic drugs or toxins or active fragments of such toxins. Suitable toxins and their corresponding fragments include diphtheria A chain, exotoxin A chain, ricin A chain, abrin A chain, curcin, croton, phenomycin, enomycin and the like. Cytotoxic agents also include radiochemicals made by conjugating radioisotopes to antibodies raised against ovarian cancer proteins, or binding of a radionuclide to a chelating agent that has been covalently attached to the antibody. Targeting the therapeutic moiety to transmembrane ovarian cancer proteins not only serves to increase the local concentration of therapeutic moiety in the ovarian cancer afflicted area, but also serves to reduce deleterious side effects that may be associated with the untargted therapeutic moiety.

In another preferred embodiment, the ovarian cancer protein against which the antibodies are raised is an intracellular protein. In this case, the antibody may be conjugated to a protein which facilitates entry into the cell. In one case, the antibody enters the cell by endocytosis. In another embodiment, a nucleic acid encoding the antibody is administered to the individual or cell. Moreover, wherein the ovarian cancer protein can be targeted within a cell, e.g., the nucleus, an antibody thereto contains a signal for that target localization, e.g., a nuclear localization signal.

The ovarian cancer antibodies of the invention specifically bind to ovarian cancer proteins. By "specifically bind" herein is meant that the antibodies bind to the protein with a K_d of at least about 0.1 mM, more usually at least about 1 μ M, preferably at least about 0.1 μ M or better, and most preferably, 0.01 μ M or better. Selectivity of binding is also important.

Detection of ovarian cancer sequence for diagnostic and therapeutic applications

In one aspect, the RNA expression levels of genes are determined for different cellular states in the ovarian cancer phenotype. Expression levels of genes in normal tissue (e.g., not undergoing ovarian cancer) and in ovarian cancer tissue (and in some cases, for varying severities of ovarian cancer that relate to prognosis, as outlined below, or in non-malignant disease are evaluated to provide expression profiles. An expression profile of a particular cell state or point of development is essentially a "fingerprint" of the state of the cell. While two states may have any particular gene similarly expressed, the evaluation of a number of genes simultaneously allows the generation of a gene expression profile that is reflective of the state of the cell. By comparing expression profiles of cells in different states,

information regarding which genes are important (including both up- and down-regulation of genes) in each of these states is obtained. Then, diagnosis may be performed or confirmed to determine whether a tissue sample has the gene expression profile of normal or cancerous tissue. This will provide for molecular diagnosis of related conditions.

5 "Differential expression," or grammatical equivalents as used herein, refers to qualitative or quantitative differences in the temporal and/or cellular gene expression patterns within and among cells and tissue. Thus, a differentially expressed gene can qualitatively have its expression altered, including an activation or inactivation, in, e.g., normal versus ovarian cancer tissue. Genes may be turned on or turned off in a particular
10 state, relative to another state thus permitting comparison of two or more states. A qualitatively regulated gene will exhibit an expression pattern within a state or cell type which is detectable by standard techniques. Some genes will be expressed in one state or cell type, but not in both. Alternatively, the difference in expression may be quantitative, e.g., in that expression is modulated, either up-regulated, resulting in an increased amount of
15 transcript, or down-regulated, resulting in a decreased amount of transcript. The degree to which expression differs need only be large enough to quantify via standard characterization techniques as outlined below, such as by use of Affymetrix GeneChip™ expression arrays. See, e.g., Lockhart (1996) Nature Biotechnology 14:1675-1680. Other techniques include, but are not limited to, quantitative reverse transcriptase PCR, northern analysis, and RNase
20 protection. As outlined above, preferably the change in expression (e.g., up-regulation or down-regulation) is at least about 50%, more preferably at least about 100%, more preferably at least about 150%, more preferably at least about 200%, with from 300 to at least 1000% being especially preferred.

Evaluation may be at the gene transcript, or the protein level. The amount of gene
25 expression may be monitored using nucleic acid probes to the DNA or RNA equivalent of the gene transcript, and the quantification of gene expression levels, or, alternatively, the final gene product itself (protein) can be monitored, e.g., with antibodies to the ovarian cancer protein and standard immunoassays (ELISAs, etc.) or other techniques, including mass spectroscopy assays, 2D gel electrophoresis assays, etc. Proteins corresponding to ovarian
30 cancer genes, e.g., those identified as being important in an ovarian cancer or disease phenotype, can be evaluated in an ovarian disease diagnostic test. In a preferred embodiment, gene expression monitoring is performed simultaneously on a number of genes. Multiple protein expression monitoring can be performed, or on an individual basis.

In this embodiment, the ovarian cancer nucleic acid probes are attached to biochips as outlined herein for the detection and quantification of ovarian cancer sequences in a particular sample. The assays are further described below in the example. PCR techniques can be used to provide greater sensitivity.

5 In a preferred embodiment nucleic acids encoding the ovarian cancer protein are detected. Although DNA or RNA encoding the ovarian cancer protein may be detected, of particular interest are methods wherein an mRNA encoding an ovarian cancer protein is detected. Probes to detect mRNA can be a nucleotide/deoxynucleotide probe that is complementary to and hybridizes with the mRNA and includes, but is not limited to, 10 oligonucleotides, cDNA or RNA. Probes also should contain a detectable label, as defined herein. In one method the mRNA is detected after immobilizing the nucleic acid to be examined on a solid support such as nylon membranes and hybridizing the probe with the sample. Following washing to remove the non-specifically bound probe, the label is detected. In another method detection of the mRNA is performed in situ. In this method 15 permeabilized cells or tissue samples are contacted with a detectably labeled nucleic acid probe for sufficient time to allow the probe to hybridize with the target mRNA. Following washing to remove the non-specifically bound probe, the label is detected. For example a digoxigenin labeled riboprobe (RNA probe) that is complementary to the mRNA encoding an ovarian cancer protein is detected by binding the digoxigenin with an anti-digoxigenin 20 secondary antibody and developed with nitro blue tetrazolium and 5-bromo-4-chloro-3-indoyl phosphate.

In a preferred embodiment, various proteins from the three classes of proteins as described herein (secreted, transmembrane or intracellular proteins) are used in diagnostic assays. The ovarian cancer proteins, antibodies, nucleic acids, modified proteins and cells 25 containing ovarian cancer sequences are used in diagnostic assays. This can be performed on an individual gene or corresponding polypeptide level. In a preferred embodiment, the expression profiles are used, preferably in conjunction with high throughput screening techniques to allow monitoring for expression profile genes and/or corresponding polypeptides.

30 As described and defined herein, ovarian cancer proteins, including intracellular, transmembrane, or secreted proteins, find use as prognostic or diagnostic markers of ovarian disease. Detection of these proteins in putative ovarian cancer tissue allows for detection, diagnosis, or prognosis of ovarian disease, and for selection of therapeutic strategy. In one

embodiment, antibodies are used to detect ovarian cancer proteins. A preferred method separates proteins from a sample by electrophoresis on a gel (typically a denaturing and reducing protein gel, but may be another type of gel, including isoelectric focusing gels and the like). Following separation of proteins, the ovarian cancer protein is detected, e.g., by immunoblotting with antibodies raised against the ovarian cancer protein. Methods of immunoblotting are well known to those of ordinary skill in the art.

In another preferred method, antibodies to the ovarian cancer protein find use in situ imaging techniques, e.g., in histology. See, e.g., Asai (ed. 1993) Methods in Cell Biology: Antibodies in Cell Biology (vol. 37) Academic Press. Cells are contacted with from one to many antibodies to the ovarian cancer protein(s). Following washing to remove non-specific antibody binding, the presence of the antibody or antibodies is detected. In one embodiment the antibody is detected by incubating with a secondary antibody that contains a detectable label. In another method the primary antibody to the ovarian cancer protein(s) contains a detectable label, e.g., an enzyme marker that can act on a substrate. In another preferred embodiment each one of multiple primary antibodies contains a distinct and detectable label. This method finds particular use in simultaneous screening for a plurality of ovarian cancer proteins. As will be appreciated by one of ordinary skill in the art, many other histological imaging techniques are also provided by the invention.

In a preferred embodiment the label is detected in a fluorometer which has the ability to detect and distinguish emissions of different wavelengths. In addition, a fluorescence activated cell sorter (FACS) can be used in the method.

In another preferred embodiment, antibodies find use in diagnosing ovarian cancer from blood, serum, plasma, stool, and other samples. Such samples, therefore, are useful as samples to be probed or tested for the presence of ovarian cancer proteins. Antibodies can be used to detect an ovarian cancer protein by previously described immunoassay techniques including ELISA, immunoblotting (western blotting), immunoprecipitation, BIAcore technology, and the like. Conversely, the presence of antibodies may indicate an immune response against an endogenous ovarian cancer protein.

In a preferred embodiment, in situ hybridization of labeled ovarian cancer nucleic acid probes to tissue arrays is done. For example, arrays of tissue samples, including ovarian cancer tissue and/or normal tissue, are made. In situ hybridization (see, e.g., Ausubel, supra) is then performed. When comparing the fingerprints between an individual and a standard, the skilled artisan can make a diagnosis, a prognosis, or a prediction based on the findings. It

is further understood that the genes which indicate the diagnosis may differ from those which indicate the prognosis and molecular profiling of the condition of the cells may lead to distinctions between responsive or refractory conditions or may be predictive of outcomes.

In a preferred embodiment, the ovarian cancer proteins, antibodies, nucleic acids, modified proteins and cells containing ovarian cancer sequences are used in prognosis assays. As above, gene expression profiles can be generated that correlate to ovarian cancer, clinical, pathological, or other information, in terms of long term prognosis. Again, this may be done on either a protein or gene level, with the use of a plurality of genes being preferred. As above, ovarian cancer probes may be attached to biochips for the detection and quantification of ovarian cancer sequences in a tissue or patient. The assays proceed as outlined above for diagnosis. PCR method may provide more sensitive and accurate quantification.

Assays for therapeutic compounds

In a preferred embodiment members of the proteins, nucleic acids, and antibodies as described herein are used in drug screening assays. The ovarian cancer proteins, antibodies, nucleic acids, modified proteins and cells containing ovarian cancer sequences are used in drug screening assays or by evaluating the effect of drug candidates on a "gene expression profile" or expression profile of polypeptides. In a preferred embodiment, the expression profiles are used, preferably in conjunction with high throughput screening techniques to allow monitoring for expression profile genes after treatment with a candidate agent. See, e.g., Zlokarnik, et al. (1998) Science 279:84-88; and Heid (1996) Genome Res. 6:986-994.

In a preferred embodiment, the ovarian cancer proteins, antibodies, nucleic acids, modified proteins and cells containing the native or modified ovarian cancer proteins are used in screening assays. That is, the present invention provides novel methods for screening for compositions which modulate the ovarian cancer phenotype or an identified physiological function of an ovarian cancer protein. As above, this can be done on an individual gene level or by evaluating the effect of drug candidates on a "gene expression profile". In a preferred embodiment, the expression profiles are used, preferably in conjunction with high throughput screening techniques to allow monitoring for expression profile genes after treatment with a candidate agent. See, e.g., Zlokarnik, supra.

Having identified the differentially expressed genes herein, a variety of assays may be executed. In a preferred embodiment, assays may be run on an individual gene or protein level. That is, having identified a particular gene as up regulated in ovarian cancer, test

compounds can be screened for the ability to modulate gene expression or for binding to the ovarian cancer protein. "Modulation" thus includes both an increase and a decrease in gene expression. The preferred amount of modulation will depend on the original change of the gene expression in normal versus tissue undergoing ovarian cancer, with changes of at least 10%, preferably 50%, more preferably 100-300%, and in some embodiments 300-1000% or greater. Thus, if a gene exhibits a 4-fold increase in ovarian cancer tissue compared to normal tissue, a decrease of about four-fold is often desired; similarly, a 10-fold decrease in ovarian cancer tissue compared to normal tissue often provides a target value of a 10-fold increase in expression to be induced by the test compound.

The amount of gene expression may be monitored using nucleic acid probes and the quantification of gene expression levels, or, alternatively, the gene product itself can be monitored, e.g., through the use of antibodies to the ovarian cancer protein and standard immunoassays. Proteomics and separation techniques may also allow quantification of expression.

In a preferred embodiment, gene expression or protein monitoring of a number of entities, e.g., an expression profile, is monitored simultaneously. Such profiles will typically involve a plurality of those entities described herein.

In this embodiment, the ovarian cancer nucleic acid probes are attached to biochips as outlined herein for the detection and quantification of ovarian cancer sequences in a particular cell. Alternatively, PCR may be used. Thus, a series, e.g., of microtiter plate, may be used with dispensed primers in desired wells. A PCR reaction can then be performed and analyzed for each well.

Expression monitoring can be performed to identify compounds that modify the expression of one or more ovarian cancer-associated sequences, e.g., a polynucleotide sequence set out in Tables 1-26. Generally, in a preferred embodiment, a test modulator is added to the cells prior to analysis. Moreover, screens are also provided to identify agents that modulate ovarian cancer, modulate ovarian cancer proteins, bind to an ovarian cancer protein, or interfere with the binding of an ovarian cancer protein and an antibody or other binding partner.

The term "test compound" or "drug candidate" or "modulator" or grammatical equivalents as used herein describes any molecule, e.g., protein, oligopeptide, small organic molecule, polysaccharide, polynucleotide, etc., to be tested for the capacity to directly or indirectly alter the ovarian cancer phenotype or the expression of an ovarian cancer sequence,

e.g., a nucleic acid or protein sequence. In preferred embodiments, modulators alter expression profiles, or expression profile nucleic acids or proteins provided herein. In one embodiment, the modulator suppresses an ovarian cancer phenotype, e.g., to a normal or non-malignant tissue fingerprint. In another embodiment, a modulator induced an ovarian cancer phenotype. Generally, a plurality of assay mixtures are run in parallel with different agent concentrations to obtain a differential response to the various concentrations. Typically, one of these concentrations serves as a negative control, e.g., at zero concentration or below the level of detection.

Drug candidates encompass numerous chemical classes, though typically they are organic molecules, preferably small organic compounds having a molecular weight of more than 100 and less than about 2,500 daltons. Preferred small molecules are less than 2000, or less than 1500 or less than 1000 or less than 500 D. Candidate agents comprise functional groups necessary for structural interaction with proteins, particularly hydrogen bonding, and typically include at least an amine, carbonyl, hydroxyl or carboxyl group, preferably at least two of the functional chemical groups. The candidate agents often comprise cyclical carbon or heterocyclic structures and/or aromatic or polyaromatic structures substituted with one or more of the above functional groups. Candidate agents are also found among biomolecules including peptides, saccharides, fatty acids, steroids, purines, pyrimidines, derivatives, structural analogs or combinations thereof. Particularly preferred are peptides.

In one aspect, a modulator will neutralize the effect of an ovarian cancer protein. By "neutralize" is meant that activity of a protein is inhibited or blocked and the consequent effect on the cell.

In certain embodiments, combinatorial libraries of potential modulators will be screened for an ability to bind to an ovarian cancer polypeptide or to modulate activity. Conventionally, new chemical entities with useful properties are generated by identifying a chemical compound (called a "lead compound") with some desirable property or activity, e.g., inhibiting activity, creating variants of the lead compound, and evaluating the property and activity of those variant compounds. Often, high throughput screening (HTS) methods are employed for such an analysis.

In one preferred embodiment, high throughput screening methods involve providing a library containing a large number of potential therapeutic compounds (candidate compounds). Such "combinatorial chemical libraries" are then screened in one or more assays to identify those library members (particular chemical species or subclasses) that

display a desired characteristic activity. The compounds thus identified can serve as conventional "lead compounds" or can themselves be used as potential or actual therapeutics.

A combinatorial chemical library is a collection of diverse chemical compounds generated by either chemical synthesis or biological synthesis by combining a number of chemical "building blocks" such as reagents. For example, a linear combinatorial chemical library, such as a polypeptide (e.g., mutein) library, is formed by combining a set of chemical building blocks called amino acids in every possible way for a given compound length (e.g., the number of amino acids in a polypeptide compound). Millions of chemical compounds can be synthesized through such combinatorial mixing of chemical building blocks. See, e.g., Gallop, et al. (1994) J. Med. Chem. 37:1233-1251.

Preparation and screening of combinatorial chemical libraries is well known to those of skill in the art. Such combinatorial chemical libraries include, but are not limited to, peptide libraries (see, e.g., U.S. Patent No. 5,010,175; Furka (1991) Pept. Prot. Res. 37:487-493; and Houghton, et al. (1991) Nature 354:84-88), peptoids (PCT Publication No WO 91/19735), encoded peptides (PCT Publication WO 93/20242), random bio-oligomers (PCT Publication WO 92/00091), benzodiazepines (U.S. Pat. No. 5,288,514), diversomers such as hydantoin, benzodiazepines and dipeptides (Hobbs, et al. (1993) Proc. Nat'l Acad. Sci. USA 90:6909-913), vinylogous polypeptides (Hagihara, et al. (1992) J. Amer. Chem. Soc. 114:6568-570), non-peptidic peptidomimetics with a Beta-D-Glucose scaffolding (Hirschmann, et al. (1992) J. Amer. Chem. Soc. 114:9217-218), analogous organic syntheses of small compound libraries (Chen, et al. (1994) J. Amer. Chem. Soc. 116:2661-662), oligocarbamates (Cho, et al. (1993) Science 261:1303-305), and/or peptidyl phosphonates (Campbell, et al. (1994) J. Org. Chem. 59:658-xxx). See, generally, Gordon, et al. (1994) J. Med. Chem. 37:1385-401, nucleic acid libraries (see, e.g., Stratagene, Corp.), peptide nucleic acid libraries (see, e.g., U.S. Patent 5,539,083), antibody libraries (see, e.g., Vaughn, et al. (1996) Nature Biotechnology 14:309-314; and PCT/US96/10287), carbohydrate libraries (see, e.g., Liang, et al. (1996) Science 274:1520-1522; and U.S. Patent No. 5,593,853), and small organic molecule libraries (see, e.g., benzodiazepines, page 33, Baum (Jan. 18, 1993) C&E News; isoprenoids, U.S. Patent No. 5,569,588; thiazolidinones and metathiazanones, U.S. Patent No. 5,549,974; pyrrolidines, U.S. Patent Nos. 5,525,735 and 5,519,134; morpholino compounds, U.S. Patent No. 5,506,337; benzodiazepines, U.S. Patent No. 5,288,514; and the like).

Devices for the preparation of combinatorial libraries are commercially available.

See, e.g., 357 MPS, 390 MPS, Advanced Chem Tech, Louisville KY; Symphony, Rainin, Woburn, MA; 433A Applied Biosystems, Foster City, CA; 9050 Plus, Millipore, Bedford, MA.

A number of well known robotic systems have also been developed for solution phase chemistries. These systems include automated workstations like the automated synthesis apparatus developed by Takeda Chemical Industries, LTD. (Osaka, Japan) and many robotic systems utilizing robotic arms (Zymate II, Zymark Corporation, Hopkinton, MA; Orca, Hewlett-Packard, Palo Alto, CA), which mimic the manual synthetic operations performed by a chemist. Any of the above devices are suitable for use with the present invention. The nature and implementation of modifications to these devices (if any) so that they can operate as discussed herein will be apparent to persons skilled in the relevant art. In addition, numerous combinatorial libraries are themselves commercially available (see, e.g., ComGenex, Princeton, N.J.; Asinex, Moscow, RU; Tripos, Inc., St. Louis, MO; ChemStar, Ltd, Moscow, RU; 3D Pharmaceuticals, Exton, PA; Martek Biosciences, Columbia, MD; etc.).

The assays to identify modulators are amenable to high throughput screening. Preferred assays thus detect enhancement or inhibition of ovarian cancer gene transcription, inhibition or enhancement of polypeptide expression, and inhibition or enhancement of polypeptide activity.

High throughput assays for the presence, absence, quantification, or other properties of particular nucleic acids or protein products are well known to those of skill in the art. Similarly, binding assays and reporter gene assays are similarly well known. Thus, e.g., U.S. Patent No. 5,559,410 discloses high throughput screening methods for proteins, U.S. Patent No. 5,585,639 discloses high throughput screening methods for nucleic acid binding (e.g., in arrays), while U.S. Patent Nos. 5,576,220 and 5,541,061 disclose high throughput methods of screening for ligand/antibody binding.

In addition, high throughput screening systems are commercially available (see, e.g., Zymark Corp., Hopkinton, MA; Air Technical Industries, Mentor, OH; Beckman Instruments, Inc. Fullerton, CA; Precision Systems, Inc., Natick, MA, etc.). These systems typically automate entire procedures, including all sample and reagent pipetting, liquid dispensing, timed incubations, and final readings of the microplate in detector(s) appropriate for the assay. These configurable systems provide high throughput and rapid start up as well as a high degree of flexibility and customization. The manufacturers of such systems provide

detailed protocols for various high throughput systems. Thus, e.g., Zymark Corp. provides technical bulletins describing screening systems for detecting the modulation of gene transcription, ligand binding, and the like.

In one embodiment, modulators are proteins, often naturally occurring proteins or fragments of naturally occurring proteins. Thus, e.g., cellular extracts containing proteins, or random or directed digests of proteinaceous cellular extracts, may be used. In this way libraries of proteins may be made for screening in the methods of the invention. Particularly preferred in this embodiment are libraries of bacterial, fungal, viral, and mammalian proteins, with the latter being preferred, and human proteins being especially preferred. Particularly useful test compound will be directed to the class of proteins to which the target belongs, e.g., substrates for enzymes or ligands and receptors.

In a preferred embodiment, modulators are peptides of from about 5 to about 30 amino acids, with from about 5 to about 20 amino acids being preferred, and from about 7 to about 15 being particularly preferred. The peptides may be digests of naturally occurring proteins as is outlined above, random peptides, or "biased" random peptides. By "randomized" or grammatical equivalents herein is meant that each nucleic acid and peptide consists of essentially random nucleotides and amino acids, respectively. Since generally these random peptides (or nucleic acids, discussed below) are chemically synthesized, they may incorporate any nucleotide or amino acid at any position. The synthetic process can be designed to generate randomized proteins or nucleic acids, to allow the formation of all or most of the possible combinations over the length of the sequence, thus forming a library of randomized candidate bioactive proteinaceous agents.

In one embodiment, the library is fully randomized, with no sequence preferences or constants at any position. In a preferred embodiment, the library is biased. That is, some positions within the sequence are either held constant, or are selected from a limited number of possibilities. For example, in a preferred embodiment, the nucleotides or amino acid residues are randomized within a defined class, e.g., of hydrophobic amino acids, hydrophilic residues, sterically biased (either small or large) residues, towards the creation of nucleic acid binding domains, the creation of cysteines, for cross-linking, prolines for SH-3 domains, serines, threonines, tyrosines or histidines for phosphorylation sites, etc., or to purines, etc.

Modulators of ovarian cancer can also be nucleic acids, as defined above.

As described above generally for proteins, nucleic acid modulating agents may be naturally occurring nucleic acids, random nucleic acids, or "biased" random nucleic acids.

For example, digests of procaryotic or eucaryotic genomes may be used as is outlined above for proteins.

In a preferred embodiment, the candidate compounds are organic chemical moieties, a wide variety of which are available in the literature.

5 After the candidate agent has been added and the cells allowed to incubate for some period of time, the sample containing a target sequence to be analyzed is added to the biochip. If required, the target sequence is prepared using known techniques. For example, the sample may be treated to lyse the cells, using known lysis buffers, electroporation, etc., with purification and/or amplification such as PCR performed as appropriate. For example, 10 an in vitro transcription with labels covalently attached to the nucleotides is performed. Generally, the nucleic acids are labeled with biotin-FTTC or PE, or with cy3 or cy5.

In a preferred embodiment, the target sequence is labeled with, e.g., a fluorescent, a chemiluminescent, a chemical, or a radioactive signal, to provide a means of detecting the target sequence's specific binding to a probe. The label also can be an enzyme, such as, 15 alkaline phosphatase or horseradish peroxidase, which when provided with an appropriate substrate produces a product that can be detected. Alternatively, the label can be a labeled compound or small molecule, such as an enzyme inhibitor, that binds but is not catalyzed or altered by the enzyme. The label also can be a moiety or compound, such as, an epitope tag or biotin which specifically binds to streptavidin. For the example of biotin, the streptavidin 20 is labeled as described above, thereby, providing a detectable signal for the bound target sequence. Unbound labeled streptavidin is typically removed prior to analysis.

As will be appreciated by those in the art, these assays can be direct hybridization assays or can comprise "sandwich assays", which include the use of multiple probes, as is generally outlined in U.S. Patent Nos. 5,681,702; 5,597,909; 5,545,730; 5,594,117; 25 5,591,584; 5,571,670; 5,580,731; 5,571,670; 5,591,584; 5,624,802; 5,635,352; 5,594,118; 5,359,100; 5,124,246; and 5,681,697, each of which is hereby incorporated by reference. In this embodiment, in general, the target nucleic acid is prepared as outlined above, and then added to the biochip comprising a plurality of nucleic acid probes, under conditions that allow the formation of a hybridization complex.

30 A variety of hybridization conditions may be used in the present invention, including high, moderate and low stringency conditions as outlined above. The assays are generally run under stringency conditions which allows formation of the label probe hybridization complex only in the presence of target. Stringency can be controlled by altering a step

parameter that is a thermodynamic variable, including, but not limited to, temperature, formamide concentration, salt concentration, chaotropic salt concentration pH, organic solvent concentration, etc.

These parameters may also be used to control non-specific binding, as is generally outlined in U.S. Patent No. 5,681,697. Thus it may be desirable to perform certain steps at higher stringency conditions to reduce non-specific binding.

The reactions outlined herein may be accomplished in a variety of ways. Components of the reaction may be added simultaneously, or sequentially, in different orders, with preferred embodiments outlined below. In addition, the reaction may include a variety of other reagents. These include salts, buffers, neutral proteins, e.g., albumin, detergents, etc. which may be used to facilitate optimal hybridization and detection, and/or reduce non-specific or background interactions. Reagents that otherwise improve the efficiency of the assay, such as protease inhibitors, nuclease inhibitors, anti-microbial agents, etc., may also be used as appropriate, depending on the sample preparation methods and purity of the target.

The assay data are analyzed to determine the expression levels, and changes in expression levels as between states, of individual genes, forming a gene expression profile.

Screens are performed to identify modulators of the ovarian cancer phenotype. In one embodiment, screening is performed to identify modulators that can induce or suppress a particular expression profile, thus preferably generating the associated phenotype. In another embodiment, e.g., for diagnostic applications, having identified differentially expressed genes important in a particular state, screens can be performed to identify modulators that alter expression of individual genes. In another embodiment, screening is performed to identify modulators that alter a biological function of the expression product of a differentially expressed gene. Again, having identified the importance of a gene in a particular state, screens are performed to identify agents that bind and/or modulate the biological activity of the gene product.

In addition screens can be done for genes that are induced in response to a candidate agent. After identifying a modulator based upon its ability to suppress an ovarian cancer expression pattern leading to a normal expression pattern, or to modulate a single ovarian cancer gene expression profile so as to mimic the expression of the gene from normal tissue, a screen as described above can be performed to identify genes that are specifically modulated in response to the agent. Comparing expression profiles between normal tissue and agent treated ovarian cancer tissue reveals genes that are not expressed in normal tissue

or ovarian cancer tissue, but are expressed in agent treated tissue. These agent-specific sequences can be identified and used by methods described herein for ovarian cancer genes or proteins. In particular these sequences and the proteins they encode find use in marking or identifying agent treated cells. In addition, antibodies can be raised against the agent induced
5 proteins and used to target novel therapeutics to the treated ovarian cancer tissue sample.

Thus, in one embodiment, a test compound is administered to a population of ovarian cancer cells, that have an associated ovarian cancer expression profile. By "administration" or "contacting" herein is meant that the candidate agent is added to the cells in such a manner as to allow the agent to act upon the cell, whether by uptake and intracellular action, or by
10 action at the cell surface. In some embodiments, nucleic acid encoding a proteinaceous candidate agent (e.g., a peptide) may be put into a viral construct such as an adenoviral or retroviral construct, and added to the cell, such that expression of the peptide agent is accomplished, e.g., PCT US97/01019. Regulatable gene therapy systems can also be used.

Once the test compound has been administered to the cells, the cells can be washed if
15 desired and are allowed to incubate under preferably physiological conditions for some period of time. The cells are then harvested and a new gene expression profile is generated, as outlined herein.

Thus, e.g., ovarian cancer or non-malignant tissue may be screened for agents that modulate, e.g., induce or suppress the ovarian cancer phenotype. A change in at least one
20 gene, preferably many, of the expression profile indicates that the agent has an effect on ovarian cancer activity. By defining such a signature for the ovarian cancer phenotype, screens for new drugs that alter the phenotype can be devised. With this approach, the drug target need not be known and need not be represented in the original expression screening platform, nor does the level of transcript for the target protein need to change.

In a preferred embodiment, as outlined above, screens may be done on individual genes and gene products (proteins). That is, having identified a particular differentially expressed gene as important in a particular state, screening of modulators of either the expression of the gene or the gene product itself can be done. The gene products of differentially expressed genes are sometimes referred to herein as "ovarian cancer proteins"
25 or a "ovarian cancer modulatory protein". The ovarian cancer modulatory protein may be a fragment, or alternatively, be the full length protein to the fragment encoded by the nucleic acids of the Tables. Preferably, the ovarian cancer modulatory protein is a fragment. In a preferred embodiment, the ovarian cancer amino acid sequence which is used to determine
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sequence identity or similarity is encoded by a nucleic acid of the Tables. In another embodiment, the sequences are naturally occurring allelic variants of a protein encoded by a nucleic acid of the Tables. In another embodiment, the sequences are sequence variants as further described herein.

5 Preferably, the ovarian cancer modulatory protein is a fragment of approximately 14 to 24 amino acids long. More preferably the fragment is a soluble fragment. Preferably, the fragment includes a non-transmembrane region. In a preferred embodiment, the fragment has an N-terminal Cys to aid in solubility. In another embodiment, the C-terminus of the fragment is kept as a free acid and the N-terminus is a free amine to aid in coupling, e.g., to
10 cysteine. Or, the ovarian cancer proteins are conjugated to an immunogenic agent, e.g., to BSA.

Measurements of ovarian cancer polypeptide activity, or of ovarian cancer or the ovarian cancer phenotype can be performed using a variety of assays. For example, the effects of the test compounds upon the function of the ovarian cancer polypeptides can be
15 measured by examining parameters described above. A suitable physiological change that affects activity can be used to assess the influence of a test compound on the polypeptides of this invention. When the functional consequences are determined using intact cells or animals, one can also measure a variety of effects such as, in the case of ovarian cancer associated with tumors, tumor growth, tumor metastasis, neovascularization, hormone
20 release, transcriptional changes to both known and uncharacterized genetic markers (e.g., northern blots), changes in cell metabolism such as cell growth or pH changes, and changes in intracellular second messengers such as cGMP. In the assays of the invention, mammalian ovarian cancer polypeptide is typically used, e.g., mouse, preferably human.

Assays to identify compounds with modulating activity can be performed in vitro.
25 For example, an ovarian cancer polypeptide is first contacted with a potential modulator and incubated for a suitable amount of time, e.g., from 0.5 to 48 hours. In one embodiment, the ovarian cancer polypeptide levels are determined in vitro by measuring the level of protein or mRNA. The level of protein is measured using immunoassays such as western blotting, ELISA and the like with an antibody that selectively binds to the ovarian cancer polypeptide
30 or a fragment thereof. For measurement of mRNA, amplification, e.g., using PCR, LCR, or hybridization assays, e.g., northern hybridization, RNase protection, dot blotting, are preferred. The level of protein or mRNA is detected using directly or indirectly labeled detection agents, e.g., fluorescently or radioactively labeled nucleic acids, radioactively or

enzymatically labeled antibodies, and the like, as described herein.

Alternatively, a reporter gene system can be devised using the ovarian cancer protein promoter operably linked to a reporter gene such as luciferase, green fluorescent protein, CAT, or β -gal. The reporter construct is typically transfected into a cell. After treatment with a potential modulator, the amount of reporter gene transcription, translation, or activity is measured according to standard techniques known to those of skill in the art.

In a preferred embodiment, as outlined above, screens may be done on individual genes and gene products (proteins). That is, having identified a particular differentially expressed gene as important in a particular state, screening of modulators of the expression of the gene or the gene product itself can be done. The gene products of differentially expressed genes are sometimes referred to herein as "ovarian cancer proteins." The ovarian cancer protein may be a fragment, or alternatively, be the full length protein to a fragment shown herein.

In one embodiment, screening for modulators of expression of specific genes is performed. Typically, the expression of only one or a few genes are evaluated. In another embodiment, screens are designed to first find compounds that bind to differentially expressed proteins. These compounds are then evaluated for the ability to modulate differentially expressed activity. Moreover, once initial candidate compounds are identified, variants can be further screened to better evaluate structure activity relationships.

In a preferred embodiment, binding assays are done. In general, purified or isolated gene product is used; that is, the gene products of one or more differentially expressed nucleic acids are made. For example, antibodies are generated to the protein gene products, and standard immunoassays are run to determine the amount of protein present. Alternatively, cells comprising the ovarian cancer proteins can be used in the assays.

Thus, in a preferred embodiment, the methods comprise combining an ovarian cancer protein and a candidate compound, and determining the binding of the compound to the ovarian cancer protein. Preferred embodiments utilize the human ovarian cancer protein, although other mammalian proteins, e.g., counterparts, may also be used, e.g., for the development of animal models of human disease. In some embodiments, as outlined herein, variant or derivative ovarian cancer proteins may be used.

Generally, in a preferred embodiment of the methods herein, the ovarian cancer protein or the candidate agent is non-diffusably bound to an insoluble support having isolated sample receiving areas (e.g., a microtiter plate, an array, etc.). The insoluble supports may be

made of any composition to which the compositions can be bound, is readily separated from soluble material, and is otherwise compatible with the overall method of screening. The surface of such supports may be solid or porous and of any convenient shape. Examples of suitable insoluble supports include microtiter plates, arrays, membranes and beads. These are typically made of glass, plastic (e.g., polystyrene), polysaccharides, nylon or nitrocellulose, teflon™, etc. Microtiter plates and arrays are especially convenient because a large number of assays can be carried out simultaneously, using small amounts of reagents and samples. The particular manner of binding of the composition is not crucial so long as it is compatible with the reagents and overall methods of the invention, maintains the activity of the composition and is non-diffusible. Preferred methods of binding include the use of antibodies (which do not sterically block either the ligand binding site or activation sequence when the protein is bound to the support), direct binding to "sticky" or ionic supports, chemical crosslinking, the synthesis of the protein or agent on the surface, etc. Following binding of the protein or agent, excess unbound material is removed by washing. The sample receiving areas may then be blocked through incubation with bovine serum albumin (BSA), casein or other innocuous protein or other moiety.

In a preferred embodiment, the ovarian cancer protein is bound to the support, and a test compound is added to the assay. Alternatively, the candidate agent is bound to the support and the ovarian cancer protein is added. Novel binding agents include specific antibodies, non-natural binding agents identified in screens of chemical libraries, peptide analogs, etc. Of particular interest are screening assays for agents that have a low toxicity for human cells. A wide variety of assays may be used for this purpose, including labeled in vitro protein-protein binding assays, electrophoretic mobility shift assays, immunoassays for protein binding, functional assays (phosphorylation assays, etc.) and the like.

The determination of the binding of the test modulating compound to the ovarian cancer protein may be done in a number of ways. In a preferred embodiment, the compound is labeled, and binding determined directly, e.g., by attaching all or a portion of the ovarian cancer protein to a solid support, adding a labeled candidate agent (e.g., a fluorescent label), washing off excess reagent, and determining whether the label is present on the solid support. Various blocking and washing steps may be utilized as appropriate.

In some embodiments, only one of the components is labeled, e.g., the proteins (or proteinaceous candidate compounds) can be labeled. Alternatively, more than one

component can be labeled with different labels, e.g., ¹²⁵I for the proteins and a fluorophore for the compound. Proximity reagents, e.g., quenching or energy transfer reagents are also useful.

In one embodiment, the binding of the test compound is determined by competitive binding assay. The competitor is a binding moiety known to bind to the target molecule (e.g., an ovarian cancer protein), such as an antibody, peptide, binding partner, ligand, etc. Under certain circumstances, there may be competitive binding between the compound and the binding moiety, with the binding moiety displacing the compound. In one embodiment, the test compound is labeled. Either the compound, or the competitor, or both, is added first to the protein for a time sufficient to allow binding, if present. Incubations may be performed at a temperature which facilitates optimal activity, typically 4-40° C. Incubation periods are typically optimized, e.g., to facilitate rapid high throughput screening. Typically between 0.1 and 1 hr will be sufficient. Excess reagent is generally removed or washed away. The second component is then added, and the presence or absence of the labeled component is followed, to indicate binding.

In a preferred embodiment, the competitor is added first, followed by the test compound. Displacement of the competitor is an indication that the test compound is binding to the ovarian cancer protein and thus is capable of binding to, and potentially modulating, the activity of the ovarian cancer protein. In this embodiment, either component can be labeled. Thus, e.g., if the competitor is labeled, the presence of label in the wash solution indicates displacement by the agent. Alternatively, if the test compound is labeled, the presence of the label on the support indicates displacement.

In an alternative embodiment, the test compound is added first, with incubation and washing, followed by the competitor. The absence of binding by the competitor may indicate that the test compound is bound to the ovarian cancer protein with a higher affinity. Thus, if the test compound is labeled, the presence of the label on the support, coupled with a lack of competitor binding, may indicate that the test compound is capable of binding to the ovarian cancer protein.

In a preferred embodiment, the methods comprise differential screening to identify agents that are capable of modulating the activity of the ovarian cancer proteins. In this embodiment, the methods comprise combining an ovarian cancer protein and a competitor in a first sample. A second sample comprises a test compound, an ovarian cancer protein, and a

competitor. The binding of the competitor is determined for both samples, and a change, or difference in binding between the two samples indicates the presence of an agent capable of binding to the ovarian cancer protein and potentially modulating its activity. That is, if the binding of the competitor is different in the second sample relative to the first sample, the agent is capable of binding to the ovarian cancer protein.

Alternatively, differential screening is used to identify drug candidates that bind to the native ovarian cancer protein, but cannot bind to modified ovarian cancer proteins. The structure of the ovarian cancer protein may be modeled, and used in rational drug design to synthesize agents that interact with that site. Drug candidates that affect the activity of an ovarian cancer protein are also identified by screening drugs for the ability to either enhance or reduce the activity of the protein.

Positive controls and negative controls may be used in the assays. Preferably control and test samples are performed in at least triplicate to obtain statistically significant results. Incubation of all samples is for a time sufficient for the binding of the agent to the protein. Following incubation, samples are washed free of non-specifically bound material and the amount of bound, generally labeled agent determined. For example, where a radiolabel is employed, the samples may be counted in a scintillation counter to determine the amount of bound compound.

A variety of other reagents may be included in the screening assays. These include reagents like salts, neutral proteins, e.g., albumin, detergents, etc. which may be used to facilitate optimal protein-protein binding and/or reduce non-specific or background interactions. Also reagents that otherwise improve the efficiency of the assay, such as protease inhibitors, nuclease inhibitors, anti-microbial agents, etc., may be used. The mixture of components may be added in an order that provides for the requisite binding.

In a preferred embodiment, the invention provides methods for screening for a compound capable of modulating the activity of an ovarian cancer protein. The methods comprise adding a test compound, as defined above, to a cell comprising ovarian cancer proteins. Preferred cell types include almost any cell. The cells contain a recombinant nucleic acid that encodes an ovarian cancer protein. In a preferred embodiment, a library of candidate agents are tested on a plurality of cells.

In one aspect, the assays are evaluated in the presence or absence or previous or subsequent exposure of physiological signals, e.g., hormones, antibodies, peptides, antigens, cytokines, growth factors, action potentials, pharmacological agents including

chemotherapeutics, radiation, carcinogenics, or other cells (e.g., cell-cell contacts). In another example, the determinations are determined at different stages of the cell cycle process.

In this way, compounds that modulate ovarian cancer agents are identified.

- 5 Compounds with pharmacological activity are able to enhance or interfere with the activity of the ovarian cancer protein. Once identified, similar structures are evaluated to identify critical structural feature of the compound.

In one embodiment, a method of inhibiting ovarian cancer cell division is provided.

- The method comprises administration of an ovarian cancer inhibitor. In another embodiment, 10 a method of inhibiting ovarian cancer is provided. The method comprises administration of an ovarian cancer inhibitor. In a further embodiment, methods of treating cells or individuals with ovarian cancer are provided. The method comprises administration of an ovarian cancer inhibitor.

In one embodiment, an ovarian cancer inhibitor is an antibody as discussed above. In

- 15 another embodiment, the ovarian cancer inhibitor is an antisense or RNAi molecule.

A variety of cell viability, growth, proliferation, and metastasis assays are known to those of skill in the art, as described below.

Soft agar growth or colony formation in suspension

- 20 Normal cells require a solid substrate to attach and grow. When the cells are transformed, they lose this phenotype and grow detached from the substrate. For example, transformed cells can grow in stirred suspension culture or suspended in semi-solid media, such as semi-solid or soft agar. The transformed cells, when transfected with tumor suppressor genes, regenerate normal phenotype and require a solid substrate to attach and 25 grow. Soft agar growth or colony formation in suspension assays can be used to identify modulators of ovarian cancer sequences, which when expressed in host cells, inhibit abnormal cellular proliferation and transformation. A therapeutic compound would reduce or eliminate the host cells' ability to grow in stirred suspension culture or suspended in semi-solid media, such as semi-solid or soft.

- 30 Techniques for soft agar growth or colony formation in suspension assays are described in Freshney (1994) Culture of Animal Cells: A Manual of Basic Technique (3d ed.) Wiley-Liss, herein incorporated by reference. See also, the methods section of Garkavtsev, et al. (1996), supra, herein incorporated by reference.

Contact inhibition and density limitation of growth

Normal cells typically grow in a flat and organized pattern in a petri dish until they touch other cells. When the cells touch one another, they are contact inhibited and stop growing. When cells are transformed, however, the cells are not contact inhibited and continue to grow to high densities in disorganized foci. Thus, the transformed cells grow to a higher saturation density than normal cells. This can be detected morphologically by the formation of a disoriented monolayer of cells or rounded cells in foci within the regular pattern of normal surrounding cells. Alternatively, labeling index with (^3H)-thymidine at saturation density can be used to measure density limitation of growth. See, e.g., Freshney (1994), supra. The transformed cells, when transfected with tumor suppressor genes, regenerate a normal phenotype and become contact inhibited and would grow to a lower density.

In this assay, labeling index with (^3H)-thymidine at saturation density is a preferred method of measuring density limitation of growth. Transformed host cells are transfected with an ovarian cancer-associated sequence and are grown for 24 hr at saturation density in non-limiting medium conditions. The percentage of cells labeling with (^3H)-thymidine is determined autoradiographically. See, e.g., Freshney (1994), supra.

Growth factor or serum dependence

Transformed cells typically have a lower serum dependence than their normal counterparts. See, e.g., Temin (1966) J. Nat'l Cancer Inst. 37:167-175; Eagle, et al. (1970) J. Exp. Med. 131:836-879; and Freshney, supra. This is in part due to release of various growth factors by the transformed cells. Growth factor or serum dependence of transformed host cells can be compared with that of control.

Tumor specific markers levels

Tumor cells release an increased amount of certain factors (hereinafter "tumor specific markers") than their normal counterparts. For example, plasminogen activator (PA) is released from human glioma at a higher level than from normal brain cells (see, e.g., Gullino, pp. 178-184 "Angiogenesis, tumor vascularization, and potential interference with tumor growth" in Mihich (ed. 1985) Biological Responses in Cancer Plenum. Similarly,

tumor angiogenesis factor (TAF) is released at a higher level in tumor cells than their normal counterparts. See, e.g., Folkman (1992) Sem Cancer Biol. 3:89-96.

Various techniques which measure the release of these factors are described in Freshney (1994), *supra*. Also, see, Unkeless, et al. (1974) J. Biol. Chem. 249:4295-4305; Strickland and Beers (1976) J. Biol. Chem. 251:5694-5702; Whur, et al. (1980) Br. J. Cancer 42:305-312; Gullino, pp. 178-184 "Angiogenesis, tumor vascularization, and potential interference with tumor growth" in Mihich (ed. 1985) Biological Responses in Cancer Plenum; and Freshney (1985) Anticancer Res. 5:111-130.

10 Invasiveness into Matrigel

The degree of invasiveness into Matrigel or some other extracellular matrix constituent can be used as an assay to identify compounds that modulate ovarian cancer-associated sequences. Tumor cells exhibit a good correlation between malignancy and invasiveness of cells into Matrigel or some other extracellular matrix constituent. In this assay, tumorigenic cells are typically used as host cells. Expression of a tumor suppressor gene in these host cells would decrease invasiveness of the host cells.

Alternatively, the level of invasion of host cells can be measured by using filters coated with Matrigel or some other extracellular matrix constituent. Penetration into the gel, or through to the distal side of the filter, is rated as invasiveness, and rated histologically by number of cells and distance moved, or by pre-labeling the cells with ¹²⁵I and counting the radioactivity on the distal side of the filter or bottom of the dish. See, e.g., Freshney (1984), *supra*.

Tumor growth in vivo

Effects of ovarian cancer-associated sequences on cell growth can be tested in transgenic or immune-suppressed mice. Knock-out transgenic mice can be made, in which the ovarian cancer gene is disrupted or in which an ovarian cancer gene is inserted. Knock-out transgenic mice can be made by insertion of a marker gene or other heterologous gene into the endogenous ovarian cancer gene site in the mouse genome via homologous recombination. Such mice can also be made by substituting the endogenous ovarian cancer gene with a mutated version of the ovarian cancer gene, or by mutating the endogenous ovarian cancer gene, e.g., by exposure to carcinogens.

A DNA construct is introduced into the nuclei of embryonic stem cells. Cells containing the newly engineered genetic lesion are injected into a host mouse embryo, which is re-implanted into a recipient female. Some of these embryos develop into chimeric mice that possess germ cells partially derived from the mutant cell line. By breeding the chimeric mice it is possible to obtain a new line of mice containing the introduced genetic lesion. See, e.g., Capecchi, et al. (1989) Science 244:1288-1292. Chimeric targeted mice can be derived according to Hogan, et al. (1988) Manipulating the Mouse Embryo: A Laboratory Manual CSH Press; and Robertson (ed. 1987) Teratocarcinomas and Embryonic Stem Cells: A Practical Approach IRL Press, Washington, D.C.

Alternatively, various immune-suppressed or immune-deficient host animals can be used. For example, genetically athymic "nude" mouse (see, e.g., Giovanella, et al. (1974) J. Nat'l Cancer Inst. 52:921-930), a SCID mouse, a thymectomized mouse, or an irradiated mouse (see, e.g., Bradley, et al. (1978) Br. J. Cancer 38:263-272; Selby, et al. (1980) Br. J. Cancer 41:52-61) can be used as a host. Transplantable tumor cells (typically about 10^6 cells) injected into isogenic hosts will produce invasive tumors in a high proportions of cases, while normal cells of similar origin will not. In hosts which developed invasive tumors, cells expressing an ovarian cancer-associated sequences are injected subcutaneously. After a suitable length of time, preferably 4-8 weeks, tumor growth is measured (e.g., by volume or by its two largest dimensions) and compared to the control. Tumors that have statistically significant reduction (using, e.g., Student's T test) are said to have inhibited growth.

Polynucleotide modulators of ovarian cancer

Antisense and RNAi Polynucleotides

In certain embodiments, the activity of an ovarian cancer-associated protein is down-regulated, or entirely inhibited, by the use of antisense polynucleotide, e.g., a nucleic acid complementary to, and which can preferably hybridize specifically to, a coding mRNA nucleic acid sequence, e.g., an ovarian cancer protein mRNA, or a subsequence thereof. Binding of the antisense polynucleotide to the mRNA reduces the translation and/or stability of the mRNA.

In the context of this invention, antisense polynucleotides can comprise naturally-occurring nucleotides, or synthetic species formed from naturally-occurring subunits or their close homologs. Antisense polynucleotides may also have altered sugar moieties or inter-

sugar linkages. Exemplary among these are the phosphorothioate and other sulfur containing species which are known for use in the art. Analogs are comprehended by this invention so long as they function effectively to hybridize with the ovarian cancer protein mRNA. See, e.g., Isis Pharmaceuticals, Carlsbad, CA; Sequitor, Inc., Natick, MA.

5 Such antisense polynucleotides can readily be synthesized using recombinant means, or can be synthesized in vitro. Equipment for such synthesis is sold by several vendors, including Applied Biosystems. The preparation of other oligonucleotides such as phosphorothioates and alkylated derivatives is also well known to those of skill in the art.

Antisense molecules as used herein include antisense or sense oligonucleotides.

10 Sense oligonucleotides can, e.g., be employed to block transcription by binding to the antisense strand. The antisense and sense oligonucleotide comprise a single-stranded nucleic acid sequence (either RNA or DNA) capable of binding to target mRNA (sense) or DNA (antisense) sequences for ovarian cancer molecules. A preferred antisense molecule is for an ovarian cancer sequences in Tables 1-26, or for a ligand or activator thereof. Antisense or
15 sense oligonucleotides, according to the present invention, comprise a fragment generally at least about 14 nucleotides, preferably from about 14 to 30 nucleotides. An antisense or a sense oligonucleotide can be developed based upon a cDNA sequence encoding a given protein. See, e.g., Stein and Cohen (1988) Cancer Res. 48:2659-2668; and van der Krol, et al. (1988) BioTechniques 6:958-976.

20 RNA interference is a mechanism to suppress gene expression in a sequence specific manner. See, e.g., Brumelkamp, et al. (2002) Sciencexpress (21March2002); Sharp (1999) Genes Dev. 13:139-141; and Cathew (2001) Curr. Op. Cell Biol. 13:244-248. In mammalian cells, short, e.g., 21 nt, double stranded small interfering RNAs (siRNA) have been shown to be effective at inducing an RNAi response. See, e.g., Elbashir, et al. (2001) Nature 411:494-
25 498. The mechanism may be used to down-regulate expression levels of identified genes, e.g., treatment of or validation of relevance to disease.

Ribozymes

In addition to antisense polynucleotides, ribozymes can be used to target and inhibit
30 transcription of ovarian cancer-associated nucleotide sequences. A ribozyme is an RNA molecule that catalytically cleaves other RNA molecules. Different kinds of ribozymes have been described, including group I ribozymes, hammerhead ribozymes, hairpin ribozymes, RNase P, and axhead ribozymes (see, e.g., Castanotto, et al. (1994) Adv. Pharmacol. 25: 289-

317 for a general review of the properties of different ribozymes).

The general features of hairpin ribozymes are described, e.g., in Hampel, et al. (1990) Nucl. Acids Res. 18:299-304; European Patent Publication No. 0 360 257; U.S. Patent No. 5,254,678. Methods of preparing them are well known to those of skill in the art. See, e.g.,
5 WO 94/26877; Ojwang, et al. (1993) Proc. Nat'l Acad. Sci. USA 90:6340-6344; Yamada, et al. (1994) Hum. Gene Ther. 1:39-45; Leavitt, et al. (1995) Proc. Nat'l Acad. Sci. USA 92:699-703; Leavitt, et al. (1994) Hum. Gene Ther. 5:1151-120; and Yamada, et al. (1994) Virology 205:121-126.

Polynucleotide modulators of ovarian cancer may be introduced into a cell containing
10 the target nucleotide sequence by formation of a conjugate with a ligand binding molecule, as described in WO 91/04753. Suitable ligand binding molecules include, but are not limited to, cell surface receptors, growth factors, other cytokines, or other ligands that bind to cell surface receptors. Preferably, conjugation of the ligand binding molecule does not substantially interfere with the ability of the ligand binding molecule to bind to its
15 corresponding molecule or receptor, or block entry of the sense or antisense oligonucleotide or its conjugated version into the cell. Alternatively, a polynucleotide modulator of ovarian cancer may be introduced into a cell containing the target nucleic acid sequence, e.g., by formation of an polynucleotide-lipid complex, as described in WO 90/10448. It is understood that the use of antisense molecules or knock out and knock in models may also be
20 used in screening assays as discussed above, in addition to methods of treatment.

Thus, in one embodiment, methods of modulating ovarian cancer in cells or organisms are provided. In one embodiment, the methods comprise administering to a cell an anti-ovarian cancer antibody that reduces or eliminates the biological activity of an endogenous ovarian cancer protein. Alternatively, the methods comprise administering to a
25 cell or organism a recombinant nucleic acid encoding an ovarian cancer protein. This may be accomplished in any number of ways. In a preferred embodiment, e.g., when the ovarian cancer sequence is down-regulated in ovarian cancer, such state may be reversed by increasing the amount of ovarian cancer gene product in the cell. This can be accomplished, e.g., by over-expressing the endogenous ovarian cancer gene or administering a gene
30 encoding the ovarian cancer sequence, using known gene-therapy techniques, e.g.. In a preferred embodiment, the gene therapy techniques include the incorporation of the exogenous gene using enhanced homologous recombination (EHR), e.g., as described in PCT/US93/03868, hereby incorporated by reference in its entirety. Alternatively, e.g., when

the ovarian cancer sequence is up-regulated in ovarian cancer, the activity of the endogenous ovarian cancer gene is decreased, e.g., by the administration of an ovarian cancer antisense or RNAi nucleic acid.

In one embodiment, the ovarian cancer proteins of the present invention may be used to generate polyclonal and monoclonal antibodies to ovarian cancer proteins. Similarly, the ovarian cancer proteins can be coupled, using standard technology, to affinity chromatography columns. These columns may then be used to purify ovarian cancer antibodies useful for production, diagnostic, or therapeutic purposes. In a preferred embodiment, the antibodies are generated to epitopes unique to an ovarian cancer protein; that is, the antibodies show little or no cross-reactivity to other proteins. The ovarian cancer antibodies may be coupled to standard affinity chromatography columns and used to purify ovarian cancer proteins. The antibodies may also be used as blocking polypeptides, as outlined above, since they will specifically bind to the ovarian cancer protein.

Methods of identifying variant ovarian cancer-associated sequences

Without being bound by theory, expression of various ovarian cancer sequences is correlated with ovarian cancer. Accordingly, disorders based on mutant or variant ovarian cancer genes may be determined. In one embodiment, the invention provides methods for identifying cells containing variant ovarian cancer genes, e.g., determining all or part of the sequence of at least one endogenous ovarian cancer genes in a cell. This may be accomplished using any number of sequencing techniques. In a preferred embodiment, the invention provides methods of identifying the ovarian cancer genotype of an individual, e.g., determining all or part of the sequence of at least one ovarian cancer gene of the individual. This is generally done in at least one tissue of the individual, and may include the evaluation of a number of tissues or different samples of the same tissue. The method may include comparing the sequence of the sequenced ovarian cancer gene to a known ovarian cancer gene, e.g., a wild-type gene.

The sequence of all or part of the ovarian cancer gene can then be compared to the sequence of a known ovarian cancer gene to determine if any differences exist. This can be done using any number of known homology programs, such as Bestfit, etc. In a preferred embodiment, the presence of a difference in the sequence between the ovarian cancer gene of the patient and the known ovarian cancer gene correlates with a disease state or a propensity for a disease state, as outlined herein.

In a preferred embodiment, the ovarian cancer genes are used as probes to determine the number of copies of the ovarian cancer gene in the genome.

In another preferred embodiment, the ovarian cancer genes are used as probes to determine the chromosomal localization of the ovarian cancer genes. Information such as chromosomal localization finds use in providing a diagnosis or prognosis in particular when chromosomal abnormalities such as translocations, and the like are identified in the ovarian cancer gene locus.

Administration of pharmaceutical and vaccine compositions

In one embodiment, a therapeutically effective dose of an ovarian cancer protein or modulator thereof, is administered to a patient. By "therapeutically effective dose" herein is meant a dose that produces effects for which it is administered. The exact dose will depend on the purpose of the treatment, and will be ascertainable by one skilled in the art using known techniques. See, e.g., Ansel, et al. (1999) Pharmaceutical Dosage Forms and Drug Delivery Systems Lippincott; Lieberman (1992) Pharmaceutical Dosage Forms (vols. 1-3) Dekker, ISBN 0824770846, 082476918X, 0824712692, 0824716981; Lloyd (1999) The Art, Science and Technology of Pharmaceutical Compounding Amer. Pharmaceutical Assn.; and Pickar (1999) Dosage Calculations Thomson. Adjustments for ovarian cancer degradation, systemic versus localized delivery, and rate of new protease synthesis, as well as the age, body weight, general health, sex, diet, time of administration, drug interaction, and the severity of the condition may be necessary, and will be ascertainable with routine experimentation by those skilled in the art. U.S. Patent Application No. 09/687,576, further discloses the use of compositions and methods of diagnosis and treatment in ovarian cancer is hereby expressly incorporated by reference.

A "patient" for the purposes of the present invention includes both humans and other animals, particularly mammals. Thus the methods are applicable to both human therapy and veterinary applications. In the preferred embodiment the patient is a mammal, preferably a primate, and in the most preferred embodiment the patient is human.

The administration of the ovarian cancer proteins and modulators thereof of the present invention can be done in a variety of ways as discussed above, including, but not limited to, orally, subcutaneously, intravenously, intra-nasally, transdermally, intraperitoneally, intramuscularly, intrapulmonary, vaginally, rectally, or intraocularly. In some instances, e.g., in the treatment of wounds and inflammation, the ovarian cancer

proteins and modulators may be directly applied as a solution or spray.

The pharmaceutical compositions of the present invention comprise an ovarian cancer protein in a form suitable for administration to a patient. In the preferred embodiment, the pharmaceutical compositions are in a water soluble form, such as being present as pharmaceutically acceptable salts, which is meant to include both acid and base addition salts. "Pharmaceutically acceptable acid addition salt" refers to those salts that retain the biological effectiveness of the free bases and that are not biologically or otherwise undesirable, formed with inorganic acids such as hydrochloric acid, hydrobromic acid, sulfuric acid, nitric acid, phosphoric acid and the like, and organic acids such as acetic acid, propionic acid, glycolic acid, pyruvic acid, oxalic acid, maleic acid, malonic acid, succinic acid, fumaric acid, tartaric acid, citric acid, benzoic acid, cinnamic acid, mandelic acid, methanesulfonic acid, ethanesulfonic acid, p-toluenesulfonic acid, salicylic acid, and the like. "Pharmaceutically acceptable base addition salts" include those derived from inorganic bases such as sodium, potassium, lithium, ammonium, calcium, magnesium, iron, zinc, copper, manganese, aluminum salts and the like. Particularly preferred are the ammonium, potassium, sodium, calcium, and magnesium salts. Salts derived from pharmaceutically acceptable organic non-toxic bases include salts of primary, secondary, and tertiary amines, substituted amines including naturally occurring substituted amines, cyclic amines and basic ion exchange resins, such as isopropylamine, trimethylamine, diethylamine, triethylamine, tripropylamine, and ethanolamine.

The pharmaceutical compositions may also include one or more of the following: carrier proteins such as serum albumin; buffers; fillers such as microcrystalline cellulose, lactose, corn and other starches; binding agents; sweeteners and other flavoring agents; coloring agents; and polyethylene glycol.

The pharmaceutical compositions can be administered in a variety of unit dosage forms depending upon the method of administration. For example, unit dosage forms suitable for oral administration include, but are not limited to, powder, tablets, pills, capsules, and lozenges. It is recognized that ovarian cancer protein modulators (e.g., antibodies, antisense constructs, ribozymes, small organic molecules, etc.) when administered orally, should be protected from digestion. This is typically accomplished either by complexing the molecule(s) with a composition to render it resistant to acidic and enzymatic hydrolysis, or by packaging the molecule(s) in an appropriately resistant carrier, such as a liposome or a protection barrier. Means of protecting agents from digestion are well known in the art.

The compositions for administration will commonly comprise an ovarian cancer protein modulator dissolved in a pharmaceutically acceptable carrier, preferably an aqueous carrier. A variety of aqueous carriers can be used, e.g., buffered saline and the like. These solutions are sterile and generally free of undesirable matter. These compositions may be sterilized by conventional, well known sterilization techniques. The compositions may contain pharmaceutically acceptable auxiliary substances as required to approximate physiological conditions such as pH adjusting and buffering agents, toxicity adjusting agents and the like, e.g., sodium acetate, sodium chloride, potassium chloride, calcium chloride, sodium lactate and the like. The concentration of active agent in these formulations can vary widely, and will be selected primarily based on fluid volumes, viscosities, body weight, and the like in accordance with the particular mode of administration selected and the patient's needs. See, e.g., Remington's Pharmaceutical Science (15th ed., 1980) and Hardman and Limbird (eds. 2001) Goodman and Gillman: The Pharmacological Basis of Therapeutics (10th ed.) McGraw-Hill. Thus, a typical pharmaceutical composition for intravenous administration would be about 0.1 to 10 mg per patient per day. Dosages from 0.1 up to about 100 mg per patient per day may be used, particularly when the drug is administered to a secluded site and not into the blood stream, such as into a body cavity or into a lumen of an organ. Substantially higher dosages are possible in topical administration. Actual methods for preparing parenterally administrable compositions are readily available.

The compositions containing modulators of ovarian cancer proteins can be administered for therapeutic or prophylactic treatments. In therapeutic applications, compositions are administered to a patient suffering from a disease (e.g., a cancer) in an amount sufficient to cure or at least partially arrest the disease and/or its complications. An amount adequate to accomplish this is defined as a "therapeutically effective dose." Amounts effective for this use will depend upon the severity of the disease and the general state of the patient's health. Single or multiple administrations of the compositions may be administered depending on the dosage and frequency as required and tolerated by the patient. In any event, the composition should provide a sufficient quantity of the agents of this invention to effectively treat the patient. An amount of modulator that is capable of preventing or slowing the development of cancer in a mammal is referred to as a "prophylactically effective dose." The particular dose required for a prophylactic treatment will depend upon the medical condition and history of the mammal, the particular cancer being prevented, as well as other factors such as age, weight, gender, administration route, efficiency, etc. Such prophylactic

treatments may be used, e.g., in a mammal who has previously had cancer to prevent a recurrence of the cancer, or in a mammal who is suspected of having a significant likelihood of developing cancer based, e.g., in part, upon gene expression profiles. Vaccine strategies may be used, in either a DNA vaccine form, or protein vaccine.

5 It will be appreciated that the present ovarian cancer protein-modulating compounds can be administered alone or in combination with additional ovarian cancer modulating compounds or with other therapeutic agent, e.g., other anti-cancer agents or treatments.

 In numerous embodiments, one or more nucleic acids, e.g., polynucleotides comprising nucleic acid sequences set forth in Tables 1-26, such as RNAi, antisense
10 polynucleotides or ribozymes, will be introduced into cells, in vitro or in vivo. The present invention provides methods, reagents, vectors, and cells useful for expression of ovarian cancer-associated polypeptides and nucleic acids using in vitro (cell-free), ex vivo or in vivo (cell or organism-based) recombinant expression systems.

 The particular procedure used to introduce the nucleic acids into a host cell for
15 expression of a protein or nucleic acid is application specific. Many procedures for introducing foreign nucleotide sequences into host cells may be used. These include the use of calcium phosphate transfection, spheroplasts, electroporation, liposomes, microinjection, plasma vectors, viral vectors and any of the other well known methods for introducing cloned genomic DNA, cDNA, synthetic DNA or other foreign genetic material into a host cell. See,
20 e.g., Berger and Kimmel (1987) Guide to Molecular Cloning Techniques from Methods in Enzymology (vol. 152) Academic Press; Ausubel, et al. (eds. 1999 and supplements) Current Protocols Lippincott; and Sambrook, et al. (2001) Molecular Cloning: A Laboratory Manual (3d ed., Vol. 1-3) CSH Press.

 In a preferred embodiment, ovarian cancer proteins and modulators are administered
25 as therapeutic agents, and can be formulated as outlined above. Similarly, ovarian cancer genes (including both the full-length sequence, partial sequences, or regulatory sequences of the ovarian cancer coding regions) can be administered in a gene therapy application. These ovarian cancer genes can include antisense applications, either as gene therapy (e.g., for incorporation into the genome) or as antisense compositions, as will be appreciated by those
30 in the art.

 Ovarian cancer polypeptides and polynucleotides can also be administered as vaccine compositions to stimulate HTL, CTL, and antibody responses.. Such vaccine compositions can include, e.g., lipidated peptides (see, e.g., Vitiello, et al. (1995) J. Clin. Invest. 95:341-

- 349), peptide compositions encapsulated in poly(D,L-lactide-co-glycolide, "PLG") microspheres (see, e.g., Eldridge, et al. (1991) Molec. Immunol. 28:287-294; Alonso, et al. (1994) Vaccine 12:299-306; Jones, et al. (1995) Vaccine 13:675-681), peptide compositions contained in immune stimulating complexes (ISCOMS; see, e.g., Takahashi, et al. (1990) Nature 344:873-875; Hu, et al. (1998) Clin. Exp. Immunol. 113:235-243), multiple antigen peptide systems (MAPs; see, e.g., Tam (1988) Proc. Nat'l Acad. Sci. USA 85:5409-5413; Tam (1996) J. Immunol. Methods 196:17-32), peptides formulated as multivalent peptides; peptides for use in ballistic delivery systems, typically crystallized peptides, viral delivery vectors (Perkus, et al., p. 379, in Kaufmann (ed. 1996) Concepts in Vaccine Development de Gruyter; Chakrabarti, et al. (1986) Nature 320:535-537; Hu, et al. (1986) Nature 320:537-540; Kieny, et al. (1986) AIDS Bio/Technology 4:790-795; Top, et al. (1971) J. Infect. Dis. 124:148-154; Chanda, et al. (1990) Virology 175:535-547), particles of viral or synthetic origin (see, e.g., Kofler, et al. (1996) J. Immunol. Methods 192:25-35; Eldridge, et al. (1993) Sem. Hematol. 30:16-24; Falo, et al. (1995) Nature Med. 7:649-653), adjuvants (Warren, et al. (1986) Ann. Rev. Immunol. 4:369-388; Gupta, et al. (1993) Vaccine 11:293-306), liposomes (Reddy, et al. (1992) J. Immunol. 148:1585-1589; Rock (1996) Immunol. Today 17:131-137), or, naked or particle absorbed cDNA (Ulmer, et al. (1993) Science 259:1745-1749; Robinson, et al. (1993) Vaccine 11:957-960; Shiver, et al., p. 423, in Kaufmann (ed. 1996) Concepts in Vaccine Development de Gruyter; Cease and Berzofsky (1994) Ann. Rev. Immunol. 12:923-989; and Eldridge, et al. (1993) Sem. Hematol. 30:16-24). Toxin-targeted delivery technologies, also known as receptor mediated targeting, such as those of Avant Immunotherapeutics, Inc. (Needham, Massachusetts) may also be used.

- Vaccine compositions often include adjuvants. Many adjuvants contain a substance designed to protect the antigen from rapid catabolism, such as aluminum hydroxide or mineral oil, and a stimulator of immune responses, such as lipid A, Bortadella pertussis, or Mycobacterium tuberculosis derived proteins. Certain adjuvants are commercially available as, e.g., Freund's Incomplete Adjuvant and Complete Adjuvant (Difco Laboratories, Detroit, MD); Merck Adjuvant 65 (Merck and Company, Inc., Rahway, NJ); AS-2 (SmithKline Beecham, Philadelphia, PA); aluminum salts such as aluminum hydroxide gel (alum) or aluminum phosphate; salts of calcium, iron or zinc; an insoluble suspension of acylated tyrosine; acylated sugars; cationically or anionically derivatized polysaccharides; polyphosphazenes; biodegradable microspheres; monophosphoryl lipid A and quil A. Cytokines, such as GM-CSF, interleukin-2, -7, -12, and other like growth factors, may also be

used as adjuvants.

Vaccines can be administered as nucleic acid compositions wherein DNA or RNA encoding one or more of the polypeptides, or a fragment thereof, is administered to a patient. See, e.g., Wolff et al. (1990) Science 247:1465-1468; U.S. Patent Nos. 5,580,859; 5,589,466; 5,804,566; 5,739,118; 5,736,524; 5,679,647; and WO 98/04720. Examples of DNA-based delivery technologies include "naked DNA", facilitated (bupivacaine, polymers, peptide-mediated) delivery, cationic lipid complexes, and particle-mediated ("gene gun") or pressure-mediated delivery (see, e.g., U.S. Patent No. 5,922,687).

For therapeutic or prophylactic immunization purposes, the peptides of the invention can be expressed by viral or bacterial vectors. Examples of expression vectors include attenuated viral hosts, such as vaccinia or fowlpox. This approach involves the use of vaccinia virus, e.g., as a vector to express nucleotide sequences that encode ovarian cancer polypeptides or polypeptide fragments. Upon introduction into a host, the recombinant vaccinia virus expresses the immunogenic peptide, and thereby elicits an immune response. Vaccinia vectors and methods useful in immunization protocols are described in, e.g., U.S. Patent No. 4,722,848. Another vector is BCG (Bacille Calmette Guerin). BCG vectors are described in Stover, et al. (1991) Nature 351:456-460. A wide variety of other vectors useful for therapeutic administration or immunization e.g., adeno and adeno-associated virus vectors, retroviral vectors, Salmonella typhi vectors, detoxified anthrax toxin vectors, and the like, will be apparent. See, e.g., Shata, et al. (2000) Mol. Med. Today 6:66-71; Shedlock, et al. (2000) J. Leukoc. Biol. 68:793-806; and Hipp, et al. (2000) In Vivo 14:571-85.

Methods for the use of genes as DNA vaccines are well known, and include placing an ovarian cancer gene or portion of an ovarian cancer gene under the control of a regulatable promoter or a tissue-specific promoter for expression in an ovarian cancer patient. The ovarian cancer gene used for DNA vaccines can encode full-length ovarian cancer proteins, but more preferably encodes portions of the ovarian cancer proteins including peptides derived from the ovarian cancer protein. In one embodiment, a patient is immunized with a DNA vaccine comprising a plurality of nucleotide sequences derived from an ovarian cancer gene. For example, ovarian cancer-associated genes or sequence encoding subfragments of an ovarian cancer protein are introduced into expression vectors and tested for their immunogenicity in the context of Class I MHC and an ability to generate cytotoxic T cell responses. This procedure provides for production of cytotoxic T cell responses against cells which present antigen, including intracellular epitopes.

In a preferred embodiment, the DNA vaccines include a gene encoding an adjuvant molecule with the DNA vaccine. Such adjuvant molecules include cytokines that increase the immunogenic response to the ovarian cancer polypeptide encoded by the DNA vaccine. Additional or alternative adjuvants are available.

- 5 In another preferred embodiment ovarian cancer genes find use in generating animal models of ovarian cancer. When the ovarian cancer gene identified is repressed or diminished in cancer tissue, gene therapy technology, e.g., wherein antisense RNA directed to the ovarian cancer gene will also diminish or repress expression of the gene. Animal models of ovarian cancer find use in screening for modulators of an ovarian cancer-
- 10 associated sequence or modulators of ovarian cancer. Similarly, transgenic animal technology including gene knockout technology, e.g., as a result of homologous recombination with an appropriate gene targeting vector, will result in the absence or increased expression of the ovarian cancer protein. When desired, tissue-specific expression or knockout of the ovarian cancer protein may be necessary.
- 15 It is also possible that the ovarian cancer protein is overexpressed in ovarian cancer. As such, transgenic animals can be generated that overexpress the ovarian cancer protein. Depending on the desired expression level, promoters of various strengths can be employed to express the transgene. Also, the number of copies of the integrated transgene can be determined and compared for a determination of the expression level of the transgene.
- 20 Animals generated by such methods find use as animal models of ovarian cancer and are additionally useful in screening for modulators to treat ovarian cancer.

Kits for Use in Diagnostic and/or Prognostic Applications

- For use in diagnostic, research, and therapeutic applications suggested above, kits are
- 25 also provided by the invention. In the diagnostic and research applications such kits may include any or all of the following: assay reagents, buffers, ovarian cancer-specific nucleic acids or antibodies, hybridization probes and/or primers, siRNA or antisense polynucleotides, ribozymes, dominant negative ovarian cancer polypeptides or polynucleotides, small molecules inhibitors of ovarian cancer-associated sequences etc. A therapeutic product may
- 30 include sterile saline or another pharmaceutically acceptable emulsion and suspension base.

In addition, the kits may include instructional materials containing directions (e.g., protocols) for the practice of the methods of this invention. While the instructional materials typically comprise written or printed materials they are not limited to such. Any medium

capable of storing such instructions and communicating them to an end user is contemplated by this invention. Such media include, but are not limited to electronic storage media (e.g., magnetic discs, tapes, cartridges, chips), optical media (e.g., CD ROM), and the like. Such media may include addresses to internet sites that provide such instructional materials.

The present invention also provides for kits for screening for modulators of ovarian cancer-associated sequences. Such kits can be prepared from readily available materials and reagents. For example, such kits can comprise one or more of the following materials: an ovarian cancer-associated polypeptide or polynucleotide, reaction tubes, and instructions for testing ovarian cancer-associated activity. Optionally, the kit contains biologically active ovarian cancer protein. A wide variety of kits and components can be prepared according to the present invention, depending upon the intended user of the kit and the particular needs of the user. Diagnosis would typically involve evaluation of a plurality of genes or products. The genes will be selected based on correlations with important parameters in disease which may be identified in historical or outcome data.

EXAMPLES

Example 1: Gene Chip Analysis

Molecular profiles of various normal and cancerous tissues were determined and analyzed using gene chips. RNA was isolated and gene chip analysis was performed as described (Glynn, et al. (2000) *Nature* 403:672-676; Zhao, et al. (2000) *Genes Dev.* 14:981-993).

TABLE 1A lists about 1119 genes up-regulated in ovarian cancer compared to normal adult tissues. These were selected from 59000 probesets on the Affymetrix/Eos Hu03 GeneChip array such that the ratio of "average" ovarian cancer to "average" normal adult tissues was greater than or equal to 5.0. The "average" ovarian cancer level was set to the 50th percentile value amongst various ovarian cancers. The "average" normal adult tissue level was set to the 55th percentile amongst various non-malignant tissues.

TABLE 1A: ABOUT 1119 UP-REGULATED OVARIAN CANCER GENES

Phy: Primkey
Ex. Acc: Exemplar Accession
UG ID: UniGene ID
Title: UniGene title
ratio: ratio tumor vs normal tissues

Phy	Ex. Accn	UG ID	Title	ratio
423634	AW559908	Hs.1690	heparin-binding growth factor binding protein	65.7
423017	AW178751	Hs.227548	serine (or cysteine) proteinase inhibitor, clade B(ovabumi	63.6
432538	T77013	Hs.3132	steroidogenic acute regulatory protein	61.3
445910	AW265700	Hs.155660	ESTs	35.9
431938	AA938471	Hs.115242	developmentally regulated GTP-binding protein 1	32.0
407112	AA070801	Hs.51615	ESTs, Weakly similar to ALU7_HUMAN ALU SUBFAM	31.3
425630	NM_001944	Hs.1925	desmoglein 3 (permpilous vulgaris antigen)	30.0
462075			predicted exon	27.9
400301	X03635	Hs.1657	estrogen receptor 1	26.4

	402639			predicted exon	25.3
	421848	LA2583	Hs.111758	keratin 5A	24.7
	414540	BE379050		"gb:50123655F1 NIH_MGC_44 Homo sapiens cDNA clone	24.6
	418994	AA296520	Hs.29546	ectoderm E (ectodermal adhesion molecule 1)	24.5
5	401575			predicted exon	23.6
	457024	AA397546	Hs.119151	ESTs	23.2
	440684	AD253123	Hs.127356	"ESTs, Highly similar to NEST_HUMAN NEST1 [H.sapien	23.1
	459006	AW298631	Hs.27721	hypothetical protein FLJ20353	22.8
10	402954			predicted exon	22.5
	402421			predicted exon	20.9
	437329	AA811977	Hs.291761	ESTs	20.8
	414605	BE390440		"gb:50128305F1 NIH_MGC_44 Homo sapiens cDNA clone	20.7
	411004	AW813242		"gb:MR3-GT0191-020200-207-g10 ST0191 Homo sapiens	20.4
	401263			predicted exon	20.3
15	440533	AI140666	Hs.263320	ESTs	19.9
	445603	H08345	Hs.106234	ESTs	19.7
	403786			predicted exon	19.7
	435508	AW604361	Hs.121121	ESTs	19.6
	459390	BE385725		"gb:501276347F1 NIH_MGC_20 Homo sapiens cDNA clone	19.2
20	421823	NA0850	Hs.28625	ESTs	19.0
	417366	BE185289	Hs.1078	small proline-rich protein 1B (corniflin)	18.9
	422525	AA759757	Hs.192807	ESTs	18.6
	456121	SA2416	Hs.74647	Human T-cell receptor active alpha-chain mRNA from JM c	18.3
	430520	NM_016190	Hs.742057	chromosome 1 open reading frame 10	18.1
25	450192	AA253143	Hs.24596	RAD51-interacting protein	18.0
	416839	H94900	Hs.17882	ESTs	17.9
	440788	AI065894	Hs.176577	ESTs	17.9
	451072	AA013451	Hs.117929	ESTs	17.7
30	402203			predicted exon	17.3
	417611	AW993963		"gb:RC1-BN0035-130400-013-a04 BN0035 Homo sapiens	17.3
	436658	AD22598	Hs.123571	ESTs	17.2
	403747			predicted exon	17.2
	444958	AW292643	Hs.167047	ESTs	17.2
35	404037			predicted exon	17.1
	458375	BE251770		"gb:501112470F1 NIH_MGC_16 Homo sapiens cDNA clone	16.9
	434198	AI039813		gb:3495D06.1 Soares fetal_liver, 2w2Hf8_9w Homo sapi	16.9
	441557	AW452647	Hs.270482	ESTs	16.9
	433871	W02410	Hs.205558	ESTs	16.8
40	429153	AA854766		gb:am20a10.s1 Soares_NFL_T_GBC_S1 Homo sapiens cD	16.7
	434306	AI056238	Hs.143316	ESTs	16.7
	400613			predicted exon	16.6
	448372	AW445168	Hs.170802	ESTs	16.5
	410029	HA7233	Hs.30543	ESTs	16.5
	445887	AI263105	Hs.145597	ESTs	16.1
45	422036	AA302647	Hs.271891	ESTs	16.0
	404787			predicted exon	15.9
	420531	AA280824	Hs.190035	ESTs	15.8
	405196			predicted exon	15.8
50	452947	AW130413		"gb:5000Lx1 NCL_CGAP_Gas4 Homo sapiens cDNA clo	15.8
	425538	BE102552	Hs.139322	small proline-rich protein 3	15.8
	435313	AI769400	Hs.169729	ESTs	15.7
	449535	AI889942	Hs.232150	ESTs	15.6
	424208	AF077374	Hs.139322	small proline-rich protein 3	15.4
55	411650	AW855718		"gb:RC1-C10279-070100-021-a05 CT0279 Homo sapiens c	15.4
	442659	BE269247	Hs.170226	Homo sapiens clone 23579 mRNA sequence	15.4
	443534	AI076123		gb:oy92a04.x1 Soares fetal_liver, spleen, INFLS_S1 Homo	15.4
	458012	AI424859	Hs.108211	ESTs	15.3
	441018	AI005887	Hs.148762	ESTs	15.3
60	429572	BE391563	Hs.165433	"ESTs, Highly similar to T17342 hypothetical protein DKFZ	15.1
	418092	RA5154	Hs.106804	ESTs	15.1
	410009	AW898161	Hs.53112	"ESTs, Weakly similar to ALU_HUMAN ALU SUBFAM	15.1
	458234	BE351408	Hs.127196	ESTs	15.0
	434208	T92641	Hs.127648	hypothetical protein PRO2176	15.0
	403177			predicted exon	15.0
65	432725	AI403106	Hs.132127	hypothetical protein LOC57822	14.9
	425099	AA305052		"gb:EST157885 Infant brain Homo sapiens cDNA 5' end, mR	14.7
	409723	AW885757	Hs.257862	ESTs	14.6
	423735	AA302059		"gb:EST133963 Embryo, 12 week II Homo sapiens cDNA 5'	14.6
70	444266	AI424984	Hs.125465	ESTs	14.5
	443341	AW814659	Hs.3688	ESTs	14.4
	457336	AW959557	Hs.291029	ESTs	14.4
	405000	AA972165	Hs.150308	ESTs	14.4
	446292	AF061497	Hs.279682	Rh type C glycoprotein	14.3
	430086	AA336819	Hs.201167	"Homo sapiens cDNA: FLJ121545 fs, clone COL06195"	14.3
75	434715	BE005346	Hs.116410	ESTs	14.2
	409387	AW384900	Hs.123526	ESTs	14.2
	409272	AB014569	Hs.52526	RAA0669 gene product	14.2
	454913	AW814659		"gb:RC8-CA0014-080300-012-809 CA0014 Homo sapiens	14.0
	439846	T63359	Hs.228320	"Homo sapiens cDNA: FLJ23537 fs, clone LUNG07690"	14.0
80	409655	AA299961		"gb:EST112514 Adrenal gland tumor Homo sapiens cDNA	13.9
	422897	AA677994	Hs.4290	ESTs	13.9
	404654			predicted exon	13.9
	468829	AI557388		"gb:PT2.1_8_G03.r tumor2 Homo sapiens cDNA 3', mRNA	13.8
	407327	AA487182	Hs.269414	ESTs	13.8

455435	AW939445		*gbcV1-DT0072-310100-056-b07 DT0072 Homo sapiens	13.7
455327	AJ383143	Ha.224672	ESTs	13.7
411693	AW857271		*gbcCMO-CT0307-210100-158-g09 CT0307 Homo sapiens	13.7
407463	AJ272034		gbcHomo sapiens mRNA for putative capacitative calcium c	13.6
446767	AL380107	Ha.158954	ESTs	13.6
433540	H70423	Ha.300511	ESTs	13.5
435205	AW027859	Ha.187658	*ESTs, Highly similar to cytomegalovirus partial fusion reoe	13.5
441458	AB191142	Ha.214233	ESTs	13.5
401269			predicted exon	13.4
436653	AI199675	Ha.153070	ESTs	13.4
426898	AA354104	Ha.97489	ESTs	13.4
423637	AL137279	Ha.130187	Homo sapiens mRNA; cDNA DKFZp434O1214 (from clon	13.2
448543	AW897741	Ha.21380	Homo sapiens mRNA; cDNA DKFZp458P1124 (from clon	13.2
456714	AW897265		*gbcCMO-HN0057-150400-335-a04 HN0057 Homo sapiens	13.2
455358	A024555	Ha.131575	ESTs	13.2
431822	AA516049		*gbcg655001.s1 NCL_CGAP_Lip2 Homo sapiens cDNA do	13.1
454822	AW833783		*gbcCV4-TT0008-130100-080-a06 TT0008 Homo sapiens c	13.1
455358	AF990738	Ha.240086	ESTs	13.1
435542	AA817316	Ha.209533	ESTs	13.1
421286	AA905554	Ha.187835	ESTs	13.0
452798	AF548829	Ha.213786	ESTs	13.0
444335	BE383686	Ha.191621	ESTs	13.0
444271	AW452559	Ha.149804	ESTs	12.9
443950	AW865532		*gbcCV4-SN0024-210400-181-g04 SN0024 Homo sapiens	12.9
428719	AA358193	Ha.193128	hypothetical protein FLJ10805	12.8
418282	AA215535	Ha.98133	ESTs	12.8
437308	AA749417	Ha.292353	ESTs	12.7
400584			predicted exon	12.7
426306	AA447310	Ha.164059	*Homo sapiens cDNA FLJ13338 fs, clone OVARC100188	12.7
448466	AJ522109	Ha.171066	ESTs	12.7
402738			predicted exon	12.7
451531	AA018311	Ha.114762	ESTs	12.6
435243	AW292886	Ha.261373	adenosine A2b receptor pseudogene	12.6
431725	X55724	Ha.28439	Norrie disease (pseudoglioma)	12.6
425108	AW00489	Ha.95967	ESTs	12.5
422330	D03078	Ha.115263	epiregulin	12.5
432949	AA570749	Ha.298866	ESTs	12.5
417008	AA191719	Ha.171872	DEAD(H) (Asp-Glu-Ala-Asp/His) box polypeptide 8 (RVA	12.4
455378	AA943387	Ha.87278	ESTs	12.4
423266	AA650114		*gbcns9208.s1 NCL_CGAP_P4.31 Homo sapiens cDNA don	12.4
440571	AA904461	Ha.130798	ESTs	12.3
411178	AW820852		*gbcRC2-ST0301-120200-011-112 ST0301 Homo sapiens c	12.3
445334	AF131173	Ha.13475	hypothetical protein	12.3
433917	AB053325	Ha.122814	Human DNA sequence from clone RP5-102B015 on chrom	12.2
402018			predicted exon	12.2
424101	AA335354		*gbcEST39787 Epikidymus Homo sapiens cDNA 5' end, mR	12.1
445533	AL119710	Ha.21335	nucleosome assembly protein 1-like 3	12.1
458154	AW816379		*gbcCV4-ST0234-181199-035-g01 ST0234 Homo sapiens c	12.1
440919	AW291274	Ha.262826	ESTs	12.0
415747	AA381209		*gbcEST94257 Activated T-cells I Homo sapiens cDNA 5' e	12.0
411748	AW859320		*gbcCV1-CT0364-250100-052-g05 CT0364 Homo sapiens	12.0
452975	M95521	Ha.69469	dendritic cell protein	12.0
427276	AA400269	Ha.49598	ESTs	12.0
454315	AW373564	Ha.251928	nuclear pore complex Interacting protein	12.0
450786	H96632	Ha.33954	ESTs	12.0
402578			predicted exon	11.9
455591	AL037185		gbcDKFZp564A1169_r1 554 (synonym: htr2) Homo sapie	11.9
433449	AW772282		*gbcH11605.s1 NCL_CGAP_P6111 Homo sapiens cDNA c	11.9
425108	AA692921	Ha.126035	ESTs	11.9
454555	AW807073		*gbcMR4-ST0632-031199-018-d06 ST0602 Homo sapiens	11.7
443613	AB078355		gbcx39b05.s1 Soares_NHMPu_S1 Homo sapiens cDNA c	11.7
404385	NM_020399	Ha.283104	putative capacitative calcium channel	11.6
411725	AW858356		*gbcCMO-CT0341-181228-130-c06 CT0341 Homo sapiens	11.5
455174	AB934575	Ha.147801	ESTs	11.5
412402	AW584748		*gbcRC1-HN0015-120400-021-c07 HN0015 Homo sapiens	11.5
434205	AF119891	Ha.263832	hypothetical protein PRO2015	11.5
454046	AW449251	Ha.257131	ESTs	11.5
411149	N68715	Ha.269128	ESTs	11.5
414210	BE383592		*gbc0123971F1 NH_MGC_19 Homo sapiens cDNA clon	11.4
405994	D88884	Ha.57735	acylyl LDL receptor; SREC	11.3
453945	AL187568		gbcCMO-CT0341-181228-130-c06 CT0341 Homo sapi	11.3
443849			predicted exon	11.3
442824	BE178065	Ha.144081	EST	11.3
426548	AA430358	Ha.58649	ESTs	11.3
434804	AA546530		*gbcns44EDS.s1 NCL_CGAP_Alv1 Homo sapiens cDNA do	11.3
430486	BE092109	Ha.241551	*chloride channel, calcium activated, family member 2"	11.3
400174			predicted exon	11.2
424324	AA346316		*gbcEST52440 Greater omentum tumor Homo sapiens cDN	11.2
447724	AW298375	Ha.24477	ESTs	11.2
457028	AW449838	Ha.979562	ESTs	11.2
429900	AA460421	Ha.30875	ESTs	11.2
452240	AJ911147	Ha.61232	ESTs	11.2
450057	AA333603	Ha.36752	*Homo sapiens cDNA: FLJ22834 fs, clone KAA4314"	11.1
402222			predicted exon	11.1

	446745	AW118189	Hs.156400	ESTs	11.1
	453050	AW294092	Hs.21594	ESTs	11.1
	443482	AW180353	Hs.250385	ESTs	11.1
5	436843	AA824588	Hs.gbc83302.s1 NCL_CGAP_GCB1 Homo sapiens cDNA c	11.0	11.0
	416320	H47867	Hs.34024	ESTs	11.0
	435772	AA700019	Hs.132932	"ATP-binding cassette, sub-family G (WHITE), member 5 (11.0
	451542	AA015355	Hs.32713	ESTs	11.0
	408522	AS541214	Hs.46320	"Small proline-rich protein SPRK [human, odontogenic kerat	11.0
	414712	NB8858.comp	Hs.77039	ribosomal protein S3A	10.9
10	411940	AW876686	Hs.254290	"gbcM4-P70031-180200-507-e05 P70031 Homo sapiens c	10.9
	408733	AW264812	Hs.27607	ESTs	10.9
	452030	AL131578	Hs.27607	Homo sapiens mRNA; cDNA DKFZp564N2464 (from don	10.9
	458175	AW296224	Hs.150434	ESTs	10.9
	400612	AS37559	Hs.126127	predicted exon	10.9
15	440159	AB026987	Hs.202687	"potassium voltage-gated channel, Shal-related subfamily, m	10.8
	429443	AB026987	Hs.202687	"CD83 antigen (activated B lymphocytes, immunoglobulin s	10.8
	416319	AB15501	Hs.79197	predicted exon	10.7
	405783			predicted exon	10.6
20	405708			"Homo sapiens cDNA FLJ13872 fa, clone THYR0100132	10.6
	433266	AB53224	Hs.298677	ESTs	10.6
	456900	AA355442	Hs.169054	ESTs	10.6
	432408	N91217	Hs.76391	"myxovirus (influenza) resistance 1, homolog of murine (Int	10.6
	451702	AW865452	Hs.246503	ESTs	10.6
	418179	AS15330	Hs.1145	Wilms tumor 1	10.6
25	408987	H95615		gbyT03F11.r1 Soares retina N2bSHR Homo sapiens cDNA	10.6
	405285	BE165909	Hs.134862	predicted exon	10.5
	419276	BE165909	Hs.134862	"Homo sapiens cDNA: FLJ23161 fa, clone LNC097303	10.5
	407287	AB78812	Hs.301658	ESTs, Weakly similar to ALUA_HUMAN ALU SUBFAM	10.5
	403065			predicted exon	10.5
30	414195	BE263283	"gbc01144881F2 NIH_MGC_19 Homo sapiens cDNA clone	10.4	10.4
	454258	AB457286	Hs.143979	ESTs, Weakly similar to KIAA1276 protein (Lisaplan)	10.4
	412351	BE011811	Hs.251946	"Homo sapiens cDNA: FLJ23107 fa, clone LNC07738"	10.4
	428688	AA437010	Hs.266584	ESTs	10.4
	440834	AA807027	Hs.128806	ESTs	10.4
35	437096	AA744406		gbyM51h02.s1 NCL_CGAP_P118 Homo sapiens cDNA do	10.4
	400135			predicted exon	10.3
	447849	AS35147	Hs.164277	ESTs	10.3
	400993			predicted exon	10.3
40	427469	AA403894	Hs.269347	ESTs	10.3
	402794			predicted exon	10.2
	452743	AW965082	Hs.61455	ESTs	10.2
	448983	AB11654	Hs.224908	ESTs	10.2
	422696	AF242524	Hs.26323	hypothetical nuclear factor SBN22	10.2
45	428940	AA442153	Hs.104744	"ESTs, Weakly similar to AF208855 1 BM-013 (Lisaplan)	10.2
	409191	AW818390	"gbcRC1-ST0278-180200-014-410 ST0278 Homo sapiens c	10.2	10.2
	428493	AK001745	Hs.184628	hypothetical protein FLJ10863	10.2
	406076	AL301719	Hs.137011	Homo sapiens mRNA; cDNA DKFZp547P134 (from clone	10.2
	410620	BE477277	"gbc0126977/F1 NIH_MGC_21 Homo sapiens cDNA clone	10.1	10.1
	458335	AW290399	Hs.145534	chromosome 21 open reading frame 23	10.1
50	452507	AB904646	Hs.282633	"gbcOV-BT065-020399-103 BT065 Homo sapiens cDNA, m	10.1
	433297	AB555581	Hs.282633	ESTs	10.1
	428724	AS358303	Hs.282633	ESTs	10.0
	436559	AB217900	Hs.144464	ESTs	10.0
	405675			predicted exon	10.0
55	413468	BE141737	Hs.254105	"cardiac 1, (alpha)"	10.0
	447198	DS1523	Hs.283435	ESTs	10.0
	403306	NM_006825	Hs.74368	"transmembrane protein (B3D), endoplasmic reticulum/Go	10.0
	413544	BE147225	"gbcPM2-HT0225-031299-003-F11 HT0225 Homo sapiens	9.9	9.9
	437094	AW103746	Hs.136907	ESTs	9.9
60	401407			predicted exon	9.9
	416203	H27794	Hs.265055	ESTs	9.9
	426882	AA393108	Hs.97355	ESTs	9.9
	454874	AW838407	"gbcPM3-LT0031-301299-002-b09 LT0031 Homo sapiens	9.9	9.9
	403022	Z33558	Hs.278432	"myosin, heavy polypeptide 6, cardiac muscle, alpha (cardio	9.9
65	404952			predicted exon	9.9
	430691	C14187	Hs.103538	ESTs	9.9
	444518	AB150278	Hs.146894	ESTs	9.8
	419565	H72974		gbyu28a10.s1 Soares fetal liver spleen 1NFLS Homo sapie	9.8
	438691	AA060288	Hs.212184	ESTs	9.8
70	405636			predicted exon	9.8
	437242	AA747538	Hs.187942	ESTs	9.8
	425527	AF019812	Hs.297007	ESTs	9.8
	452226	AA024898	Hs.296002	ESTs	9.8
75	418966	AB123555	Hs.81796	ESTs	9.8
	441139	AW445009	Hs.126547	ESTs	9.7
	427244	AA407400	Hs.178045	ESTs	9.7
	423756	AA828125	"gbcod71a09.s1 NCL_CGAP_Ov2 Homo sapiens cDNA do	9.7	9.7
	457940	AL360159	Hs.30445	Homo sapiens mRNA full length insert cDNA clone EURO	9.6
	413526	AW792804	Hs.134002	ESTs	9.6
80	440576	AW445775	Hs.126503	ESTs	9.6
	419088	AB336223	Hs.77496	small nuclear ribonucleoprotein polypeptide G	9.6
	454707	AW814969	"gbcMR1-ST0206-170400-024-g05 ST0206 Homo sapiens	9.6	9.6
	446252	AB283125	ESTs	9.6	9.6
	443374	AA631439	"gbcnp55802.s1 NCL_CGAP_Thy1 Homo sapiens cDNA d	9.6	9.6

	403093		predicted exon	9.6
	454633	AW811380	"gb:U3-ST0143-290999-019-005 ST0143 Homo sapiens c	9.6
	407291	AA001464	gb:z4501.1 Soares retina N2b4HR Homo sapiens cDNA	9.6
5	455203	AW865450	"gb:PM4-SN0020-010400-008-b09 SN0020 Homo sapiens	9.5
	402847		predicted exon	9.5
	401530		predicted exon	9.5
	414281	BE269751	Hs.288935	9.5
	411057	AW815098	hypothetical protein FLJ20813	9.5
10	415933	H14425	"gb:CV4-ST0212-091119-023-010 ST0212 Homo sapiens c	9.5
	456174	T82121	ESTs	9.5
	422949	AA319435	"gb:EST12657 Adrenal gland tumor Homo sapiens cDNA 5	9.5
	402112	T83624	Hs.2186	9.5
	457866	AA744279	Hs.253346	9.5
	458145	A233457	Hs.130794	9.4
15	452332	AW014859	ESTs	9.4
	434950	AW974892	"gb:EST369597 MAGe resequences, MAGN Homo sapien	9.3
	406601	AF237621	keratin 1 (epidermal hyperkeratosis)	9.3
	418958	X04430	"interleukin 6 (interleukin, beta 2)"	9.3
20	436211	AK001581	Hs.80961	9.3
	428412	AA428240	Hs.126083	9.3
	445441	AW55040	Hs.195532	9.3
	458771	AW256151	Hs.163812	9.3
	458543	AA213403	Hs.257462	9.3
	414257	AB285600	Hs.21124	9.3
25	442826	AW018777	ESTs	9.3
	446740	AB115355	Hs.102055	9.2
	408938	AA065013	Hs.22607	9.2
	434157	AS38316	Hs.159451	9.2
	406774	AW270899	ESTs	9.2
30	424268	AA357653	Hs.144339	9.2
	415715	F30364	"gb:HSPC20786 H63 Homo sapiens cDNA clone s40009	9.1
	405277		predicted exon	9.1
	412167	AW897230	"gb:CMD-NB057-150400-335-11 NN057 Homo sapiens	9.1
35	442771	AA405988	ESTs	9.1
	404898		predicted exon	9.1
	401230		predicted exon	9.1
	400523		predicted exon	9.1
40	416808	AB21836	Hs.10359	9.1
	436396	AB683487	Hs.259112	9.1
	440466	AA885871	Hs.135727	9.0
	437568	AB54795	ESTs	9.0
	405382		predicted exon	9.0
	435673	AF202951	Hs.284200	9.0
	405848		predicted exon	9.0
45	437229	AW576005	"gb:EST368114 MAGe resequences, MAGN Homo sapien	9.0
	417728	AW138437	Hs.24790	9.0
	454597	AW809548	"gb:MRA-ST0124-261099-015-001 ST0124 Homo sapiens	9.0
	427093	AA398118	Hs.97679	9.0
	408000	L11650	Hs.420	9.0
50	440556	AW026958	Hs.125568	9.0
	400163		predicted exon	8.9
	420120	AL049610	Hs.95243	8.9
	417549	AA303651	transcription elongation factor A (SII)-like 1	8.9
	406163		gb:z4501.1 Soares_fetal_liver_aplcen_1NFLS_S1 Homo	8.9
55	437918	AB71449	Hs.121629	8.9
	449419	R34910	Hs.119172	8.9
	434683	AW258724	Hs.202639	8.9
	418432	M14156	Hs.85112	8.9
	454590	AW809762	Hs.222058	8.8
60	454574	AW809109	"Homo sapiens cDNA FLJ11572 fs, clone HEMBA100337	8.8
	441433	AA333809	"gb:MRA-ST0117-070100-027-004 ST0117 Homo sapiens c	8.8
	416858	AW979294	Hs.85634	8.8
	421978	AB243662	Hs.110199	8.8
	451528	AA018297	Hs.35493	8.8
65	408751	H61553	Hs.258343	8.8
	401862		predicted exon	8.7
	417344	AW997313	"gb:RC2-BN0048-250400-018-112 BN0048 Homo sapiens	8.7
	454455	AW752710	"gb:U3-C70219-281099-024-A03 C70219 Homo sapiens c	8.7
70	455392	BE036802	"gb:GV0-BN0147-290400-214-b04 BN0147 Homo sapiens	8.7
	417650	T05870	ESTs	8.7
	458309	AA225423	"gtac:NC24r1 NCI_OGAP_P1 Homo sapiens cDNA don	8.7
	432030	AB08400	Hs.143789	8.7
	421452	BE176990	Hs.104916	8.7
75	402576		hypothetical protein FLJ21940	8.7
	428874	N67325	ESTs	8.7
	403334		predicted exon	8.7
	403562	AA36323	Hs.31141	8.7
	439443	AF086351	Hs.127892	8.7
	428600	AW853261	Hs.15036	8.7
80	414539	BE379046	"ESTs. Highly similar to AF161358 1 HSPC095 (H)sapiens	8.6
	423237	AW975028	Hs.102754	8.6
	403273		predicted exon	8.6
	452077	BE144949	"gb:RC2-HT0187-041059-011-42 HT0187 Homo sapiens	8.6
	444598	A288830	ESTs	8.6

434066	AF116649	Hs.283944	"Homo sapiens PRO0566 mRNA, complete cds"	8.6
425943	AA455889	Hs.187548	ESTs	8.6
432340	AA534222		gb:U21602.1 NCL_CGAP_AA1 Homo sapiens cDNA clone	8.6
446142	AF754693	Hs.145968	ESTs	8.6
417412	U16856	Hs.82112	"telodendin 1 receptor, type I"	8.6
416913	AW347114		"gb:RCH1-070001-031259-011-a11 DT0001 Homo sapiens	8.5
451318	AA025888	Hs.95071	ESTs	8.5
405547			predicted exon	8.5
423843	AA332652		"gb:EST36627 Embryo, 8 week 1 Homo sapiens cDNA 5' en	8.5
454145	AA046872	Hs.62798	ESTs	8.4
401200			predicted exon	8.4
404166			predicted exon	8.4
412761	AW950562		"gb:OV2-BND041-030300-145-a10 BND041 Homo sapiens	8.4
412333	AW573485		"gb:OV2-DT0044-221259-045-b09 DT0044 Homo sapiens	8.4
455092	BE152428		"gb:CMO-H70323-151299-126-b04 HT0323 Homo sapiens	8.4
419281	H96452	Hs.42189	ESTs	8.4
446171	A074927		gb:nt66c64.x.1 Soares_tetal_fetus_Nb2HF8_9w Homo sapie	8.3
437332	AL359551	Hs.16493	hypothetical protein DKFZp762N2316	8.3
402631			predicted exon	8.3
458573	AV653838	Hs.295131	ESTs	8.3
439185	AW079796	Hs.233343	ESTs	8.3
458811	AA252029	Hs.210089	ESTs	8.3
449737	AI668581	Hs.246316	ESTs	8.3
401830	AJ004832	Hs.5038	neuropathy target esterase	8.3
421991	NM_014918	Hs.110458	KIAA0990 protein	8.2
416996	W61092	Hs.59609	ESTs	8.2
443626	AA540544	Hs.138479	"ESTs, Moderately similar to ALU7_HUMAN ALU SUBF	8.2
407471	DS5644		gb:Human spleen PAA (pseudautosomal boundary)-like se	8.2
402664			predicted exon	8.2
417892	W69561		gb:nt4768r.1 Soares_tetal_haad_NbHH19W Homo sapien	8.2
424983	AT742434	Hs.169911	ESTs	8.2
434353	AA630863	Hs.131375	"ESTs, Weakly similar to ALLB_HUMAN IIII ALU CLAS	8.2
435448	AL036710	Hs.209527	ESTs	8.2
455121	BE155459		"gb:OV2-H70368-040100-082-036 HT0368 Homo sapiens	8.1
404270			predicted exon	8.1
438297	AW515196	Hs.258238	"ESTs, Moderately similar to ALU1_HUMAN ALU SUBF	8.1
418122	R42778	Hs.22217	ESTs	8.1
419929	U90256	Hs.53810	cerebral cavernous malformations 1	8.1
409525			predicted exon	8.1
403350			predicted exon	8.1
426116	AA068729	Hs.144694	ESTs	8.1
441518	AW151697	Hs.294150	ESTs	8.1
421888	AA259780	Hs.121036	ESTs	8.1
402745			predicted exon	8.1
402671			predicted exon	8.1
444781	NM_014400	Hs.11950	GPI-anchored metastasis-associated protein homolog	8.0
430372	AA206173	Hs.211375	ESTs	8.0
449867	AB72379	Hs.73919	"clathrin, light polypeptide (Lcb)"	8.0
422174	AL049325	Hs.112493	Homo sapiens mRNA, cDNA DKFZp564D036 (from clone	8.0
413382	BE059689		"gb:RCH1-070020-280300-011-b08 DT0020 Homo sapiens c	8.0
455602	AF786511	Hs.157277	ESTs	8.0
405336			predicted exon	8.0
403917			predicted exon	8.0
436807	AJ247716	Hs.232168	ESTs	8.0
439192	AW970536	Hs.105413	ESTs	8.0
437724	AW444828	Hs.184323	ESTs	8.0
452755	AW138937	Hs.213436	ESTs	8.0
401781			predicted exon	7.9
409057			predicted exon	7.9
405289	AW063311	Hs.82582	"integrin, beta-like 1 (with EGF-like repeat domains)"	7.9
421459	AB215339	Hs.97249	Hs.97249	7.9
442651	BE230486	Hs.84045	"Homo sapiens cDNA FLJ11579 fs, clone HEMBB100128	7.9
429125	AA446854	Hs.278004	ESTs	7.9
440154	BE077129	Hs.126119	"Homo sapiens cDNA FLJ13273 fs, clone OVARC100101	7.9
413233	AW587813	Hs.117354	"ESTs, Weakly similar to CRF_Yd.2016 [S.cerevisiae]"	7.9
438048	AJ782103	Hs.293502	ESTs	7.9
452466	NB4635	Hs.29664	Human DNA sequence from clone 682115 on chromosome 6	7.9
441194	BE274581		"gb:01120870F1 NIH_MGC_20 Homo sapiens cDNA clone	7.9
425252	NM_005824	Hs.155645	3T Moa leucine-rich repeat (LRR) protein	7.9
445080	AW050208	Hs.147293	ESTs	7.9
431292	AA370141	Hs.251453	Human DNA sequence from clone 957M21 on chromosome	7.9
414266	BE267834		"gb:01124428F1 NIH_MGC_8 Homo sapiens cDNA clone	7.8
407839	AA051544	Hs.161566	ESTs	7.8
455101	AA152478		gb:nt7405.s1 Stratagene pancreas (937236) Homo sapiens	7.8
455853	BE147225		"gb:PM2-HT0225-031299-003-f11 HT0225 Homo sapiens	7.8
414595	C18200		gb:C18200 Human placenta cDNA (TFP4)wara) Homo sapie	7.8
447247	AW069351	Hs.287955	"Homo sapiens cDNA FLJ13390 fs, clone NT28P3002142	7.8
416151	T26951		"gb:A065CTR Infant brain, LLN, array of Dr. M. Soares 1	7.8
446435	AW206737	Hs.253382	ESTs	7.8
403698			predicted exon	7.8
424914	AA348410	Hs.119065	ESTs	7.8
405731	AA125985	Hs.55145	"Thymosin, beta, identified in neuroblastoma cells"	7.8
461604			predicted exon	7.8
413025	AA805265	Hs.291646	ESTs	7.8

405896			predicted exon	7.8
454505	AW601385		"gblLS-UM0067-240300-050-a01 UM0057 Homo sapiens	7.7
445283	A334062	Hs.182979	ribosomal protein L12	7.7
434088	AA525499		"gbrat69g08Lr1 Soares_NIHMPV_S1 Homo sapiens cDNA	7.7
431673	AW971302	Hs.232323	ESTs	7.7
421029	AW357782	Hs.230353	ESTs	7.7
405391	AW552276		"gbrMRI-CT0352-240200-105-002 CT0352 Homo sapiens	7.7
422529	AW015128	Hs.256703	ESTs	7.7
454389	AW752571		"gblL3-CT0213-170100-055-F02 CT0213 Homo sapiens c	7.7
427821	AA470158	Hs.98202	ESTs	7.7
434657	AA641876	Hs.191840	ESTs	7.7
445628	AS44166	Hs.155743	ESTs	7.7
424872	AA347923		"gbrEST54302 Fetal heart II Homo sapiens cDNA 5' end, m	7.7
439232	N48690	Hs.46593	ESTs	7.7
441417	AF33297	Hs.144474	ESTs	7.7
453596	AA441838	Hs.82905	ESTs	7.7
430440	XS2599	Hs.2561	"nerva growth factor, beta polypeptide"	7.7
413306	AW303544	Hs.118654	ESTs	7.7
400968			predicted exon	7.7
446726	AW300144	Hs.209209	"Homo sapiens cDNA FLJ11629 fs, clone HEMBA100424	7.7
427504	AA776743	Hs.191569	ESTs	7.7
405621			predicted exon	7.6
414127	AA431853	Hs.135270	ESTs	7.6
409868	AW502152		"gblULHF-BRDp-ajr-4-11-4-ULr1 NIH_MGC_52 Homo sap	7.6
446232	AA281848	Hs.165547	ESTs	7.6
403568			predicted exon	7.6
451458	AF787555	Hs.270820	ESTs	7.6
439157	AS12737	Hs.20160	ESTs	7.6
401793			predicted exon	7.6
428839	AI190291	Hs.112143	ESTs	7.6
445072	A907438	Hs.282862	ESTs	7.6
449444	AA18436	Hs.23550	"soluble carrier family 16 (monocarboxylic acid transporters)	7.6
447499	AW262880	Hs.147674	KAA1621 protein	7.6
421773	W89233	Hs.112457	ESTs	7.6
439708	AW572527	Hs.59761	ESTs	7.6
432189	AA527841		"gblm30c04.s1 NCI_CGAP_Pv3 Homo sapiens cDNA clone	7.5
402050			predicted exon	7.5
429587	AI675749	Hs.211608	nucleoporin 153kD	7.5
427193	AF7229	Hs.254637	"Homo sapiens cDNA FLJ13502 fs, clone PLACE1004636	7.5
410548	H62953		"gbyr4706Lr1 Soares fetal liver spleen INFLS Homo sapien	7.5
443236	AA079496	Hs.134169	ESTs	7.5
439503	AW57224	Hs.15443	ESTs	7.5
427191	NA_008486	Hs.5476	"serine protease inhibitor, Kazal type, 5"	7.4
451829	AW564081	Hs.247377	ESTs	7.4
443151	AB27193	Hs.132714	ESTs	7.4
452055	AS377431	Hs.293772	ESTs	7.4
445285	A216255	Hs.144942	ESTs	7.4
401032			predicted exon	7.4
448184	BE541249	Hs.109597	ESTs	7.4
414808	T59545		"gbye4262Lr1 Soares fetal liver spleen INFLS Homo sapien	7.4
410540	AS21197	Hs.90877	ESTs, Weakly similar to ALU1_HUMAN ALU SUBFAM	7.4
410449	AW748554	Hs.18192	Set/Arg-related nuclear matrix protein (plenty of prolines 1	7.4
435585	AA688048	Hs.294080	ESTs	7.4
459160	A304723		"gblCM4-ET056-120299-092 ET056 Homo sapiens cDNA,	7.4
419163	NA0251		"gby1112Lr1 Soares melanocyte 2/Nb1Hf Homo sapiens cD	7.4
432383	AQ000144	Hs.274448	"Homo sapiens cDNA FLJ20137 fs, clone COL07137"	7.4
404893			predicted exon	7.4
425349	AA422334	Hs.78886	ribosome 5-phosphate isomerase A (ribosome 5-phosphate epimer	7.4
413864	BE175582		"gbrPCS-HT0589-100500-022-C01 HT0589 Homo sapiens	7.3
426871	AA353041	Hs.216493	ESTs	7.3
415613	R20233		"gbyg18b11Lr1 Soares infant brain 1/Nb1Hf Homo sapiens cDN	7.3
427625	AA397589	Hs.97523	ESTs	7.3
444683	A375101	Hs.158721	"ESTs, Weakly similar to ALU1_HUMAN ALU SUBFAM	7.3
447700	AI420183	Hs.171077	"ESTs, Weakly similar to similar to serine/threonine kinase	7.3
412740	AW993984		"gbrCR1-BN0035-130400-013-e05 BN0035 Homo sapiens	7.3
418642	T98118	Hs.226313	ESTs, Weakly similar to ALU1_HUMAN ALU SUBFAM	7.3
416506	H65878	Hs.237306	ESTs	7.3
426130	AA853282		"gblNTECae0407r1 Normal Human Trabecular Bone Cell	7.3
407392	AB032369		"gbrHomo sapiens MST mRNA, partial cds."	7.3
423265	AQ001108	Hs.274419	hypothetical protein FLJ10244	7.3
451221	A916701	Hs.210599	ESTs	7.3
443161	AIC83816		"gbrhox4c08Lr1 Soares_total_fetus_Nb2Hf_9w Homo sapi	7.3
418186	BE541042	Hs.23240	"Homo sapiens cDNA FLJ13496 fs, clone PLACE1004471	7.3
439152	H65014		"gbyu6610Lr1 Woltmann Olfactory Epithelium Homo sapie	7.2
459534	BE368608	Hs.147905	ESTs	7.2
443326	BE156494	Hs.188478	ESTs	7.2
417351	T90278	Hs.15049	ESTs	7.2
454182	AW177335		"gbrCM1-CTC129-180899-005-008 CTC129 Homo sapiens	7.2
402298			predicted exon	7.2
459562	N34128	Hs.145268	ESTs	7.2
407021	US2077		"gbrHuman mariner1 transposase gene, complete consensus	7.2
449376	AW241610	Hs.252713	ESTs	7.2
418051	AA8321129	Hs.177723	ESTs	7.2
402788	AA937957	Hs.193367	ESTs	7.2

	401881	AA251079	Hs.158386	predicted exon	7.2
	456436	F29556	Hs.158386	ESTs	7.2
	448966	AW372914	Hs.287452	"Homo sapiens cDNA FLJ11875 fls, clone HEMBA100707"	7.2
5	429340	N35938	Hs.199429	Homo sapiens mRNA; cDNA DKFZP434M2216 (from clone)	7.2
	405053			predicted exon	7.2
	405551			predicted exon	7.2
	431009	BE149762	Hs.248213	"gap junction protein, beta 6 (connexin 30)"	7.2
	426662	AA879474	Hs.122710	ESTs	7.2
10	408536	AW361532	Hs.135188	ESTs	7.1
	455013	B5013550		"gbtAR0.8T0551-060300-102-e05 BTO551 Homo sapiens	7.1
	428910	W03567	Hs.193792	ESTs	7.1
	424634	NM_003513	Hs.151407	"cardiac intermediate layer protein, nucleoside pyrophosph	7.1
	449794	AW444502	Hs.256982	"ESTs, Highly similar to AF116865.1 hedgehog-interacting	7.1
15	423410	AF069899	Hs.128231	"G antigen, family B, 1 (prostate associated)"	7.1
	445460	AT97473	Hs.209468	ESTs	7.1
	447285	AT371845	Hs.200696	"ATPase, Class VI, type 11C"	7.1
	419750	AL079741	Hs.183114	"Homo sapiens cDNA FLJ14236 fls, clone NT2R2400515	7.1
20	432856	AF083888	Hs.263307	ESTs	7.1
	420787	X78592	Hs.59915	androgen receptor (dihydrotestosterone receptor, testicular	7.1
	432479	AL042844	Hs.275675	kutakin p80 (WD40-containing) subunit B 1	7.1
	449733	R74546	Hs.29438	"Homo sapiens cDNA FLJ12094 fls, clone HEMBB100290	7.1
	437846	AW773866	Hs.244569	ESTs	7.1
	454634	AW646980		"gbtMR3-CT0178-081099-002-b09 CT0176 Homo sapiens	7.1
25	421929	AA300543	Hs.247360	ESTs	7.1
	401780			predicted exon	7.1
	448106	AB03470	Hs.171941	ESTs	7.0
	448835	BE277929	Hs.11081	"ESTs, Weakly similar to S57447 HPBR8-7 protein [Hsap	7.0
	400842			predicted exon	7.0
30	429354	AA451787	Hs.201202	"ESTs, Moderately similar to Pro-Pol-dUTPase polyprotein	7.0
	454983	AW947647		"gbtL3-CT0213-280100-058-A02 CT0213 Homo sapiens c	7.0
	423891	AK002042	Hs.134796	"Homo sapiens cDNA FLJ11180 fls, clone PLACE1007452	7.0
	407506	U71600		"gbtHuman zinc finger protein zfp31 (zfp31) mRNA, partial	7.0
35	413802	AW964450	Hs.32241	ESTs	7.0
	440051	B5559950		"gbt01345293F1 NIH_MGC_8 Homo sapiens cDNA clone	7.0
	446283	AA48801	Hs.171073	ESTs	7.0
	419236	AA330447	Hs.135159	"Homo sapiens cDNA FLJ11481 fls, clone HEMBA100180	7.0
	405472			predicted exon	7.0
40	435024	AB63516	Hs.127743	"ESTs, Weakly similar to V-ATPase G-subunit beta protein	7.0
	453589	AW050783	Hs.301731	"Homo sapiens cDNA FLJ11738 fls, clone HEMBA100547	7.0
	404992			predicted exon	7.0
	428129	A244311	Hs.265912	ESTs	7.0
	414315	Z24678		"gbtH3B66DQ62 STRATAGENE Human skeletal muscle cD	7.0
45	400491	H25530	Hs.50868	"solute carrier family 22 [organic cation transporter], memb	6.9
	459275	AB08913	Hs.118321	ESTs	6.9
	450853	AA479629	Hs.44243	ESTs	6.9
	457460	AI143512	Hs.164004	ESTs	6.9
	434168	A204525	Hs.116156	ESTs	6.9
50	445153	AI214671		"gbtgm32602.x1 NCI_CGAP_Lus Homo sapiens cDNA cl	6.9
	450028	AB115456	Hs.200737	ESTs	6.9
	414954	DB1422		"gbtHUM162A03B Human fetal brain (TFujwara) Homo sa	6.9
	459478	AW195566	Hs.253182	ESTs	6.9
	426269	HI5302	Hs.165950	Homo sapiens mRNA; cDNA DKFZp556A1046 (from clone	6.9
	401050			predicted exon	6.9
55	447588	AI304154	Hs.279659	"ESTs, Weakly similar to unknown protein [Lsapine]"	6.9
	449002	AB520018	Hs.117461	ESTs	6.9
	452759	AW590773	Hs.258958	ESTs	6.9
	443220	R65304	Hs.132032	"Homo sapiens cDNA FLJ11683 fls, clone HEMBA100490	6.9
	402749			predicted exon	6.8
60	426727			predicted exon	6.8
	433785	BE044593	Hs.112704	ESTs	6.8
	434129	AB07757	Hs.221041	ESTs	6.8
	453389	BE551650	Hs.232630	ESTs	6.8
	411722	AW875942		"gbtCM1-PT0013-131299-067-b10 PT0013 Homo sapiens	6.8
65	455152	AW858621		"gbt.CMD-CT0342-021299-115-004 CT0342 Homo sapiens	6.8
	412670	AA115456		"gbt2k89B05.r1 Soares adult brain N2b4HB55Y Homo sapi	6.8
	419084	W02349	Hs.191510	ESTs, Weakly similar to ORF2 [Mus musculus]"	6.8
	421316	AA287203	Hs.251397	SMAS	6.8
	432363	AA534489		"gbtbf76g11.x1 NCI_CGAP_Co3 Homo sapiens cDNA clone	6.8
	458503	AW103046	Hs.6162	KIAA0771 protein	6.8
	435527	AW269119	Hs.202636	ESTs	6.8
70	408520	AL120071	Hs.48958	Bromocain leucine rich transmembrane protein 2	6.7
	439127	AW576465	Hs.292368	ESTs	6.7
	434890	AF161345	Hs.282930	"Homo sapiens HSPC082 mRNA, partial cds"	6.7
75	429413	NM_014058	Hs.201877	DES/C1 protein	6.7
	407798	BES14082		S100 calcium-binding protein A2	6.7
	447252	R80916		"gbtyn01e10.r1 Soares adult brain N2b4HB55Y Homo sapi	6.7
	455851	BE146879		"gbtQV4-HT0222-251099-014-c11 HT0222 Homo sapiens	6.7
	436009	AF063332	Hs.58314	ESTs	6.7
80	418858	AW961605	Hs.21145	"Homo sapiens cDNA: FLJ22489 fls, clone HRC10551"	6.7
	419323	AO52379	Hs.135275	ESTs	6.7
	415317	Z43368	Hs.5570	hypothetical protein FLJ10006	6.7
	418654	AA226334	Hs.154291	ESTs	6.7
	407413	AF067801		"gbtHomo sapiens HDGC21P mRNA, complete cds."	6.7

	439694	AA843915	Hs.54707	ESTs	6.7
	451191	N67900	Hs.118446	ESTs	6.7
	454006	U12775	Hs.37006	agouti (mouse)-signaling protein	6.7
5	443657	R14973		gb:Y4210.s1 Soares fetal liver spleen (NFILS Homo sapien	6.7
	459879	BE153275		"gb:PM0-H10335-180408-008-e11 HT0336 Homo sapiens	6.7
	451368	BE242152	Hs.268417	protein serine threonine kinase Csk4	6.7
	453509	AL040021		gb:DKFZp434N1812.r1 434 (synonym: Ites3) Homo sapie	6.7
	420892	AW575076	Hs.172589	nuclear phosphoprotein similar to S. cerevisiae PWP1	6.7
10	423372	AD245375	Hs.154458	ESTs	6.7
	453316	W84445	Hs.17853	ESTs	6.7
	447795	AW295151	Hs.163612	ESTs	6.7
	413252	BE074910		"gb:RC5-BT0560-170300-021-F12 BT0560 Homo sapiens	6.7
	405771			predicted exon	6.6
15	411483	AW848115		"gb:U3-CT0214-301299-048-C09 CT0214 Homo sapiens c	6.6
	420271	A1954355	Hs.42892	ESTs	6.6
	431948	AA917706	Hs.194616	ESTs	6.6
	409529	AW445589	Hs.279724	ESTs	6.6
	458841	W29555		gb:54410 Human retina cDNA randomly primed sublibrary	6.6
	416565	AW003950	Hs.44970	ESTs	6.6
20	409057	AA677927	Hs.144269	ESTs	6.6
	441832	A1018249	Hs.128062	ESTs	6.6
	457285	A1038658	Hs.228780	"ESTs, Highly similar to AF199597 1 A-type potassium cha	6.6
	406504			predicted exon	6.6
25	414606	BE387771		"gb:50128325.F1 NIH_MGC_44 Homo sapiens cDNA clon	6.6
	452956	AW003578	Hs.231972	ESTs	6.6
	410743	AA089474	Hs.272153	ESTs	6.6
	404599			predicted exon	6.6
	423575	C18663	Hs.163443	"Homo sapiens cDNA FLJ11576 fs, clone HEMBA100354	6.6
30	443027	AA021847	Hs.253350	ESTs	6.6
	458663	AV558444	Hs.280776	"Homo sapiens cDNA FLJ13684 fs, clone PLACE2000021	6.6
	431277	AA501805	Hs.249565	ESTs	6.6
	445232	BE284357		"gb:50112787BF1 NIH_MGC_17 Homo sapiens cDNA don	6.6
	459170	AV525418		"gb:RC-BT091-210159-098 BT091 Homo sapiens cDNA, m	6.6
35	437876	AA770151	Hs.126424	ESTs	6.6
	406752	A1285598	Hs.217493	annexin A2	6.6
	401245			predicted exon	6.6
	446102	AW168067	Hs.252956	ESTs	6.5
40	446898	AV001898	Hs.16740	hypothetical protein FLJ11035	6.5
	421160	AL080215	Hs.102301	Homo sapiens mRNA; cDNA DKFZ586J0323 (from clone	6.5
	458831	H71739	Hs.200227	ESTs	6.5
	408914	AV483009		gb:U1-HB3-alc-q-08-0-U1.s1 NCL_CGAP_Bub5 Homo sa	6.5
	411016	AA813428		"gb:MR3-ST0152-010200-210-c05 ST0152 Homo sapiens c	6.5
	435682	H71937	Hs.169756	"complement component 1, a subcomponent"	6.5
	457620	AA602711		"gb:np03305.s1 NCL_CGAP_P12 Homo sapiens cDNA clon	6.5
45	438847	AA613118	Hs.163230	ESTs	6.5
	433570	T7925	Hs.269165	ESTs	6.5
	419273	BE271190	Hs.293490	ESTs	6.5
	443745	AB039670	Hs.9728	ALEX1 protein	6.5
	431029	BE392725	Hs.248571	Homo sapiens PAC clone RP5-1163J12 from 7q21.2-q31.1	6.5
50	458595	AV660159	Hs.262294	ESTs	6.5
	410956	AW812088		"gb:RC4-ST0173-191099-032-007 ST0173 Homo sapiens c	6.4
	417135	AA422067	Hs.50547	ESTs	6.4
	418441	BE407197		"gb:501301552.F1 NIH_MGC_21 Homo sapiens cDNA clon	6.4
55	413702	BE170213		"gb:OV4-HT0335-040503-193-g02 HT0336 Homo sapiens	6.4
	452563	A1907552		"gb:RC-BT147-120499-044 BT147 Homo sapiens cDNA, m	6.4
	408956	AK001868	Hs.295306	"ESTs, Highly similar to unnamed protein product [Lsapien	6.4
	406349			predicted exon	6.4
	425420	BE535911	Hs.234545	"ESTs, Weakly similar to AF155135 1 novel retina pigmen	6.4
60	459430	AW652886		gb:U182H1.1.x1 Soares_NFL_U_GBC_S1 Homo sapiens cDN	6.4
	425733	F13287	Hs.195388	Homo sapiens clone Z3578 mRNA sequence	6.4
	458678	AA061622	Hs.170938	"ESTs, Weakly similar to KIA00705 protein [Lsapiens]"	6.4
	429855	AA855714	Hs.253556	ESTs	6.4
	426872	AA410446	Hs.112011	"ESTs, Weakly similar to unknown [Lsapiens]"	6.4
65	437152	AL050027		gb:Homo sapiens mRNA; cDNA DKFZp556C0324 (from c	6.4
	440517	AW139532	Hs.132246	ESTs	6.4
	459877	AV796081	Hs.29178	ESTs	6.4
	410654	NM_006033	Hs.65370	"lspase, endothelial"	6.4
	405783			predicted exon	6.4
70	418709	AA227394		gb:R7c10.r1 Striatagene NT2 neuronal precursor 937230 H	6.4
	426884	AA431792	Hs.44784	ESTs	6.4
	448516	AW898595		"gb:RC1-NN0073-260400-011-g09 NN0073 Homo sapiens	6.3
	400983	AF035537		gb:R3 (yeast homolog) Rse, catalytic subunit of DNA poly	6.3
75	422365	BE004257	Hs.115521	"gb:Cub-BN0103-160300-298-c04 BN0103 Homo sapiens	6.3
	401521			predicted exon	6.3
	430290	AF134110	Hs.136355	ESTs	6.3
	414831	AK000342	Hs.77646	Homo sapiens mRNA; cDNA DKFZp761M2223 (from don	6.3
	437539	AW298600	Hs.141940	"ESTs, Weakly similar to S95S01 Interferon receptor JFNA	6.3
	451842	AB295339	Hs.267087	"ESTs, Moderately similar to ALU4_HUMAN ALU SUBF	6.3
80	405810			predicted exon	6.3
	443747	AV646352		"gb:AV646352 GLC Homo sapiens cDNA clone GLCAME	6.3
	427287	NM_014903	Hs.174188	KIA04035 protein	6.3
	413621	BE145814		"gb:MFO-HT0208-101298-202-d04 HT0208 Homo sapiens	6.3
	429090	AW820278	Hs.99066	ESTs	6.3

	451488	H22999	Hs.208846	ESTs	6.3
	455713	BE009891		"gbrCv4-BT0401-201299-064-b01 BT0401 Homo sapiens	6.3
	452161	RA3077	Hs.221747	ESTs	6.3
	428647	AA830050	Hs.124344	ESTs	6.3
5	445053	AI246275	Hs.149196	ESTs	6.3
	455671	AB011142	Hs.114293	KIAA0570 gene product	6.3
	401508			predicted exon	6.3
	412677	AW025608	Hs.17384	ESTs	6.3
10	441720	AI346487	Hs.28739	ESTs	6.3
	418251	AW182535	Hs.19479	ESTs	6.3
	438014	N71163	Hs.121505	"Homo sapiens cDNA FLJ11971 fls, clone HEM88100120	6.3
	432101	AI918950	Hs.111092	"Homo sapiens cDNA FLJ14250 fa, clone PLACE1006795	6.3
	421032	AW293133	Hs.101340	ESTs	6.3
	435532	AA721622		"gbrv54h12.r1 NCL CGAP_Ew1 Homo sapiens cDNA clo	6.3
15	431318	AA592700	Hs.293147	ESTs	6.3
	413470	N20934		gbrv54c11.a1 Soares melanocyte 2N01M Homo sapiens c	6.3
	402425			predicted exon	6.3
	455593	BE179065		"gbrRCO-HT0613-140300-021-006 HT0613 Homo sapiens	6.3
	400160			predicted exon	6.3
20	413795	AL040178	Hs.142003	ESTs	6.2
	405071			predicted exon	6.2
	403741			predicted exon	6.2
	432469	AJ804855	Hs.207530	ESTs	6.2
	402296			predicted exon	6.2
25	446091	AW022192	Hs.200197	ESTs	6.2
	444768	AJ871122	Hs.207821	ESTs	6.2
	404972			predicted exon	6.2
	400227			predicted exon	6.2
30	433804	AJ365561	Hs.112740	ESTs	6.2
	448807	AJ571940	Hs.7549	ESTs	6.2
	404340			predicted exon	6.2
	424632	AB014523	Hs.151406	KIAA0523 gene product	6.2
	449547	H93543	Hs.117963	ESTs	6.2
	409945	K01363	Hs.203967	metallothionein 1A [functional]	6.2
35	433863	AF053131	Hs.225535	CAT-15 protein	6.2
	407809	AW082279	Hs.244106	ESTs	6.2
	418342	BE002723	Hs.293504	"ESTs, Moderately similar to ALU1_HUMAN ALU SUBF	6.2
	438007	AA133008	Hs.158675	ribosomal protein L14	6.2
	410536	K25533		gbrv204a.s1 Soares fetal liver spleen 1NFLS Homo sapie	6.2
40	448005	AW207437	Hs.170376	ESTs	6.2
	414083	AL121282	Hs.257786	ESTs	6.2
	405382			predicted exon	6.2
	410102	AW248508	Hs.279727	"Homo sapiens cDNA FLJ14405 fls, clone HEMBA100463	6.2
45	457868	AW975133		"gbrEST3677239 MAGE resequences, MAGN Homo sapien	6.2
	407395	AF025082		"gbrHomo sapiens skin-specific protein (p33) mRNA, part	6.2
	443503	BE392691	Hs.134269	"ESTs, Weakly similar to KIAA1063 protein [H.sapiens]	6.2
	433051	AA454611	Hs.52515	transducin (beta)-like 2	6.1
	434569	AJ311295	Hs.58609	ESTs	6.1
	430481	AA479678	Hs.203269	"ESTs, Moderately similar to ALU8_HUMAN ALU SUBF	6.1
50	402859			predicted exon	6.1
	401280			predicted exon	6.1
	406544			predicted exon	6.1
	428446	AJ024600	Hs.98612	ESTs	6.1
55	412246	AI168873	Hs.69223	"ESTs, Weakly similar to KIAA1064 protein [H.sapiens]	6.1
	404020	AJ277247	Hs.287369	Inteinidin 22	6.1
	455682	BE065387		"gbrRC1-BT0314-030500-016-003 BT0314 Homo sapiens	6.1
	428613	AB037749	Hs.186928	KIAA1328 protein	6.1
	443267	AAW50630	Hs.133851	ESTs	6.1
	433405	AY167666	Hs.156892	ESTs	6.1
60	416795	AA577778	Hs.168053	"ESTs, Highly similar to AF227948 1 HBV pX associated p	6.1
	435705	W31254	Hs.7046	GL004 protein	6.1
	450769	AA257418	Hs.136554	ESTs	6.1
	427174	AJ359848	Hs.87541	ESTs	6.1
	425369	AA974499	Hs.192183	ESTs	6.1
65	416675	H73802	Hs.35381	ESTs	6.1
	432749	NM_014438		Interleukin-1 Superfamily e	6.1
	401809			predicted exon	6.1
	403041			predicted exon	6.0
70	485823	AW833259		"gbrRC2-TT0007-131099-011-c01 TT0007 Homo sapiens c	6.0
	416515	N91716	Hs.194140	ESTs	6.0
	425291	BE173164	Hs.1518	heparin-like growth factor-binding protein 4	6.0
	437146	AA730977		"gbrv55105.s1 NCL CGAP_Ew1 Homo sapiens cDNA clo	6.0
	450094	AI174947	Hs.295789	Homo sapiens mRNA; cDNA DKFZp564D1164 (from clon	6.0
	402529			predicted exon	6.0
75	430706	NM_003540	Hs.247616	"H4 histone family, member C"	6.0
	459186	AY08287		"gbrRC-BT168-020499-035 BT168 Homo sapiens cDNA, m	6.0
	452158	AB99120	Hs.61188	ESTs	6.0
	411237	AW833576		"gbrCv4-TT0008-181159-038-004 TT0008 Homo sapiens	6.0
	400441	MI1530	Hs.99879	B-cell growth factor 1 (12kD)	6.0
80	439398	AA284267	Hs.221504	ESTs	6.0
	440862	H39048	Hs.127432	ESTs	6.0
	415451	II19415	Hs.266920	"ESTs, Moderately similar to ALU1_HUMAN ALU SUBF	6.0
	459387	AA031658		gbrv15c0a.s1 Soares prenatant mouse_NH-FPU Homo sapl	6.0
	456072	HS4381		gbrv38a03.s1 Soares fetal liver spleen 1NFLS Homo sapio	6.0

5	409954	AW512770	Hs.286457	ESTs	6.0
	443486	AU73408	Hs.133912	"ESTs, Weakly similar to methyl-CpG binding domain-cont	6.0
	430625	AF734186	Hs.185105	ESTs	6.0
	454466	AA984138	Hs.279895	"Homo sapiens mRNA for KIAA1578 protein, partial cds"	6.0
	456508	AA278277	Hs.194212	ESTs	6.0
10	449228	AJ432107	Hs.146950	"ESTs, Weakly similar to AF208946 1 BM-004 [H.sapiens], "g1:EST386776 MAGE sequences, MAGM Homo sapien	6.0
	457727	AW974387	Hs.146180	"ESTs, Weakly similar to non-receptor protein tyrosine kina	6.0
	424440	BE464435		"g1:PKM0-IT0343-281299-003-e06 HT0343 Homo sapiens	5.9
	455110	BE154506		predicted exon	5.9
	422700			"g1:RC2-BN0120-250400-012-03 BN0120 Homo sapiens	5.9
15	405982	BE005839		lumen protein p53-binding protein	5.9
	427635	BE397988	Hs.179982	predicted exon	5.9
	408948	AW296713	Hs.221441	ESTs	5.9
	402046			predicted exon	5.9
	416438	R89238	Hs.34262	ESTs	5.9
20	403083			predicted exon	5.9
	402481			predicted exon	5.9
	420867	AW502161		"g1:HF-BR09-df-p-12-0-Ulr1 NIH_MGC_S2 Homo sap	5.9
	420362	U97734	Hs.97206	huntinglin interacting protein 1	5.9
	421375	AA489200	Hs.100595	"ESTs, Moderately similar to ALU1_HUMAN ALU SURF	5.9
25	437630	AC257282	Hs.163029	ESTs	5.9
	443500	AV464388	Hs.137071	ESTs	5.9
	448595	AB133276	Hs.5662	"guanine nucleotide binding protein (G protein), beta poly	5.9
	439214	H06076	Hs.26320	TRIAB1 protein	5.9
	428046	AW812795	Hs.155381	"ESTs, Moderately similar to 136022 hypothetical protein p1	5.9
30	431941	AK000106	Hs.272227	"Homo sapiens cDNA FLJ20099 fs, clone COL04544"	5.9
	403355			predicted exon	5.9
	439031	AF075079		g1:Homo sapiens full length insert cDNA YQ80A08	5.9
	430032	AW936136	Hs.99810	ESTs	5.9
	422457	F08208	Hs.165608	paired mesoderm homeo box 1	5.9
35	422169	L10343	Hs.112341	"protease inhibitor 3, skin-derived (SKALP)"	5.9
	406592			predicted exon	5.9
	418636	AW749855		"g1:CV4-ET0534-281299-053-c05 ET0534 Homo sapiens	5.8
	428395	AA52244	Hs.161727	ESTs	5.8
	408590	AW291652	Hs.263873	ESTs	5.8
40	422168	AA586894	Hs.112408	S100 calcium-binding protein A7 (psoriasin 1)	5.8
	417421	AL138201	Hs.82120	"nuclear receptor subfamily 4, group A, member 2"	5.8
	401129			predicted exon	5.8
	434745	AW974445	Hs.185155	"ESTs, Weakly similar to HuEMAP [H.sapiens]"	5.8
	402800			predicted exon	5.8
45	436185	AW753380	Hs.49753	"Homo sapiens mRNA for KIAA1661 protein, partial cds"	5.8
	418519	AI198719	Hs.176376	ESTs	5.8
	425242	AW812256		"g1:RC0-ST0174-191099-031-a07 ST0174 Homo sapiens c	5.8
	427166	AA431576	Hs.165656	ESTs	5.8
	418168	H23587	Hs.266398	g1:cyt72h12r1 Soares adult brain N26S9H6597 Homo saple	5.8
50	431467	NT1851	Hs.266398	Homo sapiens mRNA; cDNA DN72p43HE0528 (from clon	5.8
	421558	AB011125	Hs.105746	KIA09553 protein	5.8
	458055	AW979121	Hs.131375	"ESTs, Weakly similar to ALU8_HUMAN III ALU CLAS	5.8
	418345	AJ001696	Hs.241407	"serine (or cysteine) proteinase inhibitor, clade B (ovalbumi	5.8
	425544	AA402325		g1:ngb11h1.s1 NCI_CGAP_P6 Homo sapiens cDNA clone	5.8
55	433544	AJ793211	Hs.165372	"ESTs, Moderately similar to ALU1_HUMAN ALU SURF	5.8
	442007	AA301116	Hs.142838	"Homo sapiens cDNA: FLJ23444 fs, clone HSI01343"	5.8
	443422	R10288	Hs.301529	ESTs	5.8
	434311	BE543469	Hs.266263	"Homo sapiens cDNA FLJ11115 fs, clone MAMMA10017	5.8
	424968	AJ077312	Hs.153985	"solute carrier family 7 (cationic amino acid transporter, y+	5.8
60	441744	AA960922	Hs.200938	ESTs	5.7
	413101	BE085215		"g1:RC1-BT0314-310300-015-01 BT0314 Homo sapiens c	5.7
	456587	W03032	Hs.145297	ESTs	5.7
	441369	AA931535		g1:ov056d04.s1 NCI_CGAP_Lu5 Homo sapiens cDNA clone	5.7
	414428	BE269606	Hs.182625	VAMP (vesicle-associated membrane protein)-associated pr	5.7
65	431211	M05849	Hs.5566	"gap junction protein, beta 2, 29kD (connexin 26)"	5.7
	411541	W03940		g1:zab2602r1 Soares fetal liver spleen INFLS Homo sapien	5.7
	448612	AI096363	Hs.171285	ESTs	5.7
	419118	AA234223	Hs.139204	ESTs	5.7
	405322			predicted exon	5.7
70	454990	AW854639		"g1:MRI-CT0258-140100-203-010 CT0258 Homo sapiens	5.7
	450313	AD039893	Hs.24809	hypothetical protein FLJ10826	5.7
	416292	AA179233	Hs.42390	nasopharyngeal carcinoma susceptibility protein	5.7
	443009	AW589823	Hs.224189	ESTs	5.7
	408416	AW953897	Hs.44743	KIAA1435 protein	5.7
75	416100	HI18700	Hs.266799	ESTs	5.7
	437845	AA769578	Hs.90488	ESTs	5.7
	443345	AA052508	Hs.164482	"ESTs, Weakly similar to contains similarity to TFR domain	5.7
	418407	AL044818	Hs.94929	"nuclear transcription factor Y, beta"	5.7
	434557	AW854666	Hs.271866	"ESTs, Weakly similar to ALU1_HUMAN ALU SURFAM	5.7
80	431658	AA513506		g1:ngb7c08.s1 NCI_CGAP_Lip2 Homo sapiens cDNA do	5.7
	437841	AA811452	Hs.291911	ESTs	5.7
	405319	AW972706	Hs.133665	ESTs	5.7
	403957	AF030107	Hs.17165	regulator of G-protein signaling 13	5.7
	445189	AJ935450	Hs.147482	ESTs	5.7
	414418	HE2643	Hs.154188	ESTs	5.7
	446563	BE326508	Hs.141454	ESTs	5.7
	446075	AAW451457	Hs.279179	ESTs	5.7
	428058	AW016437	Hs.233462	ESTs	5.7

438425	A4292922	Hs.293170	ESTs	5.7
415532	R14780	Hs.12826	ESTs	5.7
441442	AL043282	Hs.131824	ESTs	5.7
443380	AJ792478	Hs.135377	ESTs	5.7
445527	W33694	Hs.83286	ESTs	5.7
414376	BC383856	Hs.68915	ESTs, Weakly similar to 16.7kd protein [Lsapiens]	5.7
457960	AA771881	Hs.298149	ESTs	5.6
453293	AA382267	Hs.10553	ESTs	5.6
452503	AB000509	Hs.29736	TNF receptor-associated factor 5	5.6
405227			predicted exon	5.6
442257	AW503831		gb:U44F-BN0-atb-b-05-0-U1r1 NIH_MGC_50 Homo sap	5.6
403403			predicted exon	5.6
454377	AA076811		gb:7B03C12 Chromosome 7 Fetal Brain cDNA Library Hom	5.6
430656	H85310	Hs.209456	"ESTs, Weakly similar to NC22 [Lsapiens]"	5.6
419936	AJ792788		"gc:bc11d05.y5 NC1_CGAP_JG45 Homo sapiens cDNA clo	5.6
437267	AW511443	Hs.258110	ESTs	5.6
430583	AA481269	Hs.178381	ESTs	5.6
444835	AI190904	Hs.155479	ESTs	5.6
444902	AJ132099	Hs.12114	varin 1	5.6
451800	AW577435	Hs.31850	ESTs	5.6
405485			predicted exon	5.6
403891			predicted exon	5.6
425557	AB594300	Hs.45730	ESTs	5.6
432182	AA584052	Hs.272798	hypothetical protein FLJ20413	5.6
450152	AJ139635	Hs.22368	ESTs	5.6
410063	AW573107	Hs.29332	ESTs	5.6
421285	NM_000102	Hs.1363	"cytochrome P450, subfamily XVII (steroid 17-alpha-hydro	5.6
425264	AA363953	Hs.20369	"ESTs, Weakly similar to gonadotropin inducible transcript	5.6
415844	M62982	Hs.1200	arachidonic 12-lipoxygenase	5.6
429816	AB92722	Hs.12045	ESTs	5.6
423528	AB011137	Hs.129740	KIAA0565 gene product	5.6
403089			predicted exon	5.6
414373	AW162907	Hs.75969	proline-rich protein with nuclear targeting signal	5.6
403687			predicted exon	5.6
417079	U65590	Hs.81134	interleukin 1 receptor antagonist	5.5
432501	BE546532	Hs.287329	Fas binding protein 1	5.5
403691			predicted exon	5.5
403845	BE296182		"gb:00117732F1 NIH_MGC_17 Homo sapiens cDNA don	5.5
435990	AI015862	Hs.131753	ESTs	5.5
444409	AJ792140	Hs.49265	ESTs	5.5
435478	AA682622		gb:20108.s1 Soares fetal liver spleen, INFL5_S1 Homo	5.5
430961	AA344008	Hs.124575	"ESTs, Weakly similar to unnamed protein product [Lsapi	5.5
433544	AW342028	Hs.256112	ESTs	5.5
441541	AA938663	Hs.199828	ESTs	5.5
400709			predicted exon	5.5
407615	AW753085		"gb:PM1-CT0247-151299-005-at03 CT0247 Homo sapiens	5.5
424153	AA651737	Hs.141496	MAGE-8a 2	5.5
452465	AA610211	Hs.34244	ESTs	5.5
406330			predicted exon	5.5
431071	AA491379		"gb:af16075.r1 NC1_CGAP_GCB1 Homo sapiens cDNA cl	5.5
418086	AA211791	Hs.269666	"Homo sapiens cDNA FLJ13415 f1s, clone PLACE1001799	5.5
453034	BE246010	Hs.184109	ribosomal protein L37a	5.5
412953	Z45794	Hs.238809	ESTs	5.5
425381	AJ206234	Hs.155924	cAMP responsive element modulator	5.5
406149			predicted exon	5.5
416533	BE244053	Hs.79362	retinoblastoma-like 2 (p13)	5.5
456378	AD040535	Hs.150624	ESTs	5.5
401213			predicted exon	5.5
405904			predicted exon	5.5
445132	Z44811		gb:HSC29G031 normalized infant brain cDNA Homo sapie	5.5
445138			predicted exon	5.5
447238	AW135374	Hs.270949	ESTs	5.5
416852	AF283776	Hs.80285	Homo sapiens mRNA; cDNA DKFpZ586C1723 (from don	5.5
446691	AA481119	Hs.283558	hypothetical protein PRO1855	5.5
452242	BC383856	Hs.68915	"ESTs, Weakly similar to AF157318 1 AD-617 protein [Ls	5.5
456994	AA383623	Hs.293616	ESTs	5.5
440913	AJ267491	Hs.160593	ESTs	5.5
435380	AA679001	Hs.192221	ESTs	5.5
453375	AA029647	Hs.28550	a disintegrin and metalloproteinase domain 12 (meltrin alph	5.5
414035	Y00530	Hs.75716	"serine (or cysteine) proteinase inhibitor, clade B (ovalbum	5.4
455084	H01699	Hs.277289	CGI-125 protein	5.4
405687	BE544857		predicted exon	5.4
447396	AJ373163	Hs.170333	"gb:001078872F1 NIH_MGC_12 Homo sapiens cDNA don	5.4
413083	BE064528		ESTs	5.4
404828			predicted exon	5.4
427543			predicted exon	5.4
421988	AW450481	Hs.161333	ESTs	5.4
413404	BE503463	Hs.297431	ESTs	5.4
459043	AB064444	Hs.208113	"ESTs, Weakly similar to N-WASP [Lsapiens]"	5.4
404410			predicted exon	5.4
453094	AA470519		"gb:07110.s1 NC1_CGAP_P1 Homo sapiens cDNA don	5.4
431499	NM_001514	Hs.258561	general transcription factor IIB	5.4
412566	AW962574		"gb:EST374547 MAGE resequences, MAGG Homo sapien	5.4

	454238	BE176420	Hs.8177	ESTs	5.4
	458183	AA484304	Hs.131163	ESTs	5.4
	446206	AW172652	Hs.145479	ESTs	5.4
	455275	AW977806		"gb:ES T388810 MAGE resequences, MAGO Homo sapien	5.4
5	415579	AA165232	Hs.222089	ESTs	5.4
	423200	AA323073	Hs.289583	ESTs	5.4
	440052	AB53744	Hs.195648	ESTs	5.4
	424717	H03754	Hs.152213	"wingless-type MMTV integration site family, member 5A"	5.4
	420111	AA355652		gb:z21h11.r1 NC_CGAP_GCB1 Homo sapiens cDNA do	5.4
10	432140	AK020404	Hs.272688	hypothetical protein FLJ20397	5.4
	414904	AA157881	Hs.143056	ESTs	5.4
	409479	BE136300	Hs.135912	ESTs	5.4
	404727			predicted exon	5.4
	440111	AB237778	Hs.145509	ESTs	5.4
15	456093	UA6922	Hs.77252	fragile histidine triad gene	5.4
	424834	AK001432	Hs.163408	"Homo sapiens cDNA FLJ10570 fs, clone NT2RP2003117	5.4
	425071	NM_013989	Hs.154424	"cisdinase, lisdihydrinase, type II"	5.4
	425065	H32045		gb:z56g96.5 Soares_placenta_8to9weeks_2NbHPSo9W	5.4
	415602	F12920	Hs.165575	ESTs	5.4
20	428939	AA579465	Hs.287332	ESTs	5.4
	416879	H98999	Hs.42599	ESTs	5.4
	456088	BE171322	Hs.156148	"Homo sapiens cDNA: FLJ23082 fs, clone LMG06451"	5.4
	423175	W27556	Hs.15853	ESTs	5.4
	424585	AA64840		gb:z43h11.r1 Soares_Jolad_fetus_Nb2HF9_9w Homo sapie	5.4
25	452281	T33500	Hs.28792	"Homo sapiens cDNA FLJ11041 fs, clone PLACE1004405	5.3
	424323	AA330791	Hs.146763	hypocell-poly(epsilon)-associated complex alpha polypeptide	5.3
	426701	AI968103	Hs.209461	"Homo sapiens cDNA FLJ12836 fs, clone NT2P2003206	5.3
	447645	AW897321	Hs.159599	ESTs	5.3
	402974			predicted exon	5.3
30	438607	AW881783	Hs.211061	ESTs	5.3
	428873	AI701609	Hs.98908	ESTs	5.3
	405454			predicted exon	5.3
	431967	AA523690	Hs.191727	ESTs	5.3
35	427282	ALD48534	Hs.48458	"ESTs, Weakly similar to ALUR_HUMAN ALU SUBFAM	5.3
	424085	NM_002914	Hs.139226	replication factor C (activator 1) 2 (40kD)	5.3
	435098	AF174394	Hs.177461	"Homo sapiens apoptotic-related protein PCAR mRNA, par	5.3
	421284	U62435	Hs.103128	"cholinergic receptor, nicotinic, alpha polypeptide 6"	5.3
	435711	AF228667	Hs.58353	CTP synthase II	5.3
	405252			predicted exon	5.3
40	410123	T18981	Hs.21963	ESTs	5.3
	435435	T89473	Hs.192326	ESTs	5.3
	417071	H58820	Hs.276133	ESTs	5.3
	438958	H50167	Hs.33113	ESTs	5.3
45	457405	AA504860		gb:ab03a10.s1 Stratagene fetal refina 937202 Homo sapiens	5.3
	413542	BE154837		"gb:PM1-11T0345-121199-001-c08 HT0345 Homo sapiens	5.3
	433868	AA512950		gb:z6g50.5.1 NC_CGAP_Co10 Homo sapiens cDNA do	5.3
	444461	R53734	Hs.25976	ESTs	5.3
	427088	AA359085	Hs.142330	ESTs	5.3
50	451307	AW293207	Hs.211516	ESTs	5.3
	402931			predicted exon	5.3
	402892			predicted exon	5.3
	433420	AB574093	Hs.293961	ESTs	5.3
	455750	BE080469		"gb:OV1-BT0630-280500-085-d06 BT0630 Homo sapiens	5.3
55	411379	AB115344	Hs.12554	"ESTs, Weakly similar to Nucleosome Assembly Protein 1-	5.3
	428483	AY908539	Hs.184592	KIAA0344 gene product	5.3
	429208	AA447990	Hs.190478	ESTs	5.3
	447572	AB311546	Hs.159732	ESTs	5.3
	434806	AW022054	Hs.136591	ESTs	5.3
	417616	R07728	Hs.286698	ESTs	5.3
60	411805	AW864183		"gb:PM0-SN0014-260400-002-d02 GN0014 Homo sapiens	5.3
	419000	T9855	Hs.286592	ESTs	5.3
	413468	BE144017	Hs.184693	"transcription elongation factor B (SII), polypeptide 1 (1k	5.3
	400975			predicted exon	5.3
	407453	AJ132087		gb:Homo sapiens mRNA for axonemal dynein heavy chain (5.3
65	430757	AA58622		"gb:h0g09.s1 NC_CGAP_Lu24 Homo sapiens cDNA do	5.3
	417753	AA054504	Hs.82575	small nuclear ribonucleoprotein polypeptide 6"	5.3
	401877	AB011094	Hs.129892	KIAA0522 protein	5.2
	457122	AD026157	Hs.33728	"ESTs, Weakly similar to ALU1_HUMAN ALU SUBFAM	5.2
	410708	AT732404	Hs.68846	ESTs	5.2
70	435907	AK032829	Hs.113814	ESTs	5.2
	428398	AA243688	Hs.98558	ESTs	5.2
	401098			predicted exon	5.2
	414501	N43991	Hs.171584	ESTs	5.2
	419053	AA073560	Hs.98613	"Homo sapiens cDNA FLJ12282 fs, clone MAMMA10018	5.2
75	421107	AA283822	Hs.55606	"ESTs, Weakly similar to ZNF91_HUMAN ZINC FINGER P	5.2
	411489	AW948346		"gb:LC1-CT0214-150200-076-F03 CT0214 Homo sapiens c	5.2
	419249	X14767	Hs.89768	"gamma-aminobutyric acid (GABA) A receptor, beta 1"	5.2
	420082	AW514083	Hs.159135	ESTs	5.2
	425638	NM_016112	Hs.159241	polycystic kidney disease 2-like 1	5.2
80	451686	AA059246	Hs.110293	ESTs	5.2
	453687	AG29383	Hs.108198	HSPD037 protein	5.2
	411985	H66373	Hs.15973	"ESTs, Highly similar to bA383316.3 [Hsapiens]"	5.2
	426650	AA382814		"gb:EST96097 Testis 1 Homo sapiens cDNA 5' end, mRNA	5.2
	424115	AA335497	Hs.293985	ESTs	5.2

	405675		predicted exon	5.2
	409584	AA076010	gbczm8912a.1 Striatagene ovarian cancer (937219) Homo sa	5.2
	454423	AW603985	Hs.179662 nucleosome assembly protein 1-like 1	5.2
	417173	U51397	Hs.81424 ubiquitin-like 1 (centrin)	5.2
5	439155	H61076	Hs.262021	5.2
	432267	AK006672	Hs.274227 "Homo sapiens cDNA FLJ10010 f1a, clone HEMBA100030	5.2
	459024	AA020799	Hs.179825 RAN binding protein 2-like 1	5.2
	404088		predicted exon	5.2
10	403525		predicted exon	5.2
	445862	AJ948717	Hs.225155 "ESTs, Weakly similar to PSF_HUMAN PTB-ASSOCIATE	5.2
	448257	AW772070	Hs.253146 ESTs	5.2
	410500	R09442	gby26c09.1 Soares fetal liver spleen 1NFLS Homo sapien	5.2
	456084	AA155559	Hs.79709 ESTs	5.2
	410523	BE143339	"gbc-hR010164-151299-012-003 HT0164 Homo sapiens	5.2
15	434623	AB023163	Hs.4014 KIAA0946 protein; Huntingtin interacting protein H	5.2
	454484	AW795196	Hs.215857 ring finger protein 14	5.2
	402131		predicted exon	5.2
	438913	AK380429	Hs.172445 ESTs	5.2
	402628		predicted exon	5.1
20	415973	R24707	Hs.250201 ESTs	5.1
	455540	BE064059	"gbc-CV3-BT0296-010300-111-e04 BT0296 Homo sapiens	5.1
	442750	AK016503	Hs.131096 ESTs	5.1
	404638		predicted exon	5.1
	431117	AF003922	Hs.250600 delta (Drosophila)-like 1	5.1
25	428819	AL135523	Hs.153914 KIAA0675 gene product	5.1
	435610	AA037118	Hs.118306 ESTs	5.1
	427335	AA448542	Hs.251677 G antigen 7B	5.1
	416450	AA180467	Hs.142556 ESTs	5.1
	440876	AW613324	Hs.279570 ESTs	5.1
30	414584	BE400585	"gbc-b01301836F1 NIH_MGC_21 Homo sapiens cDNA clone	5.1
	443175	N57863	gbc-y60C02a.1 Soares fetal liver spleen 1NFLS Homo sapie	5.1
	408998	AB052236	Hs.49376 hypothetical protein FLJ20544	5.1
	415654	AW958363	"gbc-EST380439 MAGE resequences, MAGE Homo sapiens	5.1
	440559	AW929054	Hs.125976 "ESTs, Weakly similar to metalloproteinase/dintegrin/hydel	5.1
35	421236	AB287622	Hs.151956 ESTs	5.1
	416258	N45661	Hs.275131 ESTs	5.1
	405982		predicted exon	5.1
	405589		predicted exon	5.1
40	412458	AW953229	Hs.169142 ESTs	5.1
	435693	AK031134	Hs.119887 ESTs	5.1
	449182	AW292381	Hs.224150 ESTs	5.1
	402363		predicted exon	5.1
	440830	AT733112	Hs.176101 ESTs	5.1
	415412	F08049	Hs.52132 ESTs	5.1
45	442832	AW206560	Hs.253569 ESTs	5.1
	445359	AB08725	Hs.147783 ESTs	5.1
	412088	AB089496	Hs.108932 ESTs	5.1
	428785	AK015953	Hs.125265 ESTs	5.1
50	430163	X66610	Hs.234748 "melase alpha, lung-specific"	5.1
	455441	AW545954	"gbc-CVD-ET0001-055059-228-e09 ET0001 Homo sapiens c	5.1
	400304	AF005082	Hs.113261 "Homo sapiens skin-specific protein (xp33) mRNA, partial	5.1
	403944		predicted exon	5.1
	457069	BE159191	Hs.114318 "ESTs, Weakly similar to ORF1 [Lupatini]"	5.1
	414125	BE233197	"gbc-D0116804F1 NIH_MGC_16 Homo sapiens cDNA clone	5.1
55	448566	AW291319	Hs.194574 ESTs	5.1
	457948	AA98640	Hs.159354 ESTs	5.1
	432640	N92638	Hs.124004 ESTs	5.1
	494070		predicted exon	5.1
	422709		predicted exon	5.1
60	415425	BE077308	"gbc-RC1-BT0506-060200-012-b12 BT0506 Homo sapiens	5.0
	407173	T64349	gbyc10488.s1 Striatagene lung (937210) Homo sapiens cDN	5.0
	452602	AB942956	"gbc-FM-ET0045-220199-266_1 ET0045 Homo sapiens cDNA	5.0
	446657	AK335191	Hs.260702 "ESTs, Moderately similar to ALU7_HUMAN ALU SUBF	5.0
	459124	AW201478	Hs.299178 ESTs	5.0
65	409940	BE346143	"gbc-b01073109F1 NIH_MGC_12 Homo sapiens cDNA clone	5.0
	443547	AW271273	Hs.23767 "Homo sapiens cDNA FLJ12665 f1a, clone HT2744A00225	5.0
	447452	BE561928	Hs.102480 ESTs	5.0
	414327	BE408145	Hs.185254 "ESTs, Moderately similar to NAC-1 protein [R/nonvegicus]	5.0
	416155	AB072824	Hs.205442 "ESTs, Weakly similar to AF117610 1 inner centromere pro	5.0
70	408391	AK651657	Hs.167409 ESTs	5.0
	426834	AK015333	Hs.135167 ESTs	5.0
	433368	AW677277	"gbc-MR4-PT0051-150200-001-403 PT0051 Homo sapiens	5.0
	433398	AW190593	Hs.151143 ESTs	5.0
75	439721	AW22142	Hs.271963 "ESTs, Weakly similar to ALLUS_HUMAN ALU SUBFAM	5.0
	441818	AK30451	Hs.7976 KIAA0332 protein	5.0
	458804	AL157625	gbc-DKF2p76L10L21.61 t761 (synonym: harry2) Homo sapl	5.0
	411905	BE265067	"gbc-b01193693F1 NIH_MGC_7 Homo sapiens cDNA clone	5.0
	424248	AA628151	Hs.187783 ESTs	5.0
80	423687	AW267567	Hs.11941 "Homo sapiens cDNA: FLJ21432 f1a, clone COL04219"	5.0
	456212	N51635	gbyb7b01.s1 Soares multiple sclerosis_2bNHASP Homo	5.0
	442514	AW186551	"Homo sapiens cDNA FLJ14007 f1a, clone Y73AA1002407	5.0
	436394	AK020185	"gbc-Homo sapiens cDNA FLJ20178 f1a, clone COL00999"	5.0
	442952	AW594492	Hs.253316 ESTs	5.0
	454653	AW812227	"gbc-RC2-ST0173-20199-011-g09 ST0173 Homo sapiens c	5.0

5	414698	AB15523	Hs.78930	*tryculetin, alpha (non A4 component of amyloid precursor)	5.0
	443335	T89097	Hs.16645	ESTs	5.0
	448419	AL080072	Hs.21195	Homo sapiens mRNA; cDNA DKFZ564A0616 (from clone	5.0
	425574	AA325963		"gb:ES T68717 Fetal lung II Homo sapiens cDNA 5' end, mR	5.0
	435174	AA873718	Hs.194624	ESTs	5.0
	425648	AW138812	Hs.155286	ESTs	5.0
	450613	AF020555		"gb:ta20g10.1 NCL CGAP_U11 Homo sapiens cDNA clyp	5.0
	400432	AX015809	Hs.287757	Sequence 8 from Patent WO9502025	5.0
10	421751	AW813731	Hs.159153	ESTs	5.0
	425900			predicted exon	5.0
	429430	AC01837	Hs.155335	ESTs	5.0
	439518	W76326		gb:z60d04.r1 Soares_fetal_heart_NbH19HW Homo sapiens	5.0
	432884	AF053748	Hs.248114	glial cell derived neurotrophic factor	5.0
15	427411	BC362011	Hs.33503	"Homo sapiens cDNA FLJ11344 fa, clone PLACE1010670	5.0
	441001	AW137017	Hs.126373	Human DNA sequence from clone RPS-1184F4 on chromos	5.0
	438490	AW593272	Hs.26261	ESTs	5.0
	408170	AW204516	Hs.31835	ESTs	5.0
	449104	R08702		gb:z74c06.r1 Soares fetal liver spleen 1NFLS Homo sapien	5.0
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	Phy: Unique Eos probe set identifier number				
	CAT number: Gene cluster number				
	Accession: Genbank accession numbers				
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	408391	1055687_1	AW859276 AW859274 AW190959 T91463		
	408523	1063925_1	AW833259 AW833273 AW0206845		
30	408914	1063828_1	AW540309		
	409687	105308_1	*H85615 H86300 H86263 H86282 AA059278 H86304		
	409191	1107176_1	AW818390 AW818237 AW658911 AW658977 BE072544 W26498		
	409545	1138823_1	BE298182 AW629821		
	409584	114165_1	AA076010 AA076009 AA094314		
35	409695	114676_1	AA298961 AA298669 AA076945 AA077528 AA077487		
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	409887	1158530_1	AW502181 AW502587 AW502345		
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	409982	116302_1	BE003639 AW065618 AW516815		
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	411178	1234752_1	AW8520852 AW820773 AW821088		
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			AW954789 AW954823 AW954802 AW954802 AW954800 AW954799 AW954825 AW954821 AW954820 AW954808 AW954809		
			AW954812 AW954801 AW954813 AW954778 AW954804 AW954758 AW954807 AW954807		
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	141286	143094_1	BE287834 BE51189 BE514096
	141315	143512_1	Z24578 AA49088 F1354 AA494040 AA143127
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	141594	1464086_1	BE409385
	141605	1465799_1	BE390440
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	141854	1509697_1	D81422 C16494 D61078 D61313 D80399 D81520
	151126	151126_1	C18200 D7881 R1025
	151613	1540602_1	R20233 F12901 T74740
	151654	154135_1	AW968063 AA465492 R34539 AA165411
	151715	1548918_1	F03364 F35559 T15435
15	151747	155189_1	AA31209 AA391245 AA167683
	151611	1573926_1	T26661 Z44136 H23016
	151618	1574546_1	H23687 H46460 H40239
	151625	159398_1	BE077398 AL043350 AW952170 AA180251 AA325267
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	161734	166827_1	AW939713 AA149585
25	161749	168700_1	AA203651 R89136
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	161782	1697298_1	W95951 R08466 R87183
	161836	177402_1	AW749855 AA223995 AW750208 AW750206
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	161753	187763_1	N42531 W25700 AA248574 AA569553
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	164385	241151_1	AA464840 AA343628
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	165612	253969_1	BE004457 AW811190 AA360576 BE172402 BE181703
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	169163	300543_1	AA884768 AW974271 AA922975 AA447312
	169264	315008_1	AA470519 BE303010 BE302954 BE384120
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	162363	345468_1	AA534489 AW970240 AW970323
	162966	355839_1	AA650114 AW974148 AA572946
	163398	364276_1	AW877277 AW811294
	163449	366572_1	AW772822 AW552674
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	164804	393491_1	AA649630 AA653316 H54973
	164950	398061_1	AW974892 AA654375
	165478	406683_1	AA682622 BE141695
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	167096	433005_1	AA744406 AA745347 AA465535
	167146	43371_1	AA732977 A1261564 AA334473 Z45283 AW675661 AW938044 BE150701 AW936262 AA306882 BE655075 BE567380 AA728920 AA167612
70	167152	43386_1	AA267685 A1261152 AA485791 BE568425 AW562958
	167229	434947_1	AL050027 BE089051
	169031	467898_1	AW976005 AA149264 AA747275 AA810377
	169152	469201_1	AF075079 H48601 H48755
75	169518	47334_1	H65014 A7086007 H65015
	169518	48426_2	W76326 AF086341 W72300
	169518	48426_2	BE559980 BE397203 BE268207 BE559764 BE267725 BE513654 BE268742 BE268219 BE267665 BE561356
	169518	48426_2	BE274581 BE275382 AA703515 BE166690
	169518	48426_2	AA931535 AA486801 Z49193
	169518	48426_2	AA503831 AW503317 BE565665
80	169518	48426_2	A038316 A1344631 A1261653
	169518	48426_2	N57863 A038952 W90167 N54103
	169518	48426_2	A038931 A163444 Z401 Z1 A951414 BE501049
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445232	633430_1	BE294357 V36569 A217005
446171	664826_1	A0374327 A1278380 A0301383
447252	714160_1	R90916 AL120073 R18429 Z42095 A1369730 R30824
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453845	983027_1	AL157659
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454377	114761_1	A04076611 AW814764
454389	115682_1	AW752371 AW847602 AW47979
454465	1206365_1	AW752710 BE180336 BE180186
454505	1219564_1	AW801365 AW801435 AW801372
454556	1223876_1	AW807073 AW807055 AW807067 AW807276 AW807030 AW807363 AW845892 AW807091 AW807275 AW807284 AW807287 AW845891
454574	1225636_1	AW805189 AW807072 AW809122 AW809126 AW809128 AW809133 AW809131 AW809113 AW809111 AW809132
454597	1226095_1	AW805648 AW809704 AW809643 AW809653 AW809709 AW809949 AW809939 AW810010 AW809705 AW809950 AW809922 AW809667
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454652	1229041_1	AW811380 AW811385
454690	1229106_1	AW812227 AW812294 AW812092
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455013	1246889_1	AW847547 AW847659 AW847656 AW847653 AW847717 AW847786
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455110	1253965_1	BE154205 AW855572 AW855607
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455620	1348141_1	AW846039 AW846045 AW846028 AW846036
455662	1349206_1	BE008002 BE007987 BE007998 BE008000
455713	1352512_1	BE004059 BE003903 BE003638 BE003663 BE004056 BE003974 BE003904 BE003698 BE003896 BE003906 BE003980
455759	1359316_1	AW85387 BE065310 BE065381
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457727	382596_1	AL138130 AA049795 AW939277
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458304	75903_1	AW874887 A0496558 A052145
458329	772443_1	AW875133 AA729543 AA805813
45841	784196_1	AW816379 AA888282 AA879046 AA879195
459160	920051_1	AL157625 AT72896 BE22492
459170	920646_1	A157368 BE159395
459186	922866_1	W22865 W22871
459285		A0904723 A0904725 A0904729 A0904722 A0904758 A0904736
459325		A0905518 A090516 A090547 A090515 AW176013 AW176037
459387		A0905287 BE064074 BE068820 BE068823 BE068822 BE068826

TABLE 1C:

Play: Unique number corresponding to an Eca probelet

Ref: Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham I. et al." refers to the publication entitled "The DNA sequence of human chromosome 22" Dunham, et al. (1999) Nature 402:489-495

Strand: Indicates DNA strand from which exons were predicted

NL_position: Indicates nucleotide positions of predicted exons

	Pkey	Ref	Strand	NL_position
	400584	8687612	Minus	18338-18572
	400593	9807642	Minus	25013-25127
5	400612	9929646	Minus	151513-151662
	400613	9864507	Plus	92278-92472
	400623	7228177	Plus	74195-74335,74653-74827
	400709	7249204	Plus	153075-154980
	400749	7331445	Minus	9162-9293
	400842	1927148	Plus	90462-90673
10	400925	7651921	Plus	38183-38391,43900-44086
	400964	7139719	Minus	155282-155403
	400968	7923967	Plus	19338-20043
	400975	7139779	Minus	108473-108847
	400983	8081158	Plus	107953-108632
15	401032	8117525	Minus	69451-69555
	401050	8117628	Minus	78445-79425
	401088	8492704	Plus	194659-195179
	401129	8699792	Minus	62022-62242,62325-62451,62543-62710,63072-63167
	401200	9743387	Minus	111585-111805,114791-114916,115419-115583,116351-116446,116847-116907,122853-123057,124982-125407
20	401213	9658408	Plus	98243-98380,98469-98619
	401230	9929527	Minus	33835-34006,34539-34592,36461-36745,48925-49098,52604-52758
	401245	4827300	Minus	59373-59531
	401280	8076883	Minus	86308-86355
	401289	8954206	Plus	2259-2591
25	401283	9800093	Minus	47256-47456
	401487	7381770	Plus	92897-92913
	401508	7534110	Minus	110776-110983
	401521	7705251	Plus	9127-9234
	401530	7706649	Plus	41468-42406
30	401575	7229804	Minus	76253-76384
	401604	7689963	Minus	119835-120185
	401780	7249190	Minus	28397-29617,28920-29045,29135-29296,29411-29567,29705-29787,30224-30573
	401781	7249190	Minus	83215-83435,83531-83656,83740-83901,84237-84393,84955-85037,86290-86614
35	401793	7263888	Minus	102945-103083
	401809	7342191	Minus	107548-108290
	401862	7770606	Minus	55839-55933,59145-59203
	401881	8122429	Minus	148470-148651,153418-153618,154282-154438
	402018	7528100	Plus	168728-168859
40	402046	8072415	Plus	165394-165556,168167-168395
	402050	8076888	Minus	130105-130227
	402071	8117361	Plus	85924-86039
	402075	8117407	Plus	121907-122035,122804-122921,124019-124161,124455-124610,125672-126076
	402131	7704981	Minus	33114-33205,33496-33678
45	402203	8576119	Minus	8124-8265
	402222	9958106	Plus	3251-3834,3839-4269
	402256	6598824	Plus	22587-23723
	402258	6598824	Plus	36768-37623
	402261	9796341	Minus	46699-46692,46758-46811,856293-86346,89776-89829,90046-90101,102817-102924
50	402425	9796347	Minus	50224-50385
	402481	9797406	Plus	87891-88991
	402529	7639937	Minus	165-817
	402543	9838066	Minus	89684-90893
	402576	7230225	Minus	1867-2247
55	402578	9884928	Plus	66390-66496
	402623	9931216	Plus	31753-31956
	402631	9931231	Minus	115858-116560
	402639	9958129	Minus	20167-22383
	402664	8077024	Plus	70318-70946
60	402709	6901246	Minus	56947-57055
	402738	7331557	Minus	8725-8859
	402745	9212200	Minus	76516-76680
	402750	4835258	Minus	147744-147861
	402784	6136940	Minus	131034-131794
	402800	6010175	Plus	43921-44045,46181-46273
65	402859	5588237	Minus	69821-75323
	402892	8086844	Minus	194384-194645
	402914	9953349	Plus	124035-124321
	403041	3171152	Plus	70527-71019
70	403065	8954197	Minus	71615-71773,73930-74144
	403083	8954241	Plus	163070-163251
	403089	8954241	Plus	171984-172229
	403093	8954241	Plus	177083-177373,177464-177751
	403177	9838213	Minus	142560-142726
75	403273	8018055	Plus	133899-134099
	403334	8568677	Minus	137295-137350
	403350	8569775	Minus	135374-135523
	403356	8569930	Plus	92839-93036
	403403	9436460	Plus	21240-21399
	403525	7960440	Plus	152431-153243
80	403568	8101145	Minus	85509-85568
	403647	8699843	Minus	35849-36204
	403687	7387384	Plus	9009-9534
	403691	7387384	Minus	86280-86463
	403698	4263532	Plus	10464-10507

	403741	7630932	Minus	2833-3468
	403747	7638395	Minus	20453-25621
	403766	6053636	Minus	7028-73217
5	403831	7249249	Minus	61428-61575
	403891	7331467	Minus	191508-193220
	403944	7711864	Minus	129213-129415
	403963	8589150	Plus	149466-149665
	404070	2996542	Plus	7210-7414,10043-10195
10	404088	9958257	Plus	184131-184295
	404097	7770701	Plus	55512-55781
	404166	7656622	Plus	86147-86509
	404270	9828129	Minus	3649-3750,4161-4306,5962-6043,6849-6965
	404340	7630856	Plus	10898-11506
	404410	7342122	Plus	49052-49175,58177-55273,59384-59488
15	404589	8705107	Plus	104043-110733
	404638	9796751	Minus	99433-99528,100035-100161
	404664	9797142	Minus	104257-105215
	404727	8081050	Plus	115534-115747
	404767	7652327	Minus	23344-23759
20	404828	6590415	Minus	26291-27253
	404849	7706886	Plus	144843-144864,149846-150121
	404893	6850447	Plus	65083-65223
	404898	7351420	Minus	177019-177328
25	404952	7382668	Minus	136328-136616
	404972	3213020	Plus	48711-49524
	404992	4626277	Minus	106104-106195,111659-111781
	405071	7708797	Minus	11115-11652
	405138	8575241	Plus	90303-90616
30	405196	7230083	Minus	135716-135851
	405227	6731245	Minus	22550-22802
	405277	3980473	Plus	23471-23572
	405285	6139075	Minus	65744-65903,67090-67170,61478-61560
	405292	3845420	Plus	33227-33442
35	405336	6094635	Plus	33267-33563
	405362	2337862	Minus	106008-106142,105980-106091,140445-140556,142519-142641
	405382	6530782	Plus	31523-32311
	405454	7656675	Plus	133807-134053
	405465	7767904	Plus	8935-9073,12242-12367,13364-13505,14966-15493
	405472	8439781	Plus	106237-106447,108462-108596
40	405547	1054740	Plus	124361-124520,124874-125050
	405576	4003382	Plus	84000-85009
	405621	5623811	Plus	59362-59607
	405635	5122990	Plus	56384-56587
45	405675	4557087	Plus	70304-70630
	405708	4156182	Plus	55030-55804
	405771	7018349	Plus	91191-91254,91510-91589
	405783	5730434	Minus	27228-27885
	405793	1405987	Minus	89197-89453
50	405800	2791346	Plus	19271-19813
	405810	4938307	Minus	64543-64566
	405848	7651809	Minus	28135-28244
	405851	6184995	Minus	26407-27151
	405867	6758731	Minus	74553-75173
	405896	6758795	Plus	67311-67874
55	405904	7705118	Minus	16375-16584
	405917	7712162	Minus	108829-107213
	405982	8247790	Minus	36028-36408
	406030	8312328	Minus	98123-96547
	406053	6758997	Plus	30921-31532
60	406057	6691254	Minus	20830-21222
	406149	7144791	Minus	44464-45164
	406163	7158901	Plus	66590-66835
	406277	6686030	Minus	4759-5490
	406322	9212102	Minus	130230-130418
65	406349	9256007	Minus	21251-21526
	406504	7711360	Minus	107068-107277
	406544	7711536	Plus	46576-46757
	406589	8224211	Plus	38906-39399
70	406592	4567182	Plus	352560-352963

TABLE 2A lists about 167 genes up-regulated in ovarian cancer compared to normal adult tissues that are likely to be extracellular or cell-surface proteins. These were selected as for Table 1A, except that the ratio was greater than or equal to 2.5, and the predicted protein contained a PFAM domain that is indicative of extracellular localization (e.g., Ig, fn3, egf, 7tm domains).

TABLE 2A: ABOUT 167 UP-REGULATED OVARIAN CANCER GENES ENCODING EXTRACELLULAR/CELL SURFACE PROTEINS

Phy: Primekey

Ex. Accn: Exemplar Accession

UG ID: UniGene ID

Title: UniGene Title

PFAM domains

ratio: tumor vs. normal tissues

Play	Ex. Acn No.	UG ID	Title	PFAM domain	ratio
5	423017	AW117861	serine (or cysteine) proteinase inhibitor	serpin	63.6
	431938	AA030471	developmentally regulated GTP-binding	SCP	32.0
	425580	NM_001944	desmoglein 3 (pemphigus vulgaris ant	cadherin	30.0
	418994	AA29520	selectin E (endothelial adhesion molec	EGFlectin_cushi	24.5
	452947	AW130413	gbt5004.1 x1 NCL_GCAP_Gas4 Hom	alpha-amylose	15.8
10	416952	RA1514	ESTs	phosducin/actin_rec	15.1
	431725	X55724	Narrie disease (pseudotumor)	Cys_knot	12.6
	422330	D30783	epinephrin	EGF	12.5
	446745	AW111891	ESTs	vwa	11.8
	415319	AB11861	CD33 antigen (activated B lymphocyt-	ig	10.0
15	432408	N39127	myxovirus (influenza) resistance 1, ho	lon_trans_K_beta	10.5
	405285		predicted exon	A2M/A2M_N	10.5
	406536		predicted exon	EGF_fcl_recept_actd_recept_b	9.8
	403093		predicted exon	tnfr_1	9.6
	446740	AI611635	ESTs	RYDR_JTPR	9.2
20	405547		predicted exon	ABC_tran:ABC_membrane	8.5
	412333	AW537485	gbtQV3-DT0044-221299-045-b09 DT	7tm_1	8.4
	404270		predicted exon	SCP	8.1
	402745		predicted exon	EGF_fcl_recept_b/thyroglobulin_1	8.0
	452755	AW138937	ESTs	cystatin	7.2
25	421459	A821533	ESTs	disintegrin/Reprolysin	7.9
	416151	T26661	gbtAB56GFR Infant brain, LNL, ara	laminin_G/EGF	7.8
	446232	A291848	ESTs	7tm_3	7.6
	431009	BE145762	gap junction protein, beta 6 (connexin	connexin	7.2
	424634	NM_003613	cartilage intermediate layer protein, n	lgbp_1	7.1
30	407449		predicted exon	h3_h4_recept_actd_recept_b	6.8
	419054	N40340	ESTs, Weakly similar to CRF2 [Mm	h3_SPRY	6.8
	459170	AI905518	gbt:RC-BT091-210199-098 BT091 Ho	ABC_tran:ABC_membrane	6.6
	416441	BE407197	gbt01301552F1 NBL_MGC_21 Hom	SOP	6.4
	410584	NM_009033	lipase, endothelial	Ribosomal_L22	6.4
35	402425		predicted exon	lon_trans	6.3
	415451	H19415	ESTs, Moderately similar to ALU1_H	Ephrin	6.0
	403083		predicted exon	tnfr_1	5.9
	444995	AK512976	guanine nucleotide binding protein (G	SOP	5.8
	418345	AJ001695	serine (or cysteine) proteinase inhibitor	serpin	5.8
40	424966	AU077312	solute carrier family 7 (cationic amino	aa_permeases	5.8
	431211	M65649	gap junction protein, beta 2, 26kd (co	connexin	5.7
	403563	AA481269	ESTs	ABC_tran:ABC_membrane	5.6
	459152	A113835	ESTs	epiplexin	5.6
	418644	M62982	arachidonate 12-lipoxygenase	lipoxygenase:PLAT	5.6
45	403089		predicted exon	tnfr_1	5.6
	403387		predicted exon	tnfr_1/Reprolysin	5.6
	403391		predicted exon	serpin	5.5
	414035	Y00630	serine (or cysteine) proteinase inhibitor	serpin	5.4
	421284	U62435	cholinergic receptor, nicotinic, alpha p	neur_chan	5.3
50	435435	T89473	ESTs	lipase:PLAT	5.3
	457122	AU026157	ESTs, Weakly similar to ALU1_HUM	lipoxygenase:PLAT	5.2
	419249	X14767	gamma-aminobutyric acid (GABA) A	neur_chan	5.2
	425698	NM_016112	polycystic kidney disease 2-like 1	lon_trans	5.2
	431117	AF003522	25-26500 (Thrombospondin)-like 1	EGF_DSL	5.1
55	457948	AA065040	ESTs	G-alpha12aif	5.1
	435174	AA687378	ESTs	SPRY	5.0
	408170	AW204516	ESTs	arfinas	5.0
	434351	AW974391	ESTs, Weakly similar to ALU1_HUM	arfinas	4.9
	430708	U78308	olfactory receptor, family 1, subfamily	7tm_1	4.8
60	422597	BE245909	ATP-binding cassette, sub-family B (M	ABC_tran:ABC_membrane	4.8
	403545		transforming growth factor, alpha	EGF	4.7
	426471	M22440	serine (or cysteine) proteinase inhibitor	serpin	4.7
	409632	W74001	solute carrier family 2 (facilitated gluc	sugar_tr	4.6
	420206	M91463	tissue factor pathway inhibitor 2	Kunitz_BPTTG-gamma	4.6
65	415138	C16356	inhibiting hormone/chloride/gonadotrop	Antc	4.5
	424402	M63108	putative acid-sensing ion channel	7tm_1	4.4
	436480	AJ271643	adrenergic, beta-2-, receptor, surface	SNF	4.4
	430226	BE245562	ESTs	ig	4.4
	436126	AW449757	low density lipoprotein-like recep	7tm_1	4.3
70	459812	AF000575	lysozyme immunoglobulin-like recep	TIMP	4.3
	409385	AA071267	gluc2m1g01.r1 Stratagene fibroblast (TNFR_c6	4.3
	449184	AW295295	ESTs	disintegrin/Reprolysin	4.3
	410555	U92649	a disintegrin and metalloproteinase do	cadherin	4.3
	422389	AF240553	procalcitonin 12	A2M/A2M_N	4.3
75	405291		predicted exon	EGF_fcl_recept_actd_recept_b	4.3
	413548	BE147555	Homo sapiens mRNA for KIAA1558	h4_recept_actEGF_fcl_recept_b	4.3
	449535	W15267	low density lipoprotein receptor-related	7tm_1	4.3
	425864	US5429	olfactory receptor, family 5, subfamily	7tm_1	4.2
	410611	AW954134	KIAA1628 protein	Peptidase_S9	4.2
80	430686	NM_001942	desmoglein 1	cadherin/Cadherin_C_1arm	4.1
	418693	AF750878	thrombospondin 1	vwc1SPN	4.0
	445924	AJ254871	ESTs	negc_tr	3.9
	457148	AF091035	ESTs, 184627	arfinas	3.9
	428568	AC004755	one cut domain, family member 3	E1-E2_ATPase	3.9
	412170	D16532	very low density lipoprotein receptor	EGF_fcl_recept_actd_recept_b	3.8
	442566	R37337	ESTs	ankle/titin/RHD/TIG	3.8
	437363		predicted exon	7tm_1	3.8

430374			predicted exon	3	1
431365	BE152544		gb:CM1-HT0323-250200-128-09 HT	alpha-amylose	3
442295	AB127248	Hs.224398	Hom sapiens cDNA FLJ11469 fs. c	Collagen;COL1	3
450351			c. predicted exon	7m_1, 7m_2, 7m_3, 7m_4, 7m_5, 7m_6, 7m_7, 7m_8, 7m_9, 7m_10, 7m_11, 7m_12, 7m_13, 7m_14, 7m_15, 7m_16, 7m_17, 7m_18, 7m_19, 7m_20, 7m_21, 7m_22, 7m_23, 7m_24, 7m_25, 7m_26, 7m_27, 7m_28, 7m_29, 7m_30, 7m_31, 7m_32, 7m_33, 7m_34, 7m_35, 7m_36, 7m_37, 7m_38, 7m_39, 7m_40, 7m_41, 7m_42, 7m_43, 7m_44, 7m_45, 7m_46, 7m_47, 7m_48, 7m_49, 7m_50, 7m_51, 7m_52, 7m_53, 7m_54, 7m_55, 7m_56, 7m_57, 7m_58, 7m_59, 7m_60, 7m_61, 7m_62, 7m_63, 7m_64, 7m_65, 7m_66, 7m_67, 7m_68, 7m_69, 7m_70, 7m_71, 7m_72, 7m_73, 7m_74, 7m_75, 7m_76, 7m_77, 7m_78, 7m_79, 7m_80, 7m_81, 7m_82, 7m_83, 7m_84, 7m_85, 7m_86, 7m_87, 7m_88, 7m_89, 7m_90, 7m_91, 7m_92, 7m_93, 7m_94, 7m_95, 7m_96, 7m_97, 7m_98, 7m_99, 7m_100, 7m_101, 7m_102, 7m_103, 7m_104, 7m_105, 7m_106, 7m_107, 7m_108, 7m_109, 7m_110, 7m_111, 7m_112, 7m_113, 7m_114, 7m_115, 7m_116, 7m_117, 7m_118, 7m_119, 7m_120, 7m_121, 7m_122, 7m_123, 7m_124, 7m_125, 7m_126, 7m_127, 7m_128, 7m_129, 7m_130, 7m_131, 7m_132, 7m_133, 7m_134, 7m_135, 7m_136, 7m_137, 7m_138, 7m_139, 7m_140, 7m_141, 7m_142, 7m_143, 7m_144, 7m_145, 7m_146, 7m_147, 7m_148, 7m_149, 7m_150, 7m_151, 7m_152, 7m_153, 7m_154, 7m_155, 7m_156, 7m_157, 7m_158, 7m_159, 7m_160, 7m_161, 7m_162, 7m_163, 7m_164, 7m_165, 7m_166, 7m_167, 7m_168, 7m_169, 7m_170, 7m_171, 7m_172, 7m_173, 7m_174, 7m_175, 7m_176, 7m_177, 7m_178, 7m_179, 7m_180, 7m_181, 7m_182, 7m_183, 7m_184, 7m_185, 7m_186, 7m_187, 7m_188, 7m_189, 7m_190, 7m_191, 7m_192, 7m_193, 7m_194, 7m_195, 7m_196, 7m_197, 7m_198, 7m_199, 7m_200, 7m_201, 7m_202, 7m_203, 7m_204, 7m_205, 7m_206, 7m_207, 7m_208, 7m_209, 7m_210, 7m_211, 7m_212, 7m_213, 7m_214, 7m_215, 7m_216, 7m_217, 7m_218, 7m_219, 7m_220, 7m_221, 7m_222, 7m_223, 7m_224, 7m_225, 7m_226, 7m_227, 7m_228, 7m_229, 7m_230, 7m_231, 7m_232, 7m_233, 7m_234, 7m_235, 7m_236, 7m_237, 7m_238, 7m_239, 7m_240, 7m_241, 7m_242, 7m_243, 7m_244, 7m_245, 7m_246, 7m_247, 7m_248, 7m_249, 7m_250, 7m_251, 7m_252, 7m_253, 7m_254, 7m_255, 7m_256, 7m_257, 7m_258, 7m_259, 7m_260, 7m_261, 7m_262, 7m_263, 7m_264, 7m_265, 7m_266, 7m_267, 7m_268, 7m_269, 7m_270, 7m_271, 7m_272, 7m_273, 7m_274, 7m_275, 7m_276, 7m_277, 7m_278, 7m_279, 7m_280, 7m_281, 7m_282, 7m_283, 7m_284, 7m_285, 7m_286, 7m_287, 7m_288, 7m_289, 7m_290, 7m_291, 7m_292, 7m_293, 7m_294, 7m_295, 7m_296, 7m_297, 7m_298, 7m_299, 7m_300, 7m_301, 7m_302, 7m_303, 7m_304, 7m_305, 7m_306, 7m_307, 7m_308, 7m_309, 7m_310, 7m_311, 7m_312, 7m_313, 7m_314, 7m_315, 7m_316, 7m_317, 7m_318, 7m_319, 7m_320, 7m_321, 7m_322, 7m_323, 7m_324, 7m_325, 7m_326, 7m_327, 7m_328, 7m_329, 7m_330, 7m_331, 7m_332, 7m_333, 7m_334, 7m_335, 7m_336, 7m_337, 7m_338, 7m_339, 7m_340, 7m_341, 7m_342, 7m_343, 7m_344, 7m_345, 7m_346, 7m_347, 7m_348, 7m_349, 7m_350, 7m_351, 7m_352, 7m_353, 7m_354, 7m_355, 7m_356, 7m_357, 7m_358, 7m_359, 7m_360, 7m_361, 7m_362, 7m_363, 7m_364, 7m_365, 7m_366, 7m_367, 7m_368, 7m_369, 7m_370, 7m_371, 7m_372, 7m_373, 7m_374, 7m_375, 7m_376, 7m_377, 7m_378, 7m_379, 7m_380, 7m_381, 7m_382, 7m_383, 7m_384, 7m_385, 7m_386, 7m_387, 7m_388, 7m_389, 7m_390, 7m_391, 7m_392, 7m_393, 7m_394, 7m_395, 7m_396, 7m_397, 7m_398, 7m_399, 7m_400, 7m_401, 7m_402, 7m_403, 7m_404, 7m_405, 7m_406, 7m_407, 7m_408, 7m_409, 7m_410, 7m_411, 7m_412, 7m_413, 7m_414, 7m_415, 7m_416, 7m_417, 7m_418, 7m_419, 7m_420, 7m_421, 7m_422, 7m_423, 7m_424, 7m_425, 7m_426, 7m_427, 7m_428, 7m_429, 7m_430, 7m_431, 7m_432, 7m_433, 7m_434, 7m_435, 7m_436, 7m_437, 7m_438, 7m_439, 7m_440, 7m_441, 7m_442, 7m_443, 7m_444, 7m_445, 7m_446, 7m_447, 7m_448, 7m_449, 7m_450, 7m_451, 7m_452, 7m_453, 7m_454, 7m_455, 7m_456, 7m_457, 7m_458, 7m_459, 7m_460, 7m_461, 7m_462, 7m_463, 7m_464, 7m_465, 7m_466, 7m_467, 7m_468, 7m_469, 7m_470, 7m_471, 7m_472, 7m_473, 7m_474, 7m_475, 7m_476, 7m_477, 7m_478, 7m_479, 7m_480, 7m_481, 7m_482, 7m_483, 7m_484, 7m_485, 7m_486, 7m_487, 7m_488, 7m_489, 7m_490, 7m_491, 7m_492, 7m_493, 7m_494, 7m_495, 7m_496,	
473735	AA715284		gb:U03401-102100-128-09 HT	alpha-amylose	3
457353	X65633	Hs.248144	Hom sapiens cDNA FLJ11469 fs. c	Collagen;COL1	3
431176	U026984	Hs.233662	ESTs	alpha-amylose	3
436233	UJ42878	Hs.124116	ESTs	alpha-amylose	3
431688	U026984	Hs.270833	amylglucosyl (schwannoma-derived g	alpha-amylose	3
445798	NM_012421	Hs.13321	predicted exon	7m_1, 7m_2, 7m_3, 7m_4, 7m_5, 7m_6, 7m_7, 7m_8, 7m_9, 7m_10, 7m_11, 7m_12, 7m_13, 7m_14, 7m_15, 7m_16, 7m_17, 7m_18, 7m_19, 7m_20, 7m_21, 7m_22, 7m_23, 7m_24, 7m_25, 7m_26, 7m_27, 7m_28, 7m_29, 7m_30, 7m_31, 7m_32, 7m_33, 7m_34, 7m_35, 7m_36, 7m_37, 7m_38, 7m_39, 7m_40, 7m_41, 7m_42, 7m_43, 7m_44, 7m_45, 7m_46, 7m_47, 7m_48, 7m_49, 7m_50, 7m_51, 7m_52, 7m_53, 7m_54, 7m_55, 7m_56, 7m_57, 7m_58, 7m_59, 7m_60, 7m_61, 7m_62, 7m_63, 7m_64, 7m_65, 7m_66, 7m_67, 7m_68, 7m_69, 7m_70, 7m_71, 7m_72, 7m_73, 7m_74, 7m_75, 7m_76, 7m_77, 7m_78, 7m_79, 7m_80, 7m_81, 7m_82, 7m_83, 7m_84, 7m_85, 7m_86, 7m_87, 7m_88, 7m_89, 7m_90, 7m_91, 7m_92, 7m_93, 7m_94, 7m_95, 7m_96, 7m_97, 7m_98, 7m_99, 7m_100, 7m_101, 7m_102, 7m_103, 7m_104, 7m_105, 7m_106, 7m_107, 7m_108, 7m_109, 7m_110, 7m_111, 7m_112, 7m_113, 7m_114, 7m_115, 7m_116, 7m_117, 7m_118, 7m_119, 7m_120, 7m_121, 7m_122, 7m_123, 7m_124, 7m_125, 7m_126, 7m_127, 7m_128, 7m_129, 7m_130, 7m_131, 7m_132, 7m_133, 7m_134, 7m_135, 7m_136, 7m_137, 7m_138, 7m_139, 7m_140, 7m_141, 7m_142, 7m_143, 7m_144, 7m_145, 7m_146, 7m_147, 7m_148, 7m_149, 7m_150, 7m_151, 7m_152, 7m_153, 7m_154, 7m_155, 7m_156, 7m_157, 7m_158, 7m_159, 7m_160, 7m_161, 7m_162, 7m_163, 7m_164, 7m_165, 7m_166, 7m_167, 7m_168, 7m_169, 7m_170, 7m_171, 7m_172, 7m_173, 7m_174, 7m_175, 7m_176, 7m_177, 7m_178, 7m_179, 7m_180, 7m_181, 7m_182, 7m_183, 7m_184, 7m_185, 7m_186, 7m_187, 7m_188, 7m_189, 7m_190, 7m_191, 7m_192, 7m_193, 7m_194, 7m_195, 7m_196, 7m_197, 7m_198, 7m_199, 7m_200, 7m_201, 7m_202, 7m_203, 7m_204, 7m_205, 7m_206, 7m_207, 7m_208, 7m_209, 7m_210, 7m_211, 7m_212, 7m_213, 7m_214, 7m_215, 7m_216, 7m_217, 7m_218, 7m_219, 7m_220, 7m_221, 7m_222, 7m_223, 7m_224, 7m_225, 7m_226, 7m_227, 7m_228, 7m_229, 7m_230, 7m_231, 7m_232, 7m_233, 7m_234, 7m_235, 7m_236, 7m_237, 7m_238, 7m_239, 7m_240, 7m_241, 7m_242, 7m_243, 7m_244, 7m_245, 7m_246, 7m_247, 7m_248, 7m_249, 7m_250, 7m_251, 7m_252, 7m_253, 7m_254, 7m_255, 7m_256, 7m_257, 7m_258, 7m_259, 7m_260, 7m_261, 7m_262, 7m_263, 7m_264, 7m_265, 7m_266, 7m_267, 7m_268, 7m_269, 7m_270, 7m_271, 7m_272, 7m_273, 7m_274, 7m_275, 7m_276, 7m_277, 7m_278, 7m_279, 7m_280, 7m_281, 7m_282, 7m_283, 7m_284, 7m_285, 7m_286, 7m_287, 7m_288, 7m_289, 7m_290, 7m_291, 7m_292, 7m_293, 7m_294, 7m_295, 7m_296, 7m_297, 7m_298, 7m_299, 7m_300, 7m_301, 7m_302, 7m_303, 7m_304, 7m_305, 7m_306, 7m_307, 7m_308, 7m_309, 7m_310, 7m_311, 7m_312, 7m_313, 7m_314, 7m_315, 7m_316, 7m_317, 7m_318, 7m_319, 7m_320, 7m_321, 7m_322, 7m_323, 7m_324, 7m_325, 7m_326, 7m_327, 7m_328, 7m_329, 7m_330, 7m_331, 7m_332, 7m_333, 7m_334, 7m_335, 7m_336, 7m_337, 7m_338, 7m_339, 7m_340, 7m_341, 7m_342, 7m_343, 7m_344, 7m_345, 7m_346, 7m_347, 7m_348, 7m_349, 7m_350, 7m_351, 7m_352, 7m_353, 7m_354, 7m_355, 7m_356, 7m_357, 7m_358, 7m_359, 7m_360, 7m_361, 7m_362, 7m_363, 7m_364, 7m_365, 7m_366, 7m_367, 7m_368, 7m_369, 7m_370, 7m_371, 7m_372, 7m_373, 7m_374, 7m_375, 7m_376, 7m_377, 7m_378, 7m_379, 7m_380, 7m_381, 7m_382, 7m_383, 7m_384, 7m_385, 7m_386, 7m_387, 7m_388, 7m_389, 7m_390, 7m_391, 7m_392, 7m_393, 7m_394, 7m_395, 7m_396, 7m_397, 7m_398, 7m_399, 7m_400, 7m_401, 7m_402, 7m_403, 7m_404, 7m_405, 7m_406, 7m_407, 7m_408, 7m_409, 7m_410, 7m_411, 7m_412, 7m_413, 7m_414, 7m_415, 7m_416, 7m_417, 7m_418, 7m_419, 7m_420, 7m_421, 7m_422, 7m_423, 7m_424, 7m_425, 7m_426, 7m_427, 7m_428, 7m_429, 7m_430, 7m_431, 7m_432, 7m_433, 7m_434, 7m_435, 7m_436, 7m_437, 7m_438, 7m_439, 7m_440, 7m_441, 7m_442, 7m_443, 7m_444, 7m_445, 7m_446, 7m_447, 7m_448, 7m_449, 7m_450, 7m_451, 7m_452, 7m_453, 7m_454, 7m_455, 7m_456, 7m_457, 7m_458, 7m_459, 7m_460, 7m_461, 7m_462, 7m_463, 7m_464, 7m_465, 7m_466, 7m_467, 7m_468, 7m_469, 7m_470, 7m_471, 7m_472, 7m_473, 7m_474, 7m_475, 7m_476, 7m_477, 7m_478, 7m_479, 7m_480, 7m_481, 7m_482, 7m_483, 7m_484, 7m_485, 7m_486, 7m_487, 7m_488, 7m_489, 7m_490, 7m_491, 7m_492, 7m_493, 7m_494, 7m_495, 7m_496,	
400380	NM_018465	Hs.283079	G protein-coupled receptor CS2.2	alpha-amylose	3
453393	NM_000303	Hs.30451	glutamate receptor, ionotropic, N-met	alpha-amylose	3
408452	AF208234	Hs.535	cystin B (beta II)	alpha-amylose	3
421166	AA305407	Hs.102308	cytochrome b5 (beta II)	alpha-amylose	3
445575	Z25368	Hs.172004	predicted exon	7m_1, 7m_2, 7m_3, 7m_4, 7m_5, 7m_6, 7m_7, 7m_8, 7m_9, 7m_10, 7m_11, 7m_12, 7m_13, 7m_14, 7m_15, 7m_16, 7m_17, 7m_18, 7m_19, 7m_20, 7m_21, 7m_22, 7m_23, 7m_24, 7m_25, 7m_26, 7m_27, 7m_28, 7m_29, 7m_30, 7m_31, 7m_32, 7m_33, 7m_34, 7m_35, 7m_36, 7m_37, 7m_38, 7m_39, 7m_40, 7m_41, 7m_42, 7m_43, 7m_44, 7m_45, 7m_46, 7m_47, 7m_48, 7m_49, 7m_50, 7m_51, 7m_52, 7m_53, 7m_54, 7m_55, 7m_56, 7m_57, 7m_58, 7m_59, 7m_60, 7m_61, 7m_62, 7m_63, 7m_64, 7m_65, 7m_66, 7m_67, 7m_68, 7m_69, 7m_70, 7m_71, 7m_72, 7m_73, 7m_74, 7m_75, 7m_76, 7m_77, 7m_78, 7m_79, 7m_80, 7m_81, 7m_82, 7m_83, 7m_84, 7m_85, 7m_86, 7m_87, 7m_88, 7m_89, 7m_90, 7m_91, 7m_92, 7m_93, 7m_94, 7m_95, 7m_96, 7m_97, 7m_98, 7m_99, 7m_100, 7m_101, 7m_102, 7m_103, 7m_104, 7m_105, 7m_106, 7m_107, 7m_108, 7m_109, 7m_110, 7m_111, 7m_112, 7m_113, 7m_114, 7m_115, 7m_116, 7m_117, 7m_118, 7m_119, 7m_120, 7m_121, 7m_122, 7m_123, 7m_124, 7m_125, 7m_126, 7m_127, 7m_128, 7m_129, 7m_130, 7m_131, 7m_132, 7m_133, 7m_134, 7m_135, 7m_136, 7m_137, 7m_138, 7m_139, 7m_140, 7m_141, 7m_142, 7m_143, 7m_144, 7m_145, 7m_146, 7m_147, 7m_148, 7m_149, 7m_150, 7m_151, 7m_152, 7m_153, 7m_154, 7m_155, 7m_156, 7m_157, 7m_158, 7m_159, 7m_160, 7m_161, 7m_162, 7m_163, 7m_164, 7m_165, 7m_166, 7m_167, 7m_168, 7m_169, 7m_170, 7m_171, 7m_172, 7m_173, 7m_174, 7m_175, 7m_176, 7m_177, 7m_178, 7m_179, 7m_180, 7m_181, 7m_182, 7m_183, 7m_184, 7m_185, 7m_186, 7m_187, 7m_188, 7m_189, 7m_190, 7m_191, 7m_192, 7m_193, 7m_194, 7m_195, 7m_196, 7m_197, 7m_198, 7m_199, 7m_200, 7m_201, 7m_202, 7m_203, 7m_204, 7m_205, 7m_206, 7m_207, 7m_208, 7m_209, 7m_210, 7m_211, 7m_212, 7m_213, 7m_214, 7m_215, 7m_216, 7m_217, 7m_218, 7m_219, 7m_220, 7m_221, 7m_222, 7m_223, 7m_224, 7m_225, 7m_226, 7m_227, 7m_228, 7m_229, 7m_230, 7m_231, 7m_232, 7m_233, 7m_234, 7m_235, 7m_236, 7m_237, 7m_238, 7m_239, 7m_240, 7m_241, 7m_242, 7m_243, 7m_244, 7m_245, 7m_246, 7m_247, 7m_248, 7m_249, 7m_250, 7m_251, 7m_252, 7m_253, 7m_254, 7m_255, 7m_256, 7m_257, 7m_258, 7m_259, 7m_260, 7m_261, 7m_262, 7m_263, 7m_264, 7m_265, 7m_266, 7m_267, 7m_268, 7m_269, 7m_270, 7m_271, 7m_272, 7m_273, 7m_274, 7m_275, 7m_276, 7m_277, 7m_278, 7m_279, 7m_280, 7m_281, 7m_282, 7m_283, 7m_284, 7m_285, 7m_286, 7m_287, 7m_288, 7m_289, 7m_290, 7m_291, 7m_292, 7m_293, 7m_294, 7m_295, 7m_296, 7m_297, 7m_298, 7m_299, 7m_300, 7m_301, 7m_302, 7m_303, 7m_304, 7m_305, 7m_306, 7m_307, 7m_308, 7m_309, 7m_310, 7m_311, 7m_312, 7m_313, 7m_314, 7m_315, 7m_316, 7m_317, 7m_318, 7m_319, 7m_320, 7m_321, 7m_322, 7m_323, 7m_324, 7m_325, 7m_326, 7m_327, 7m_328, 7m_329, 7m_330, 7m_331, 7m_332, 7m_333, 7m_334, 7m_335, 7m_336, 7m_337, 7m_338, 7m_339, 7m_340, 7m_341, 7m_342, 7m_343, 7m_344, 7m_345, 7m_346, 7m_347, 7m_348, 7m_349, 7m_350, 7m_351, 7m_352, 7m_353, 7m_354, 7m_355, 7m_356, 7m_357, 7m_358, 7m_359, 7m_360, 7m_361, 7m_362, 7m_363, 7m_364, 7m_365, 7m_366, 7m_367, 7m_368, 7m_369, 7m_370, 7m_371, 7m_372, 7m_373, 7m_374, 7m_375, 7m_376, 7m_377, 7m_378, 7m_379, 7m_380, 7m_381, 7m_382, 7m_383, 7m_384, 7m_385, 7m_386, 7m_387, 7m_388, 7m_389, 7m_390, 7m_391, 7m_392, 7m_393, 7m_394, 7m_395, 7m_396, 7m_397, 7m_398, 7m_399, 7m_400, 7m_401, 7m_402, 7m_403, 7m_404, 7m_405, 7m_406, 7m_407, 7m_408, 7m_409, 7m_410, 7m_411, 7m_412, 7m_413, 7m_414, 7m_415, 7m_416, 7m_417, 7m_418, 7m_419, 7m_420, 7m_421, 7m_422, 7m_423, 7m_424, 7m_425, 7m_426, 7m_427, 7m_428, 7m_429, 7m_430, 7m_431, 7m_432, 7m_433, 7m_434, 7m_435, 7m_436, 7m_437, 7m_438, 7m_439, 7m_440, 7m_441, 7m_442, 7m_443, 7m_444, 7m_445, 7m_446, 7m_447, 7m_448, 7m_449, 7m_450, 7m_451, 7m_452, 7m_453, 7m_454, 7m_455, 7m_456, 7m_457, 7m_458, 7m_459, 7m_460, 7m_461, 7m_462, 7m_463, 7m_464, 7m_465, 7m_466, 7m_467, 7m_468, 7m_469, 7m_470, 7m_471, 7m_472, 7m_473, 7m_474, 7m_475, 7m_476, 7m_477, 7m_478,	

13	alpha-amyrase	3.1
14	Collagen/COL1	3.1
15	7m_3ANF_receptor	3.1
16	phosphoSerineProtein_repeat,TIG	3.1
17	7m_1	3.1
18	laminin_EGF,laminin_B	3.1
19	lg	3.1
20	EGF	3.1
21	s2-C2H2	3.1
22	7m_1	3.1
23	lig_chan	3.1
24	cystallin	3.1
25	IRK	3.1
26	tr3	3.1
27	tp3_1wvc GFBP	3.1
28	Na ⁺ /H ⁺ Exchanger	3.1
29	ABC_tran ABC_membrane	3.1
30	intn_Irans	3.1
31	cadherin Cadherin_C_term	3.1
32	integrin Reprolysin	3.1
33	intn_Irans	3.1
34	tr3	3.1
35	cadherin	3.1
36	7m_1	3.1
37	EGF,laminin_G	3.1
38	sushi HYR	3.1
39	lg	3.1
40	phosphoserine death	3.1
41	sushi	3.1
42	tyrosine sushi CUB	3.1
43	tr3	3.1
44	kd_recept dMGCF	3.1
45	7m_1	3.1
46	Zn_carb Opept Propep_M14	3.1
47	7m_1	3.1
48	7m_1	3.1
49	7m_3ANF_receptor	3.1
50	thyroglobulin_1 GFBP	3.1
51	phosphoserine death	3.1
52	Gal-1 d_lectin	3.1
53	lg	3.1
54	7m_3ANF_receptor	3.1
55	TIF	3.1
56	hemopexin Procidase_M10	3.1
57	A2M A2M_N	3.1
58	IRK	3.1
59	C23HC4 SPRY2 B_box	3.1
60	ABC_tran ABC_membrane	3.1
61	lg	3.1
62	Procidase_S9	3.1
63	EGF	3.1
64	sushi	3.1
65	7m_1	3.1
66	lig_chan AF_receptor	3.1
67	EGF_AT Procidase	3.1
68	Ricin_B_joeth	3.1
69	rra	2.1
70	GF 2 death laminin_G	2.1
71	Transglut cora Transglutamin_N	2.1
72	transglutamin LRRCT	2.1
73	Same Protein_repeat TIG	2.1
74	TransRibosome_S17	2.1
75	7m_1	2.1
76	ABC_tran ABC_membrane	2.1
77	Transglutamin_N Transglut cora	2.1
78	COX8	2.1
79	lg	2.1
80	vw phagrin_A P2X_receptor	2.1
81	CUB MAF5_F8_Type_C	2.1
82	kazal	2.1
83	sushi	2.1
84	FGF	2.1
85	kazal	2.1
86	intn_Irans	2.1
87	lg	2.1
88	phagocyt	2.1

	401657			predicted exon	7m_1	2.6
	456711	AA033899	Hs.83938	ESTs, Moderately similar to MASP-2	wash/trypsin/CUB	2.6
	432042	AW571345	Hs.252715	ESTs	sugar_fr	2.6
	433138	AB020496	Hs.55729	semaphorin sem2	lg;Sema	2.6
5	425230	AI905818		gb:RC-BT091-210199-098 BT091 Ho	ABC_tran/ABC_membrane	2.6
	426418	M59464	Hs.189825	collagen, type IV, alpha 5 (Aport syn	CollagenC4	2.6
	403786			predicted exon	collinrin	2.6
	431728	NM_007351	Hs.268107	multimerin	EGF_C1q	2.6
10	441555	AW205035	Hs.192123	ESTs	sugar_fr	2.6
	445537	AJ245671	Hs.12844	EGF-like domain, multiple 6	EGF/MAM	2.6
	447197	F33075	Hs.83975	glycophorin a1 (Scaev placenta Nb2H	SDF	2.5
	426765	N54150	Hs.193122	Fr fragment of IgA ₁ receptor for	lg	2.5
	450245	AA007536	Hs.271767	ESTs, Moderately similar to ALU1_H	lg	2.5
15	416429	H54658	Hs.26842	ESTs	E1-E2_ATPase/Hydrolase	2.5
	417067	AJ014147	Hs.816086	swi2 earlier family 22 (extraneurons	acid_fr	2.5
	433162	AB039520	Hs.127821	BMI1 protein	ion_kinas	2.5
	403092			predicted exon	fn3	2.5
	406850	AI624300	Hs.172528	collagen, type I, alpha 1	vnc/Collagen/COL1	2.5
20	436698	AW297855	Hs.125615	ESTs	lipoygenase/PLAT	2.5
	456815	NM_013348	Hs.144011	potassium inwardly-rectifying channel	IRK	2.5

TABLE 2b:

Play: Unique Exon probe identifier number

CAT number: Gene cluster number

Accession: Genbank accession numbers

25	Play	CAT Number	Accession
	408385	112523_1	AA071267 T65940 T54515 AA071334
	412333	1269307_1	AW937485 AW937568 AW937658 AW937654 AW937492
30	413605	1379792_1	BE152644 BE152712 BE152668 BE152659 BE152810 BE152811 BE152616 BE152643 BE152706 BE152656 BE152660 BE152715 BE152652 BE152669 BE152661 BE152672 BE152653 BE152716 BE152651 BE152767 BE152677 BE152652 BE152714 BE152708 BE152665 BE152679 BE152771 BE152776 BE152666 BE152768 BE152813 BE152684 BE152678 BE152681 BE152709 BE152687 BE152674 BE152688 BE152711 BE152707 BE152815 BE152678 BE152673 BE152782 BE152671 BE152682 BE152760 BE152809 BE152778 BE152780 BE152762 BE152776 BE152781 BE152774 BE152763 BE152769
35	416151	157326_1	T26661 244136 H23016
	415441	159480_1	BE407157 AA102474 AA100369 BE275628 BE276131
	416531	1605019_1	H69466 H9384 N59694
	423573	229714_1	AA328504 AA327783 AW9562370
40	447197	711623_1	F05075 A035546 F36167
	447420	721207_1	AJ078028 N32550 H65772
	452530	920646_1	AI905518 AI905516 AI905457 AI905515 AW176013 AW176037
	452947	939810_1	AW130413 AI932362
	453420	966433_1	AJ003459 AJ003461
45	459170	929646_1	AI905518 AI905516 AI905457 AI905515 AW176013 AW176037

TABLE 2c:

Play: Unique number corresponding to an Exon probe

Ref: Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham L. et al." refers to the publication entitled "The DNA sequence of

human chromosome 22" Dunham, et al. (1999) Nature 402:469-495

Strand: Indicates DNA strand from which exons were predicted

NL_position: Indicates nucleotide positions of predicted exons

	Play	Ref	Strand	NL_position
55	400484	9929670	Plus	22074-22214
	400704	811684	Minus	63110-63241
	400749	7331445	Minus	9182-9293
	401244	4827300	Minus	55359-56376
	401537	7950358	Minus	186785-187029,190607-190773,198218-198348
60	401857	5100664	Minus	7312-8163
	402172	8575911	Minus	143378-143671
	402425	9796347	Minus	50224-50395
	402745	9212200	Minus	76516-76680
	403074	8954241	Plus	143375-143581
	403077	8954241	Plus	146923-147222,147326-147628
65	403083	8954241	Plus	163070-163351
	403089	8954241	Plus	171964-172238
	403092	8954241	Plus	174720-175015,175104-175404,175508-175813
	403093	8954241	Plus	177083-177373,177464-177751
70	403411	9438635	Minus	104247-104420
	403661	8705027	Minus	30268-30482
	403667	7367384	Plus	9009-9534
	403691	7367384	Minus	88280-88463
	403753	7229888	Minus	43575-43887
	403798	8099896	Minus	75073-77664
75	404187	4401839	Plus	7644-7991
	404243	5672609	Plus	74695-75123
	404270	9628129	Minus	3549-3750,4161-4306,5962-6049,6849-6905
	404886	4884082	Plus	30058-30598
80	405291	6139075	Minus	3400-34351,35194-35336,45412-45475,45731-45958,47296-47457,49549-49658,49790-49904,50221-50342,53583-53667,54111-54279
	405285	6139075	Minus	55744-55903,57080-57170,61478-61590
	405445	1064740	Plus	118677-118807,119091-119256,121626-121823
	405547	1064740	Plus	124361-124900,124914-125050
	405636	5123990	Plus	56384-56587

405790 1203958 Plus 136364-136509,136579-136699,136805-136941

5 TABLE 3A lists about 1643 genes up-regulated in ovarian cancer compared to normal ovaries. These were selected as for Table 1A, except that the ratio was greater than or equal to 15, and the denominator was the arithmetic mean value for various non-malignant ovary specimens obtained.

TABLE 3A: ABOUT 1643 UP-REGULATED GENES, OVARIAN CANCER VERSUS NORMAL OVARY

Play: Primkey

Ex. Accn: Exemplar Accession

UG ID: UniGene ID

Title: Unigene Title

PFAM domain

ratio: tumor vs. normal tissues

15	Play	Ex. Accn No.	UG ID	Title	ratio
	420859	AW66397	Ha.100000	S100 calcium-binding protein A8 (calgranulin A)	218.9
	422166	W72424	Ha.112405	S100 calcium-binding protein A9 (calgranulin B)	180.2
	422158	L10343	Ha.112341	protease inhibitor 3, skin-derived (SKALP)	165.0
	424789	BE550723	Ha.153179	fatty acid binding protein 6 (fatty-acid-associated)	161.5
20	424202	NM_000254	Ha.8272	prostaglandin D2 synthase (PHO), brain	150.2
	408522	A0541214	Ha.46320	Small proline-rich protein SFRK (human, odontogenic k	149.5
	431369	BE184455	Ha.251754	secretory leukocyte protease inhibitor (antileukoprotein	144.9
	430520	NM_016190	Ha.242057	chromosome 1 open reading frame 10	136.6
	428471	X77348	Ha.194510	stratfin	129.5
25	421978	AJ243562	Ha.110156	NICE-1 protein	108.7
	437191	NM_005846	Ha.5478	serine protease inhibitor, Kazal type, 5	106.2
	407788	BE514982	Ha.36991	S100 calcium-binding protein A2	105.5
	441565	AW935576	Ha.169302	solute carrier family 2 (facilitated glucose transporter),	103.6
	431211	M68649	Ha.5568	gap junction protein, beta 2, 265D (connexin 26)	102.1
30	419329	AY007220	Ha.288958	S100-type calcium binding protein A14	95.3
	430572	U33114	Ha.245158	inhibitor of metalloproteinase 3 (Serrin/handus d	87.0
	417070	UG5590	Ha.81314	interleukin 1 receptor antagonist	85.1
	412636	NM_004415	Ha.74316	desmoplakin (DPI, DFI)	84.0
	417515	L24203	Ha.82237	ataxia-telangiectasia group D-associated protein	85.8
35	426295	AW367283	Ha.75539	zinc finger protein 6 (CMFAT1)	84.5
	423569	AJ216533	Ha.252658	ESTs. Weakly similar to alternatively spliced product u	84.4
	406711	N25514	Ha.77385	myosin, light polypeptide 6, alkali, smooth muscle and n	83.8
	408810	MJ1212	Ha.77385	myosin, light polypeptide 6, alkali, smooth muscle and n	81.0
	423762	T73654	Ha.278513	interferon, alpha-inducible protein 27	81.0
40	416885	AW253318	Ha.83035	med. T-cell differentiation protein	77.8
	409453	A085516	Ha.95612	ESTs	75.3
	424670	W61215	Ha.116651	epithelial V-like antigen 1	67.5
	417130	AW276858	Ha.81256	S100 calcium-binding protein A4 (calcium protein, calv	67.0
	423634	AW959038	Ha.1690	heparin-binding growth factor binding protein	65.7
45	442379	NM_004613	Ha.8265	transglutaminase 2 (C polypeptide, protein-glutamine-g	64.7
	456898	NM_001928	Ha.155597	D component of complement (adipsin)	64.6
	423017	AW178761	Ha.227848	serine (or cysteine) proteinase inhibitor, clade B (ovastu	63.6
	447990	BE348921	Ha.20144	small inducible cytokine subfamily A (Cp-Orn), memb	60.7
50	424362	AL137646	Ha.146001	Homo sapiens mRNA: cDNA DKFZp386F0824 (from	60.3
	414438	AB979277	Ha.76135	thioredoxin	59.9
	420136	AW601090	Ha.195851	actin, alpha 2, smooth muscle, ventr	58.9
	433338	AF017386	Ha.31386	ESTs. Highly similar to J01714 flizzed protein-2 [H]aa	58.8
	403741			predicted exon	57.0
55	430537	BE160081	Ha.256290	S100 calcium-binding protein A11 (calgizarin)	56.1
	424098	AF077374	Ha.139232	small proline-rich protein 3	55.8
	441591	AF255992	Ha.183	Duffy blood group	55.6
	426521	AF161445	Ha.170219	hypothetical protein	55.5
	406713	U02629	Ha.77385	myosin, light polypeptide 6, alkali, smooth muscle and n	55.3
	406725	D51245	Ha.286851	actin, beta	54.1
60	422168	A436894	Ha.112408	S100 calcium-binding protein A7 (psoriasin 1)	54.1
	406755	N80129	Ha.94360	metallothionein 1L	54.0
	425593	AA278921	Ha.1908	proteoglycan 1, secretory granule	53.3
	424257	AW539331	Ha.109857	gelsolin-like protein 1 (GELN-1) (Homo sapiens)	53.1
	421957	AW056837	Ha.109857	hypothetical protein DKFZp334H020	52.3
65	447526	ALD48753	Ha.340	small inducible cytokine A2 (monocyte chemoattractant pro	51.2
	406722	H27458	Ha.283305	Homo sapiens SINC3 protein (SINC3) mRNA, complete	51.0
	427223	BE208189	Ha.174631	cytochrome c oxidase subunit Vb	51.0
	414420	AJ043424	Ha.76956	immediate early response 3	50.9
	417259	AW903838	Ha.81800	chondroin sulfate proteoglycan 2 (versican)	50.3
70	441491	AW250089	Ha.75907	POZ and LIM domain 1 (elfin)	49.5
	436906	H55590	Ha.151244	major histocompatibility complex, class I, A	49.0
	409070	L11690	Ha.520	inducible penicillin-binding protein 1 (230/240kD)	49.0
	414033	U00630	Ha.75716	serine (or cysteine) proteinase inhibitor, clade B (ovastu	48.8
75	432706	NM_013230	Ha.286124	CD24 antigen (small cell lung carcinoma cluster 4 antigen)	48.8
	421548	L42583	Ha.111758	keratin 1A	48.7
	414662	AL030958	Ha.76867	major histocompatibility complex, class II, DR alpha	48.5
	425071	NM_013989	Ha.154424	deiodinase, iodothyronine, type II	48.5
	404767	U07070	Ha.84136	predicted exon	48.2
80	435725	BE821807	Ha.3337	paired-like homeodomain transcription factor 1	46.4
	441183	AW557446	Ha.301711	transmembrane 4 superfamily member 1	47.7
	400163			ESTs	47.2
	433423	BE407127	Ha.8997	predicted exon	47.0
	423457	F08209	Ha.185606	heat shock T0AD protein 1A	46.9
				heat shock domain homeo box 1	46.6

	114085	AA114016	Ha.75746	aldehyde dehydrogenase 6	46.0
	423189	MS9371	Ha.171596	EphA2	45.6
	438240	NS2638	Ha.124004	ESTs	45.5
5	417366	BE165289	Ha.1076	small proline-rich protein 1B (cornifin)	45.3
	412774	AA120865	Ha.23136	ESTs	45.1
	407242	M18728		gib-human nonspecific crossreacting antigen mRNA, co	44.8
	437252	AA370141	Ha.251453	Human DNA sequence from clone 367K21 on chr6	44.8
	426396			predicted exon	43.5
10	417365	D50683	Ha.62028	transforming growth factor, beta receptor II (70-80kD)	43.4
	423231	W37862	Ha.274358	Homo sapiens mRNA; cDNA DKFZp588I1524 (from c	43.4
	424479	AF054238	Ha.148098	smoothelin	43.3
	444776	NM_006147	Ha.11801	Interferon regulatory factor 6	43.2
	432314	AA533447	Ha.285173	ESTs	43.2
	426500	U75655	Ha.289114	hexabrachion (henascin C, cyclodextrin)	43.1
15	441406	Z45957	Ha.214358	Homo sapiens cDNA FLJ10457 fs, clone NT2RP1001	42.6
	412989	AI373182	Ha.75103	tyrosine 3-monoxygenase/hydroxylase 5-monoxygenase	42.6
	423720	LD44191	Ha.23368	Homo sapiens cDNA: FLJ21310 fs, clone COL02160	42.5
	401111			predicted exon	42.4
	407207	T03551	Ha.179661	tubulin, beta polypeptide	42.4
20	417164	AA332823	Ha.81361	heterogeneous nuclear ribonucleoprotein A/B	42.2
	424971	AA478005	Ha.154036	tumor suppressing anti-transferrin candidate 3	41.9
	439394	AA145250	Ha.58105	ESTs, Weakly similar to WDNM RAT WDNM1 PROT	41.9
	406657	AI576844	Ha.277477	major histocompatibility complex, class I, C	41.8
	451092	AI207295	Ha.13766	Homo sapiens mRNA for FLJ00074 protein, partial cds	41.6
25	412596	AA161219	Ha.11969	diphtheria toxin receptor (heparin-binding epidermal gro	41.6
	422103	AA598430	Ha.79776	protein kinase H1; small stress protein-like protein HS	41.5
	428765	AI018263	Ha.126265	ESTs	41.3
	426868	BE518571	Ha.429	ATP synthase, H+-transporting, mitochondrial F0 comp	41.0
	414622	AI752666	Ha.76669	nicotinamide N-methyltransferase	40.8
30	405022			predicted exon	40.8
	482221	AA812183	Ha.47447	ESTs	40.8
	446500	U78093	Ha.15154	sushi-repeat-containing protein, X chromosome	40.7
	421416	BE302950	Ha.104125	adenylyl cyclase-associated protein	40.6
	412247	AF022375	Ha.73793	vascular endothelial growth factor	40.5
35	410541	AA065003	Ha.54179	hypothetical protein	40.5
	406658	AI202095	Ha.77961	major histocompatibility complex, class I, B	40.0
	420225	AIW243046	Ha.94789	ESTs	40.0
	406825	AI382529	Ha.84298	CD74 antigen (invariant polypeptide of major histocom	39.4
	443823	AA345155	Ha.103983	complement component 1, a subcomponent, alpha poly	39.4
	404201	AF059566	Ha.103983	solute carrier family 5 (sodium iodide symporter), mem	39.3
	405138			predicted exon	39.1
	408733	AW264812	Ha.254290	ESTs	39.0
	414044	BE514194	Ha.17271	profilin 1	38.9
45	430152	AB001325	Ha.234642	aquaporin 3	38.8
	428121	AB006622	Ha.182536	Homo sapiens cDNA: FLJ21370 fs, clone COL03092	38.8
	434311	BE543469	Ha.266263	Homo sapiens cDNA FLJ14115 fs, clone MAMMA10	38.7
	405140			predicted exon	38.5
	432918	AF077200	Ha.279813	hypothetical protein	38.4
50	420107	AL043980	Ha.7886	pellino (Drosophila) homolog 1	38.4
	427693	BE546832	Ha.186370	collin 1 (non-muscle)	38.1
	449835	BE277929	Ha.11081	ESTs, Weakly similar to S57447 HPBRII-7 protein [H	38.1
	432374	W68815	Ha.301885	Homo sapiens cDNA FLJ11346 fs, clone PLACE1010	37.9
	428383	BE616599	Ha.184029	hypothetical protein DKFZp761A052	37.7
55	436258	AW887491	Ha.107125	ESTs, Weakly similar to S57447 HPBRII-7 protein [H	37.7
	425796	V63374	Ha.59936	keratin 10 (epidermal) hyperkeratosis: keratosis palm	37.7
	400327	M18679	Ha.247942	Human variant SS rRNA-like gene and ORF, complete	37.6
	401781			predicted exon	37.6
	448257	AW772070	Ha.263146	ESTs	37.3
60	429415	AA337211	Ha.184222	Dowry syndrome critical region gene 1	37.2
	424206	NM_003734	Ha.198241	amine oxidase, copper containing 3 (vascular adhesion p	37.2
	406812	AF000575	Ha.67846	leukocyte immunoglobulin-like receptor, subfamily B (37.2
	425862	U83115	Ha.101002	absent in melanoma 1	37.2
	432501	BE546832	Ha.267329	Fas binding protein 1	37.1
65	421786	AI188553	Ha.21351	ESTs	37.1
	427981	BE275986	Ha.181311	asparaginyl-tRNA synthetase	37.0
	410143	AA118169	Ha.268819	Homo sapiens cDNA: FLJ21022 fs, clone CA050383	36.8
	451028	AW633606	Ha.109012	ESTs	36.7
	414135	NM_004419	Ha.2128	dual specificity phosphatase 5	36.7
70	414602	AW630088	Ha.76550	Homo sapiens mRNA; cDNA DKFZp564B1264 (from	36.7
	401786			predicted exon	36.5
	411469	T09997	Ha.70327	cysteine-rich protein 2	36.2
	419693	AA133749	Ha.92323	FXYD domain-containing ion transport regulator 3	36.1
	417039	AA502180	Ha.80986	ATP synthase, H+-transporting, mitochondrial F0 comp	36.1
75	406718	AA505525	Ha.169478	glyceralddehyde-3-phosphate dehydrogenase	36.0
	425543			predicted exon	35.0
	408669	AI93591	Ha.76146	platelet/endothelial cell adhesion molecule (CD31 anti	35.9
	414987	AA524394	Ha.165544	ESTs	35.9
	445810	AW265700	Ha.155560	ESTs	35.9
	406653	AA574074	Ha.77961	major histocompatibility complex, class I, B	35.6
80	407498	U29131		gib-human HMIC-C chimeric transcript mRNA, partial	35.6
	412524	AA417813	Ha.11177	ESTs	35.5
	401521			predicted exon	35.4
	428948	AW269713	Ha.221441	ESTs	35.1
	406728	AI596345	Ha.183704	ubiquitin C	34.9

440669	AI206964			glox30g66.x1 NQ_CGAP_G06 Homo sapiens cDNA	34.8
422658	AF211981	Hs.250175		homolog of yeast long chain polyunsaturated fatty acid	34.8
452924	AW580939	Hs.97199		complement component C1q receptor	34.7
428600	AW863261	Hs.15036		ESTs. Highly similar to AF161358.1 HSPC085 [Lscpi]	34.7
425928	AW501137			gbU4HF-8Pp-at-a-12-4-UL.r1 NIH_MGC_31 Homo	34.6
458390	BE827725			gbS012763471 NIH_MGC_20 Homo sapiens cDNA	34.5
445055	BE512695	Hs.109051		glycoprotein, synaptic 2	34.3
411789	AF245505	Hs.72157		Homo sapiens adican mRNA, complete cds	34.3
410626	BE407727			gbS01299771F1 NIH_MGC_21 Homo sapiens cDNA	34.2
410705	AF232494	Hs.68946		ESTs	34.2
419273	BE271180	Hs.293450		ESTs	34.2
407839	AA045144	Hs.161566		ESTs	34.0
444286	AI625304	Hs.190312		ESTs	34.0
449225	AB002365	Hs.23311		KIAA0367 protein	34.0
414290	AI568801	Hs.71721		ESTs	33.9
401245				predicted exon	33.9
425222	M65430	Hs.155191		villin 2 (actin)	33.8
409930	RI2678	Hs.301569		KIAA0564 protein	33.8
437201	F25275	Hs.177456		amyloid beta (A4) precursor protein (protease nexin-II,	33.7
406566	AF068896	Hs.11590		cathespin F	33.7
405071				predicted exon	33.7
455426	AW937792			gbCV3-DT0045-140208-082-067 DT0045 Homo sapi	33.6
416160	T82802			gbY05804.r1 Soares fetal liver spleen 1NFLS Homo s	33.5
424995	Z45023			gbHSC2FA041 normalized infant brain cDNA Homo s	33.5
453870	AW365001	Hs.8042		Homo sapiens cDNA: FLJ23173 fs, clone LNG10019	33.5
433470	AW660564	Hs.3337		transmembrane 4 superfamily member 1	33.4
428188	MS8447	Hs.27		transglutaminase 1 (K polypeptide epidermal type I, pro	33.3
417409	BE272508	Hs.82109		syndecan 1	33.3
425389	AW974499	Hs.192183		ESTs	33.3
434656	AI624436	Hs.194468		ESTs	33.2
456562	AA390409	Hs.102069		DKFZP434O125 protein	33.1
447111	AI017574	Hs.17409		cysteine-rich protein 1 (intestinal)	33.0
432360	BE045243	Hs.274416		NADH dehydrogenase (ubiquinone) 1 alpha subcomplex	32.9
442125	MG1689	Hs.1735		inhibin, beta B (activin A8 beta polypeptide)	32.7
419968	XA0430	Hs.53913		inhibin beta 5 (inhibin, beta 5)	32.7
429415	NM_002593	Hs.202097		procollagen C-endopeptidase enhancer	32.6
451541	BE279383	Hs.26557		phalloidin 3	32.6
424459	N90344	Hs.149436		kinase family member 5B	32.4
425144				predicted exon	32.4
422511	AU076442	Hs.117938		collagen, type XVII, alpha 1	32.4
402321				predicted exon	32.3
437712	XA0586	Hs.85944		neutrophilic tyrosine kinase, receptor, type 1	32.3
417433	BE270266	Hs.82128		574 oncotel lymphoblast glycoprotein	32.2
419659	AB023206	Hs.92186		Leman coiled-coil protein	32.0
428582	BE336699	Hs.185055		BENE protein	32.0
421401	AW110470	Hs.104019		transforming, acidic coiled-coil containing protein 3	32.0
414064	BE245289	Hs.16165		expressed in activated TLAK lymphocytes	32.0
431938	AA938471	Hs.115242		developmentally regulated GTP-binding protein 1	32.0
411930	F06486			gbHSC19G051 normalized infant brain cDNA Homo s	31.9
428150	AW950547	Hs.182684		cytochrome c oxidase subunit VIIa polypeptide 2 (liver)	31.8
401887				predicted exon	31.8
412570	AA033517	Hs.74047		electron-transfer-flavoprotein, beta polypeptide	31.7
422738	X09915	Hs.1573		growth differentiation factor 5 (cardiopo-derived morph	31.6
453302	XA4838	Hs.21638		resin (Roeck-Stabberg cell-expressed intermediate filam	31.5
413924	AL119984	Hs.75616		KIAA0018 gene product	31.4
402031	R08865	Hs.19813		ESTs	31.3
434715	BE005346	Hs.116410		ESTs	31.3
422831	RI2504			gbY06806.r1 Soares fetal liver spleen 1NFLS Homo sa	31.2
416854	HA0164	Hs.80296		Purkinje cell protein 4	31.2
422976	AU076657	Hs.1600		sec61 homolog	31.1
426356	BE536636			gbS01064837F1 NIH_MGC_10 Homo sapiens cDNA	31.0
433925	AF112208	Hs.44163		TSC2 differentiation-associated protein	30.9
430040	AA5053115	Hs.227823		pMS protein	30.8
406340	AA299679	Hs.180370		collin 1 (non-muscle)	30.8
426050	AF107307	Hs.160596		E74-like factor 3 (ets domain transcription factor, epith	30.7
425105	BE390666	Hs.24956		hypothetical protein FLJ22055	30.7
426066				predicted exon	30.7
429338	BE182592	Hs.139322		small proline-rich protein 3	30.6
418371	M13560	Hs.84258		CD74 antigen (invariant polypeptide of major histocom	30.4
421251	Z26913	Hs.102948		enigma (LIM domain protein)	30.3
458084	AA115859	Hs.79708		ESTs	30.3
402023				predicted exon	30.3
404356				predicted exon	30.2
415973	R24707	Hs.260201		ESTs	30.2
445983	AI269107	Hs.132219		ESTs	30.1
450440	AB024334	Hs.25001		lysine 3-monooxygenase/hypophan 5-monooxygenas	30.1
458789	AL157468	Hs.20157		Homo sapiens cDNA FLJ20848 fs, clone ADKA01732	30.1
408442				predicted exon	30.1
406828	AA419202	Hs.84288		CD74 antigen (invariant polypeptide of major histocom	30.0
423267	AL137416	Hs.126177		Homo sapiens mRNA: cDNA DKFZp434O192 (rom c	30.0
451383	AW239384	Hs.20242		hypothetical protein FLJ12788	30.0
437042	AK020702	Hs.5420		hypothetical protein FLJ26095	30.0
459399	BE407712			gbS01259749F1 NIH_MGC_21 Homo sapiens cDNA	30.0
425650	NM_001944	Hs.1925		desmoglein 3 (pemphigus vulgaris antigen)	30.0

	416511	NM_006762	Hs.79356	Lysosomal-associated multispanning membrane protein	29.9
	431009	BE149762	Hs.248213	gap junction protein, beta 6 (connexin 30)	29.7
	436851	BE045992	Hs.276598	ESTs	29.6
5	419766	BE243101	Hs.22391	chromosome 20open reading frame 3	29.5
	420747	BE294407	Hs.95910	phosphotriesterase, platelet	29.5
	435895	AF037335	Hs.5338	carbonic anhydrase XII	29.5
	412765	AK000620	Hs.14571	ADP-ribosylation factor 1	29.4
	419223	X60111	Hs.1244	CD5 antigen (p15)	29.4
10	413796	AW408094	Hs.75545	interleukin 4 receptor	29.4
	447785	AW259151	Hs.163812	ESTs	29.4
	431103	NB7897	Hs.44	pleiotrophin (heparin binding growth factor 8, neurite g	29.4
	415314	M5920	Hs.6422	glycoprotein M6B	29.3
	428411	AW291464	Hs.10338	ESTs	29.3
	435850	AA080105	Hs.140	immunoglobulin heavy constant gamma 3 (Gm marker)	29.3
15	430451	AA363472	Hs.249692	cathepsin B	29.2
	453949	AIJ077146	Hs.36927	heat shock 105kD	29.2
	413859	AW92356	Hs.8394	pyruvate dehydrogenase kinase, isoenzyme 4	29.2
	407845	ALD36518	Hs.118598	ESTs	29.1
	453500	AA176427	Hs.43125	ESTs	29.1
20	456054	B6131241	gb:501151545F1 NIH_MGC_19 Homo sapiens cDNA	29.0	
	453467	AU335997	Hs.30089	ESTs	29.0
	411794	AL118377	Hs.75658	phosphorylase, glycogen; brain	28.9
	421773	HS9223	Hs.12457	ESTs	28.9
	423621	BE002504	gb:CV4-BN0090-070400-163-c07 BN0090 Homo sapi	28.8	
25	408935	BE53708	Hs.285363	ESTs	28.8
	450847	NM_003155	Hs.25580	stannocalcin 1	28.8
	431243	U64545	Hs.352189	cyndinase 4 (amphiphysin, rydocus)	28.7
	423225	AA852604	Hs.125359	Thy-1 cell surface antigen	28.7
	433469	F12741	gb:HS30G061 normalized infant brain cDNA Homo	28.7	
30	405763			predicted exon	28.7
	417308	H60720	Hs.B1892	KIAA0101 gene product	28.7
	405749			predicted exon	28.7
	413442	BE140543	gb:RC0-HT0015-310599-016 HT0015 Homo sapiens c	28.6	
	404828			predicted exon	28.6
35	407453	AJ132087	gb:Homo sapiens mRNA for azoninein dynein heavy ch	28.6	
	418529	AW005695	Hs.250897	TRK-A fused gene (NOTE: non-standard symbol and nam	28.6
	413787	AJ325558	Hs.75544	tyrosine 3-monooxygenase/hypophan 5-monooxygenase	28.5
	450690	AA296696	Hs.25334	FXYD domain-containing ion transport regulator 5	28.5
40	402430			predicted exon	28.4
	413929	BE501689	Hs.75817	collagen, type IV, alpha 2	28.2
	423803	NM_005709	Hs.132945	PDZ-73 protein	28.2
	406086			predicted exon	28.2
	416885	X54162	Hs.79386	hormonin 1 (smooth muscle)	28.2
45	417055	N39489	Hs.7258	Homo sapiens cDNA: FLJ22021 fs, clone HEP08253	28.1
	449184	AW296295	Hs.196491	ESTs	28.1
	446542	NM_004281	Hs.15259	BCL2-associated athanogene 3	28.1
	412793	AW97986	Hs.149155	gb:RC1-BN0055-232000-021-e11 BN0055 Homo sapie	28.0
	452818	W21909	Hs.8372	ubiquitin-cytochrome c reductase (6.4kD) subunit	28.0
50	402869			predicted exon	27.9
	435810	AA353044	Hs.5321	ARF1 (actin-related protein 3, yeast) homolog	27.9
	402075			predicted exon	27.9
	410480	R97457	Hs.63984	cadherin 13, H-cadherin (heart)	27.8
	406590	M29540	Hs.220529	carcinoembryonic antigen-related cell adhesion molecu	27.8
55	439766	AB033492	Hs.301241	Homo sapiens mRNA; cDNA DKF2p566A0424 (from	27.7
	424482	BE265211	Hs.149155	voltage-dependent anion channel 1	27.6
	420737	L08056	Hs.95899	tumor necrosis factor (ligand) superfamily, member 7	27.6
	414663	BE396326	gb:G0128925F1 NIH_MGC_8 Homo sapiens cDNA c	27.6	
	409703	NM_006187	Hs.56009	2'-O-deoxyadenylate synthetase 3	27.6
60	446108	ALJ06596	Hs.102773	ESTs	27.5
	428144	BE269243	Hs.182625	VAMP (vesicle-associated membrane protein)-associate	27.5
	445688	AI248205	Hs.153244	ESTs	27.5
	405411			predicted exon	27.5
	410275	U95658	Hs.61796	transcription factor AP-2 gamma (activating enhancer-b	27.5
65	424675	NM_005512	Hs.151641	glycoprotein A repetitions predominant	27.3
	450455	AL117424	Hs.25035	chloride intracellular channel 4	27.3
	414655	AA155986	Hs.104640	HIV-1 inducer of short transcripts binding protein	27.2
	433378	BE339896	Hs.3416	adipose differentiation-related protein	27.2
	401994			predicted exon	27.2
	445033	AV652402	Hs.155145	ESTs	27.2
70	402277			predicted exon	27.1
	428105	BE620016	Hs.182470	PTD10 protein	27.1
	448625	AW970786	Hs.178470	Homo sapiens cDNA: FLJ22652 fs, clone HS108080	27.1
	422587	AB78352	Hs.118625	hexokinase 1	27.0
75	457204	BE264152	Hs.221994	ESTs	27.0
	444094	AB65754	Hs.202584	ESTs	27.0
	414053	BE391635	Hs.75725	transgelin 2	26.9
	430511	BE018156	Hs.2575	calpain 1, (mu1) large subunit	26.9
	434038	L32971	Hs.3712	ubiquitin-cytochrome c reductase, Rieske iron-sulfur po	26.9
80	424939	AW000039	Hs.153681	Homo sapiens NY-REN-62 antigen mRNA, partial cds	26.9
	414539	BE379046	gb:G012366-0F1 NIH_MGC_44 Homo sapiens cDNA	26.9	
	404675			predicted exon	26.8
	401597	AA172106	Hs.110950	Rag C protein	26.8
	401405			predicted exon	26.8
	411541	W03940	gb:za62b02.r1 Sources fetal liver spleen INFLS Homo sa	26.8	

	412025	AB27451	Hs.24143	ESTs	26.7
	414276	BE297862		gb00117480F1 NIH_MGC_17 Homo sapiens cDNA	26.7
	440065	AW449415	Hs.10260	Homo sapiens cDNA FLJ11341 fs, clone PLACE1010	26.7
	447981	RS3772	Hs.8929	hypothetical protein FLJ11382	26.7
5	410677	NM_003278	Hs.54242	tetranectin (plasminogen-binding protein)	26.5
	403982			predicted exon	26.5
	452933	AW091423	Hs.28855	Homo sapiens cDNA: FLJ22425 fs, clone HRC08666	26.5
	407233	X16354	Hs.50964	carcinoembryonic antigen-related cell adhesion molecule	26.4
	430127	AA219498	Hs.233952	proteasome (prosome, macropain) subunit, alpha type, 7	26.3
	448218	A138469		gbq409b12.x1 Soares_placenta_809weeks_29thHP8to	26.3
10	413511	AB27178	Hs.75412	Arginine-rich protein	26.2
	459511	A1142379	Hs.65403	gbxg64c01.1 Soares_testis_NHT Homo sapiens cDNA	26.2
	110668	BE379794		hypothetical protein	26.2
	458662	AUC34110	Hs.169149	karyopherin alpha 1 (Importin alpha 5)	26.2
	451219	AA064209	Hs.167904	ESTs	26.1
	448559	BE267765	Hs.22595	hypothetical protein FLJ110637	26.2
	400800	Y10262	Hs.46925	eyes absent (Drosophila) homolog 3	26.2
	446342	BE298665	Hs.14848	Homo sapiens mRNA; cDNA DKFZp564D018 (from c	26.2
	421177	AW070211	Hs.102415	Homo sapiens mRNA; cDNA DKFZp588N0121 (from	26.1
	433848	AF005719	Hs.93764	carboxypeptidase A3	26.1
20	448497	BE513269	Hs.21893	ESTs, Weakly similar to glyceral 3-phosphate permease	26.1
	415279	F04237	Hs.1447	glial fibrillary acidic protein	26.0
	119323	AI052979	Hs.132776	ESTs	26.0
	432055	L36033	Hs.237356	stromal cell-derived factor 1	25.9
25	437679	NM_014214	Hs.5753	Inositol(myo)-[or 4]-C-monomophosphate 2	25.9
	425535	AB007937	Hs.158287	KIAA0466 gene product	25.8
	412923	AA175922	Hs.75092	adaptor-related protein complex 3, delta 1 subunit	25.8
	447690	AT03397	Hs.202365	ESTs	25.8
	419118	AA234223	Hs.139204	ESTs	25.8
30	421224	AW402154	Hs.128122	ESTs	25.8
	414690	BE281095	Hs.17573	uridine phosphorylase	25.8
	447330	BE273949	Hs.16141	indolin 1	25.7
	405810			predicted exon	25.7
	447604	AW069933	Hs.293674	ESTs	25.7
	445677	H95577	Hs.6638	ras homolog gene family, member E	25.7
	465088	BE177320	Hs.155148	Homo sapiens cDNA: FLJ23032 fs, clone LING06451	25.7
	417120	N79687	Hs.46616	ESTs	25.6
	405194			predicted exon	25.6
	410687	U24389	Hs.65436	lysoyl oxidase-like 1	25.6
40	421886	AA299780	Hs.121036	ESTs	25.6
	420459	AF016045	Hs.97905	ovo (Drosophila) homolog-like 1	25.5
	416323	N72630	Hs.33981	Homo sapiens genomic DNA, chromosome 21q, section	25.5
	446292	AF381497	Hs.278682	Rib type C glycoprotein	25.5
	416274	AW160404	Hs.79126	guanine nucleotide binding protein 10	25.5
45	430028	BE564110	Hs.227750	NADH dehydrogenase (ubiquinone) 1 beta subcomplex	25.5
	438450	AK050865	Hs.65853	nodal, mouse, homolog	25.5
	400215			predicted exon	25.4
	30014	H59354	Hs.182485	actinin, alpha 4	25.4
	453582	AW554339	Hs.33476	hypothetical protein FLJ11937	25.4
50	405567			predicted exon	25.4
	459170	AI905518		gbfRC-BT091-120199-098 BT091 Homo sapiens cDNA	25.4
	407944	R34008	Hs.239727	desmocollin 2	25.4
	415748	D30086	Hs.979	pyruvate dehydrogenase (liponitide) beta	25.3
	423267	H38340		gbyp70h07.r1 Soares_adult brain N204HB55Y Homo s	25.3
	450944	AA554989	Hs.209691	aurf2 (suppressor of bin/AR, Aspergillus nidulans) homo	25.3
	432906	BE265489	Hs.3123	lethal giant larvae (Drosophila) homolog 2	25.3
	400104			predicted exon	25.3
	490919	AI549095	Hs.67776	ESTs, Weakly similar to ALU7_HUMAN ALU SUBFA	25.3
	408957	MS7417		gbf-Homo sapiens mucin (mucin) mRNA, partial cds.	25.3
	402639			predicted exon	25.3
	447147	AA910353	Hs.292815	ESTs	25.3
	453379	AA035261	Hs.81753	ESTs	25.3
	414217	A030268	Hs.279569	Homo sapiens cDNA: FLJ23165 fs, clone LING09948	25.3
	430223	NM_002514	Hs.235935	nephroblastoma overexpressed gene	25.3
65	406885	M18728		Homo sapiens nonspecific crossreacting antigen mRNA, co	25.3
	444747	AA540307	Hs.257291	ESTs, Weakly similar to PSS8_HUMAN PROSTASIN	25.2
	417083	R22519	Hs.23398	ESTs	25.2
	430235	BE268048	Hs.236494	RAB10, member RAS oncogene family	25.2
	490001	AT761313	Hs.204605	ESTs	25.2
70	434598	AW519020	Hs.212640	Homo sapiens cDNA FLJ13265 fs, clone OVARC1000	25.2
	415917	A39112		gbfHSC10A111 normalized infant brain cDNA Homo	25.2
	444409	AT921140	Hs.49265	ESTs	25.2
	426578	BE391797	Hs.82148	hypothetical protein	25.1
	433417	AA581773	Hs.136494	ESTs	25.1
	426372	BE304680	Hs.169551	DEAD1 (Asp-Glu-Ala-AspHis) box polypeptide 21	25.1
75	402131			predicted exon	25.1
	450545	AW135582	Hs.201767	ESTs	25.0
	434162	AQ21214	Hs.116136	ESTs	25.0
	406571			predicted exon	24.9
80	427600	AW530918	Hs.695	proteasome (prosome, macropain) activator subunit 2 (P	24.9
	409402	AF208234	Hs.19775	cystatin B (stafin B)	24.9
	400135			predicted exon	24.9
	429403	AI393048	Hs.239894	leucine rich repeat (in FLN) interacting protein 1	24.9
	403223			predicted exon	24.8

	435236	T03890	Hs.157208	ESTs, Highly similar to Arx homeoprotein [M.musculu	24.8
	457439	AWK10408	Hs.271167	L-ipoic acid oxidase	24.8
	446667	Z78394	Hs.4896	Homo sapiens cDNA: FLJ22045 fs, clone HEP0978	24.8
	440505	Z6094	Hs.186898	ESTs	24.8
5	426724	AA383623	Hs.293816	ESTs	24.8
	403359			predicted exon	24.7
	442826	AD18777	Hs.131241	ESTs	24.7
	411503	AW190338	Hs.28029	putative receptor P2X, ligand-gated ion channel, 4	24.6
	414540	BE379050		glb.601236655F1 NIH_MGC_44 Homo sapiens cDNA	24.6
10	421555	AB014520	Hs.103958	Homo sapiens cDNA: FLJ22735 fs, clone HUA00180	24.5
	436804	AA628976	Hs.136954	ESTs	24.5
	400481	H25530	Hs.80858	serine carrier family 22 (organic cation transporter), me	24.5
	418994	AA296520	Hs.89546	selectin E (endothelial adhesion molecule 1)	24.5
	426383	BE537380		glb.601054570F1 NIH_MGC_10 Homo sapiens cDNA	24.4
	418408	AA219321	Hs.173294	ESTs	24.4
15	418186	W07575	Hs.259177	ESTs	24.4
	416908	AA333990	Hs.80424	coagulation factor XII, A1 polypeptide	24.4
	453857	AL080235	Hs.35861	DKFZP586E1621 protein	24.4
	439706	AW672527	Hs.55971	ESTs	24.4
20	441619	NM_014056	Hs.18332	DKFZP564K247 protein	24.4
	417198	F11533	Hs.81634	ATP synthase, H+ transporting, mitochondrial F0 comp	24.3
	433662	W07162	Hs.150826	CATX-8 protein	24.3
	455986	AI13222	Hs.36989	coagulation factor VII (serum prothrombin conversion a	24.3
	457123	AA170021	Hs.7917	ESTs	24.3
25	433864	AA931550	Hs.192785	ESTs	24.3
	408655	AW502208		glb.UL-HF-8R0P-aj-u-09-0-ULr1 NIH_MGC_52 Hom	24.3
	448175	BE296174	Hs.225160	Homo sapiens cDNA FLJ13102 fs, clone NT2P3002	24.3
	405277			predicted exon	24.3
	451957	AI796320	Hs.10299	Homo sapiens cDNA FLJ13545 fs, clone PLACE1006	24.3
30	408802	AL048269	Hs.288544	Homo sapiens cDNA: FLJ20882 fs, clone ADKA0320	24.2
	401757			predicted exon	24.2
	444751	AIZ07406	Hs.11066	hypothetical protein PR01197	24.2
	408647	AW245831		glb.2B22937.Sprine NIH_MGC_7 Homo sapiens cDNA	24.2
	418870	AF147204	Hs.89414	chemokine (C-X-C motif), receptor 4 (lusin)	24.2
35	436913	AA789074	Hs.167478	ESTs	24.2
	434745	AW674445	Hs.181055	ESTs, Weakly similar to HuEMAP [H.sapiens]	24.2
	451743	AW074266	Hs.23071	ESTs	24.2
	421853	AL117472	Hs.109924	DKFZP566P1422 protein	24.2
40	407926	AW956332	Hs.23971	ESTs	24.1
	413973	BE278658	Hs.128417	Homo sapiens cDNA FLJ14009 fs, clone Y79AA1002	24.1
	439078	AF059536		glb.homo sapiens full length insert cDNA clone Y79BF	24.1
	401913			predicted exon	24.1
	435138	BE314734		glb.501152976F1 NIH_MGC_19 Homo sapiens cDNA	24.1
	405911			predicted exon	24.0
45	413127	BE066529	Hs.83484	SRY (sex determining region Y)-box 4	24.0
	430793	M83181	Hs.247940	5-hydroxytryptamine (serotonin) receptor 1A	24.0
	434445	A349306	Hs.11782	ESTs	24.0
	418166	AI754416	Hs.260024	Csk-2 effector protein 3	24.0
50	431971	BE274907	Hs.77385	myosin, light polypeptide 6, alkali, smooth muscle and n	23.9
	401167			predicted exon	23.9
	454163	AW175997		glb.CNV0-BT0078-190899-605-E02 BT0078 Homo sap	23.9
	403306	NM_008625	Hs.74368	transmembrane protein (63kd), endoplasmic reticulum	23.9
	410627	AA181339	Hs.929	myosin, heavy polypeptide 7, cardiac muscle, beta	23.9
	450796	NM_001988	Hs.25482	enkephelin	23.8
55	442189	BE277633	Hs.286027	elk-1-induced mRNA	23.8
	402899			predicted exon	23.8
	426143	BE379836	Hs.167105	prolaserone (prosome, macropain) subunit, alpha type, 3	23.8
	437592	NM_003851	Hs.5710	ocular repressor of EIA-mutated genes	23.8
	433998	AF62838	Hs.271433	ESTs, Moderately similar to ALU2_HUMAN ALU SU	23.8
	401088			predicted exon	23.8
60	449924	AZ64671	Hs.164186	ESTs	23.8
	402902	AA742277		glb.ny28a09.s1 NCL CGAP_GCB1 Homo sapiens cDN	23.8
	425369	AF134157	Hs.169487	Yesciter (mouse) mal-related leucine zipper homolog	23.7
	458698	AW451089	Hs.257628	ESTs	23.7
65	422048	NM_012445	Hs.288126	spondin 2, extracellular matrix protein	23.7
	413460	RE1610	Hs.21527	ESTs, Weakly similar to KIAA0918 protein [H.sapiens]	23.6
	401575			predicted exon	23.6
	431822	AA516049		glb.ny65801.s1 NCL CGAP_Lip2 Homo sapiens cDNA	23.6
	427276	AA400269	Hs.49598	ESTs	23.6
70	417089	AA442132	Hs.81097	cytochrome c oxidase subunit VIII	23.5
	400161			predicted exon	23.5
	417190	NM_001359	Hs.81548	2,4-dioxynyl CoA reductase 1, mitochondrial	23.5
	443667	AI129066	Hs.135457	ESTs	23.5
75	413544	BE147225		glb.PM2-HT0225-031299-003-11 HT0225 Homo sapie	23.5
	403695			predicted exon	23.5
	422050	W05345	Hs.293884	ESTs	23.4
	432517	AF275816	Hs.283096	PR domain containing 9	23.4
	405307			predicted exon	23.4
	416328	H48389	Hs.268886	ESTs	23.4
80	427174	AA398848	Hs.97541	ESTs	23.4
	426148	AI751071	Hs.167135	Homo sapiens cDNA FLJ10728 fs, clone NT2P3001	23.3
	452544	AW851888		glb.CNV0-C02225-131095-034-005 C02225 Homo sapie	23.3
	404890			predicted exon	23.3
	408725	AA131539	Hs.15669	ESTs	23.3

	428362	AA426555	Hs.169333	ESTs	23.3
	425340	AA425234	Hs.179896	ribose 5-phosphate isomerase A (ribose 5-phosphate ep	23.3
	423440	NM_004812	Hs.116724	aldo-keto reductase family 1, member B11 (aldose red	23.3
	410962	BE273748	Hs.752	FK506-binding protein 1A (150k)	23.2
5	411796	AA607197	Hs.6918	ESTs	23.2
	458954	AW379875	Hs.141742	Homo sapiens cDNA FLJ12211 fs, clone MAMMA10	23.2
	405896	AB010447	Hs.48778	ribon protein	23.2
	457024	AA397546	Hs.119151	ESTs	23.2
	414591	AB688490	Hs.55902	ESTs	23.2
10	437846	AA773866	Hs.244569	ESTs	23.2
	401120			predicted exon	23.1
	421747	AB18224	Hs.107747	DNFZP566C243 protein	23.1
	452590	AA428123	Hs.7745	17kD total brain protein	23.1
15	414327	DE08145	Hs.185254	ESTs, Moderately similar to NAC-1 protein [R.norveg	23.1
	405256			predicted exon	23.1
	452416	AA026115	Hs.114777	ESTs	23.1
	440584	AIZ53123	Hs.127356	ESTs, Highly similar to NEST_HUMAN NEST1 (HLaap	23.1
	445603	H08345	Hs.106234	ESTs	23.1
	453536	AA805939	Hs.117827	ESTs	23.1
20	434867	AF159442	Hs.103382	phospholipid scramblase 3	23.0
	404727			predicted exon	23.0
	407317	AIZ04033	Hs.271461	ESTs, Weakly similar to ALU5_HUMAN ALU SUBFA	23.0
	405580			predicted exon	23.0
	437858	W81260	Hs.43410	ESTs	22.9
25	448781	AW243419	Hs.254048	ESTs	22.9
	457287	AW568188	Hs.290999	ESTs	22.9
	405545			predicted exon	22.9
	431562	AJ884334	Hs.11637	ESTs	22.9
30	440703	AL137663	Hs.7378	Homo sapiens mRNA; cDNA DKFZP434G227 (from c	22.9
	439848	AW592426		gk:EST391359 MAGE resequences, MAGP Homo sap	22.9
	418148	AA111473	Hs.281877	ESTs	22.9
	435332	AW642747	Hs.293314	ESTs, Highly similar to unnamed protein product [H.s	22.9
	401566			predicted exon	22.8
35	425078	NM_002599	Hs.154437	phosphodiesterase 2A, cGMP-stimulated	22.8
	406684	X16354	Hs.50654	cardiac myocyte antigen-related cell adhesion molecu	22.8
	421651	AW609632	Hs.263386	ESTs	22.8
	421064	AIZ45432	Hs.101382	tumor necrosis factor, alpha-induced protein 2	22.8
	441249	AA971585	Hs.166250	ESTs	22.8
40	457624	AA609159	Hs.287591	Homo sapiens cDNA FLJ13544 fs, clone PLACE1006	22.8
	407395	AF090892		gk:Homo sapiens skin-specific protein (sp33) mRNA, p	22.8
	459006	AW295631	Hs.27721	hypothetical protein FLJ20353	22.8
	435827	H71817	Hs.5322	guanine nucleotide binding protein (G protein), gamma	22.7
	418174	L26589	Hs.83555	Rho GDP dissociation inhibitor (GDI) beta	22.7
45	416307	U70267	Hs.83974	solute carrier family 21 (prostaglandin transporter), man	22.7
	456035	N54956	Hs.271726	ESTs	22.7
	457867	AA045767	Hs.5300	bladder cancer associated protein	22.7
	440401	A1126341	Hs.143687	ESTs	22.7
	409126			predicted exon	22.7
50	414931	AK000342	Hs.77646	Homo sapiens mRNA; cDNA DKFZP751M0223 (from	22.7
	406719	AJ832982	Hs.169476	glyceraldehyde-3-phosphate dehydrogenase	22.6
	439875	W55357	Hs.133660	Rho GTPase activating protein 1	22.6
	456058	NM4987	Hs.52063	ESTs	22.6
	441926	AJ015051	Hs.130653	ESTs	22.6
55	428423	AJ078517	Hs.184276	solute carrier family 9 (sodium/hydrogen exchanger), is	22.6
	438518	BE561938	Hs.255823	immunoglobulin heavy constant mu	22.6
	420574	NM_000055	Hs.1327	butyrylcholinesterase	22.6
	422160	AW582898		gk:af07c04.y1 Human Pancreatic Islets Homo sapiens c	22.5
	412408	D51103	Hs.73851	ATP synthase, H+ transporting, mitochondrial F0 comp	22.5
	409864			predicted exon	22.5
60	434360	AW015415	Hs.127780	ESTs	22.5
	427877	AW630727	Hs.181307	H3 histone, family 3A	22.4
	450309	AJ852281	Hs.54547	ESTs	22.4
	424059	AW461265	Hs.107418	ESTs	22.4
	414626	BE410589		gk:gb01303308F1 NIH_MGC_21 Homo sapiens cDNA	22.4
	401991			predicted exon	22.4
65	419741	NM_007019	Hs.93002	ubiquitin carrier protein E2-C	22.3
	457852	U25760	Hs.210783	Human chromosome 17q21 mRNA clone 1046:1-1	22.3
	422597	BE245909	Hs.118634	ATP-binding cassette, sub-family B (MDR/TAP), mem	22.3
	426504	X99133	Hs.204238	lipocalin 2 (onco gene 24p3)	22.3
70	447306	AJ373163	Hs.170333	ESTs	22.3
	424966	AJ077312	Hs.153036	solute carrier family 7 (cationic amino acid transporter,	22.3
	422739	H20106	Hs.119591	adaptor-related protein complex 2, sigma 1 subunit	22.2
	425204	AL121015	Hs.277704	oxygen regulated protein (150MD)	22.2
	423804	AW403448	Hs.1706	interferon-stimulated transcription factor 3, gamma (48k	22.2
75	404693	AJ842294	Hs.173959	uncharacterized bone marrow protein B4053	22.2
	441624	AF220191	Hs.179566	uncharacterized hypothalamic protein HSMNP1	22.2
	425751	T18239	Hs.1940	crystallin, alpha B	22.2
	452976	RA4214	Hs.101189	ESTs	22.2
80	414642	AA158359		gk:cd3061.r1 Soares_pregnanal_uterus_NbHPU Homo	22.2
	437492	AL390127	Hs.7104	Homo sapiens mRNA; cDNA DKFZp761P06121 (from	22.2
	417426	NM_002291	Hs.82124	tannin, beta 1	22.2
	414774	X02419	Hs.77274	plasminogen activator, urokinase	22.1
	424631	AA688021	Hs.178918	ESTs	22.1
	413967	AW204431	Hs.117853	ESTs	22.1

	400174			predicted exon	22.1
	431837	T79328	Hs.298262	ESTs, Weakly similar to dJ8JUR.1 [H.sapiens]	22.1
	471626			predicted exon	22.1
5	418374	AJ011916	Hs.84359	hypothetical protein	22.0
	429297	X82494	Hs.198862	filin 2	22.0
	433508			predicted exon	22.0
	433638	AJ017717	Hs.126525	chromosome 21 open reading frame 15	22.0
	473782	AA503620		glucocorticoid-inducible NCI_CGAP_Co3 Homo sapiens cDNA	22.0
10	411492	T46848	Hs.70337	immunoglobulin superfamily, member 4	22.0
	420185	AL044036	Hs.158047	gb:601177324F1 NIH_MGC_17 Homo sapiens cDNA	22.0
	429545	BE298182		ESTs	22.0
	429662	AA579474	Hs.122710	ESTs	22.0
	424247	X14008	Hs.234734	lysosome (renal amyloidosis)	22.0
	443052	N77959	Hs.8963	Homo sapiens mRNA full length insert cDNA clone EU	21.9
15	422447	AJ301711	Hs.124340	ESTs	21.9
	421574	AJ000152	Hs.105924	defensin, beta 2	21.9
	433302	AJ076259	Hs.190337	ESTs	21.9
	414527	BE241739	Hs.76359	catalse	21.9
	441436	AW137772	Hs.185980	ESTs	21.9
20	451179	AW177274		gb:CM2-CT0128-230895-005-a02 CT0128 Homo sapie	21.8
	448338	BE514761		gb:601281335F1 NIH_MGC_39 Homo sapiens cDNA	21.8
	427889	A400968	Hs.181046	dual specificity phosphatase 3 (vaccinia virus phosphat	21.8
	441114	AJ917468	Hs.126500	ESTs	21.8
	451831	NM_001614	Hs.460	cellular transcription factor 3	21.8
25	405500			predicted exon	21.8
	446581	AJ652743	Hs.197497	ESTs	21.8
	432839	AA579405	Hs.287332	ESTs	21.8
	456208			predicted exon	21.8
30	435025	T08990	Hs.4742	anchor attachment protein 1 (Gaa1p, yeast) homolog	21.7
	413976	BE239515	Hs.75555	procollagen-proline, 2-oxoglutarate 4-dioxygenase (pro	21.7
	423515	AA320472	Hs.162204	ESTs	21.7
	425239	NJ5626	Hs.29105	mitogen-activated protein kinase phosphatase x	21.7
	423050	AA320946		gb:EST23529 Adipose tissue, brown Homo sapiens cD	21.7
	413679	BE158765	Hs.204723	gb:RC1-HT0370-120100-012-c09 HT0370 Homo sapie	21.7
35	442166	AW845280	Hs.147096	ESTs	21.6
	445385	AD33836		ESTs	21.6
	406180			predicted exon	21.6
	433025	AA374743	Hs.279920	lysine 3-mono-oxygenase/hydroxylase 5-mono-oxygenas	21.6
	446598	AK256546		gb:2821774.Sprme NIH_MGC_7 Homo sapiens cDNA	21.6
40	434483	AA633306	Hs.121574	ESTs	21.6
	429582	AJ569058	Hs.22247	ESTs	21.6
	403758			predicted exon	21.6
	405028			predicted exon	21.6
45	426597	AA382250	Hs.145601	ESTs	21.6
	437308	AA748417	Hs.292353	ESTs	21.6
	447384	AJ377221	Hs.40528	ESTs	21.6
	429060	AW139155	Hs.194955	hypothetical protein DKFZp434O0320	21.6
	437068	AA743643	Hs.291427	ESTs	21.6
50	418509	AB02624	Hs.85539	ATP synthase, H+-transporting, mitochondrial F0 comp	21.5
	432999	BE294029	Hs.279903	Ras homolog enriched in brain 2	21.5
	407653	NM_016429	Hs.37462	COP22 for nonchitin coat protein zeta-COP	21.5
	446627	AJ573016	Hs.15725	hypothetical protein SB948	21.5
	413505	BE152644		gb:CM1-HT0328-260200-128-09 HT0329 Homo sapie	21.5
55	427286	AW732802	Hs.2132	epidermal growth factor receptor pathway substrate 8	21.5
	405226			predicted exon	21.4
	402570			predicted exon	21.4
	457960	AA771881	Hs.298149	ESTs	21.4
	400694			predicted exon	21.4
	425943	H46986	Hs.31861	ESTs	21.4
60	434240	AF115912	Hs.258119	hypothetical protein PRO3073	21.4
	448376	AA64332	Hs.196983	ESTs	21.4
	400809	H59799	Hs.42644	thioredoxin-like	21.4
	403304	AF025082	Hs.113281	Homo sapiens skin-specific protein (sp33) mRNA, part	21.4
	412652	AB017777	Hs.6774	ESTs	21.4
65	483373	AJ751556	Hs.183986	poliovirus receptor-related 2 (herpesvirus entry mediato	21.3
	416138	C18946	Hs.79026	myeloid leukemia factor 2	21.3
	452184	BE278288	Hs.155048	Lutheran blood group (Aubergin b antigen included)	21.3
	411028	AW613703		gb:RC3-ST0197-130100-014-b08 ST0197 Homo sapie	21.3
	417438	Z43989	Hs.82141	Human clone 23612 mRNA sequence	21.3
70	417534	NM_004998	Hs.82251	myosin IC	21.3
	427767	AJ702983	Hs.113281	glycine N-oxidase subunit Via polypeptide 1	21.2
	433300	AA582307	Hs.180714	glucocorticoid-inducible NCI_CGAP_K06 Homo sapiens cDNA	21.2
	452061	AJ074259	Hs.469	succinate dehydrogenase complex, subunit A, flavoprot	21.2
75	411939	AJ355595	Hs.146246	ESTs	21.2
	435080	AK027119	Hs.233049	ESTs, Weakly similar to fork head like protein P/Leasp	21.2
	432412	AA470549	Hs.162201	ESTs	21.2
	407491	S82769		gb:GABA receptor gamma 3 subunit [human, fetal bra	21.2
	418960	NM_004494	Hs.89525	hepatoma-derived growth factor (high-mobility group p	21.1
	432554	BE518103	Hs.168541	Homo sapiens mRNA full length insert cDNA clone EU	21.1
80	458188	AW207226	Hs.137840	ESTs, Moderately similar to SIX1_HUMAN HOMEGB	21.1
	406215			predicted exon	21.1
	425461	AK000602	Hs.157938	hypothetical protein FLJ20295	21.1
	446236	BE522158	Hs.100849	Homo sapiens cDNA FLJ141462 fs, clone NT29344002	21.1
	409415	AA579258	Hs.6083	Homo sapiens cDNA: FLJ21028 fs, clone CAE07155	21.1

	408546	W49512	Hs.46348	bradykinin receptor B1	21.1
	450008	HS2970	Hs.36588	WAP four-disulfide core domain 1	21.1
	430789	AF128947	Hs.204308	indolethylamine N-methyltransferase	21.1
5	438901	AF085534	Hs.29038	ESTs	21.1
	440500	AA972165	Hs.150308	ESTs	21.1
	413101	BE065215		gb:RC1-BT0314-310300-015-001 BT0314 Homo sapie	21.1
	447452	BE182558	Hs.102480	ESTs	21.1
	412446	AJ780115	Hs.92127	ESTs	21.1
	418975	T75496	Hs.296880	ESTs	21.0
10	454961	AW847807		gb:IL3-CT0213-150200-040-E12 CT0213 Homo sapian	21.0
	401072			predicted exon	21.0
	401204			predicted exon	21.0
	433626	AF078859	Hs.86347	hypothetical protein	21.0
	418047	R37633	Hs.4847	ESTs	21.0
15	445380	AJ42478	Hs.135377	ESTs	21.0
	427424	AA602453	Hs.113011	ESTs	21.0
	433412	AV553729	Hs.8185	CGI-44 protein; sulfide dehydrogenase like (yeast)	21.0
	422599	BE387202	Hs.118638	non-metastatic cells 1, protein (NM23A) expressed in	20.9
	433656	RS3409	Hs.120759	ESTs	20.9
20	413745	AW247252	Hs.75514	nucleoside phosphorylase	20.9
	418874	T60872		gb:yb72h1.1 Stralagene ovary (537217) Homo sapian	20.9
	452574	AF127481	Hs.35093	lymphoid blast crisis oncogene	20.9
	409332	S06407	Hs.248032	FLT4	20.9
	402421			predicted exon	20.9
25	427138	N77624	Hs.173717	phosphatidic acid phosphatase type 2B	20.9
	432038	AA524746	Hs.162110	ESTs	20.8
	423711	AF059194	Hs.131953	v-rnf musculopaponeurotic fibrosarcoma (vnm) oncoge	20.8
	402297			predicted exon	20.8
	405133			predicted exon	20.8
30	436661	AI125270	Hs.128069	ESTs, Weakly similar to similar to collagen [C. elegans]	20.8
	437836	BE69291	Hs.252458	ESTs	20.8
	437329	AA511877	Hs.201761	ESTs	20.8
	445830	H10451	Hs.42656	Homo sapiens cDNA FLJ12667, clone NT2RM4002	20.8
	406824	AW515961	Hs.84298	CD74 antigen (Invariant polypeptide of major histocom	20.7
35	421271	AW170057	Hs.133179	ESTs	20.7
	402566			predicted exon	20.7
	414028	AA782576	Hs.4944	Homo sapiens cDNA FLJ12783, clone NT2RP2001	20.7
	456728	AL120077	Hs.122967	kelch (Drosophila)-like 2 (Mayven)	20.7
40	417707	AL035786	Hs.82425	actin related protein 2/3 complex, subunit 5 (16 kD)	20.7
	438713	H16302	Hs.6749	ESTs	20.7
	450306	AL080080	Hs.24766	DKFZP564E1962 protein	20.7
	438898	AB19863	Hs.106243	ESTs	20.7
	403273			predicted exon	20.7
45	414626	BE390440		gb:S01265201F1 NIH_MGC_44 Homo sapiens cDNA	20.7
	401283			predicted exon	20.7
	403703			predicted exon	20.6
	416959	AB15443	Hs.283404	organic cation transporter	20.6
	423400	AW381148	Hs.3993	ESTs	20.6
	447563	BE536115	Hs.160983	ESTs	20.5
50	419754	HS2299	Hs.75243	bromodomain-containing 2	20.5
	406204	AA454501	Hs.43656	protein tyrosine phosphatase type IVA, member 3	20.5
	450507	AW256603	Hs.250891	ESTs	20.5
	429612	AF062649	Hs.252587	pituitary tumor-transforming 1	20.5
55	413758	BE162391		gb:PM2-HT0451-050100-002-J04 HT0451 Homo sapie	20.5
	432140	AG000404	Hs.272698	hypothetical protein FLJ20357	20.5
	400542			predicted exon	20.4
	431582	F07136	Hs.261828	G protein-coupled receptor kinase 7	20.4
	442724	AA355525	Hs.159604	cysteinyl-GRNA synthetase	20.4
	417861	AA334551	Hs.82767	sperm specific antigen 2	20.4
60	402948			predicted exon	20.4
	411004	AW813242		gb:MR3-ST0191-020200-207-g10 ST0191 Homo sapie	20.4
	435478	AA682622		gb:p20108.s1 Scores_fetal_liver_spleen_INFLS_S1 Ho	20.4
	447955	BE542271	Hs.288390	Homo sapiens cDNA: FLJ22795, clone KIAA2543	20.3
	433592	NM_004642	Hs.3436	deleted in oral cancer (mouse, homolog)	20.3
65	420865	N73241	Hs.100001	solute carrier family 17 (sodium phosphate), member 1	20.3
	449482	AF784256	Hs.28774	ESTs	20.3
	403807			predicted exon	20.3
	419942	U25138	Hs.93841	potassium large conductance calcium-activated channel	20.3
	420783	AE659638	Hs.99923	lectin, galactose-binding, soluble, 7 (galactin 7)	20.3
70	402986	BE244598	Hs.8456	chaperonin containing TCP1, subunit 2 (beta)	20.3
	451375	AF782656	Hs.283502	Homo sapiens cDNA: clone RP11-491J13 from 2	20.3
	453586	AA248089	Hs.50841	ESTs, Weakly similar to lufkin [D.Musculus]	20.3
	433090	AF720050	Hs.145362	immortalization-upregulated protein	20.3
	425053	AF046024	Hs.154320	ubiquitin-activating enzyme E1C (homologous to yeast	20.3
75	412802	UA1518	Hs.14602	aquaporin 1 (channel-forming integral protein, 28kD)	20.3
	409738	BE222975	Hs.56205	insulin induced gene 1	20.3
	428245	AF151048	Hs.183180	hypothetical protein	20.2
	412582	BE270631	Hs.74077	prolactosome (prosome, macropain) subunit, alpha type, 6	20.2
	405207			predicted exon	20.2
80	400531			predicted exon	20.2
	410709	AL122109	Hs.65735	Homo sapiens mRNA; cDNA DKFp434M1827 (from	20.2
	428438	NM_001955	Hs.2271	endothelin 1	20.2
	446918	AL135125	Hs.13913	KIAA1577 protein	20.2
	417821	BE245149	Hs.82643	protein tyrosine kinase 9	20.2

	429113	D28235	Hs.196384	prostaglandin-endoperoxide synthase 2 (prostaglandin G	20.2
	414511	AA148725	Hs.12959	hypothetical protein	20.2
	451546	AF051782	Hs.26584	Homo sapiens clone CDABP0038 mRNA sequence	20.1
5	441899	AI372588	Hs.8022	TU3A protein	20.1
	425811	AL038104	Hs.159557	karyopherin alpha 2 (RAG cohort 1, Importin alpha 1)	20.1
	411014	AW616072		gb:AF03-ST0223-070100-021-407 ST0220 Homo sapls	20.1
	451430	BE160479		gb:CV1-HT0413-210200-081-g05 HT0413 Homo sapl	20.1
	458247	HA6243	Hs.110373	ESTs	20.1
	411633	AW558544	Hs.112242	ESTs	20.1
10	427465	AA523543	Hs.7678	cellular retinoic acid-binding protein 1	20.0
	408953	U22408		gbo:Human intestinal mucin mRNA, partial cds, clone SM	20.0
	406268			predicted exon	20.0
	403348			predicted exon	20.0
	400370			predicted exon	20.0
15	414045	NC_002951	Hs.75722	riboprotein II	20.0
	427169	AA358823	Hs.97549	EST	20.0
	405586			predicted exon	20.0
	445324	A013290	Hs.145532	ESTs, Weakly similar to Gag polyprotein [M.musculus	20.0
	422525	AA738797	Hs.192807	ESTs	20.0
20	425383	D34047	Hs.156507	Down syndrome critical region gene 1-like 1	20.0
	445990	AW809762	Hs.222056	Homo sapiens cDNA FLJ11572 fs, clone HEMBA100	20.0
	411529	AA430348	Hs.288837	Homo sapiens cDNA FLJ12927 fs, clone NTZRP2004	20.0
	425397	J04088	Hs.155346	luciferase (DNA) II alpha (170kD)	20.0
	403234			predicted exon	19.9
25	427267	AJ201185	Hs.119164	ESTs	19.9
	400203			predicted exon	19.9
	446235	AL137257	Hs.23458	Homo sapiens mRNA; cDNA DKFZp434C1613 (from	19.9
	406704	M21655	Hs.929	myosin, heavy polypeptide 7, cardiac muscle, beta	19.9
	423083	AA321774	Hs.10941	ESTs, Weakly similar to IPI1_HUMAN PROTEIN PH	19.9
30	422112	BE540240	Hs.111783	Lam1 protein	19.9
	413282	BE076149		gb:CM0-BT0165-140200-175-g05 BT0165 Homo sapls	19.9
	453702	AA037637	Hs.42128	ESTs	19.9
	403065			predicted exon	19.9
35	406533	AI140688	Hs.263320	ESTs	19.9
	455914	AA336323	Hs.25381	ESTs	19.9
	458260	RA1782	Hs.22279	ESTs	19.9
	452388	BE319596	Hs.29287	retinoblastoma-binding protein 8	19.9
	422278	AF072873	Hs.114218	fizzled (Drosophila) homolog 6	19.9
40	441989	AA306207	Hs.28524	Homo sapiens cDNA FLJ2298 fs, clone HSH12044	19.9
	418758	AW593311	Hs.87019	ESTs	19.9
	405646	M33900	Hs.180255	major histocompatibility complex, class II, DR beta 1	19.8
	433053	BE301909	Hs.273952	glutathione S-transferase subunit 13 homolog	19.8
	414194	BE175494	Hs.73811	N-acylserine amidohydrolase (acid ceramidase)	19.8
	452321	AW844498	Hs.289052	Homo sapiens LENG8 mRNA, variant C, partial sequen	19.8
45	449713	AW027025	Hs.239282	ESTs	19.8
	458827	AW970785	Hs.178470	Homo sapiens cDNA: FLJ22552 fs, clone HSH08080	19.8
	414022	Z14244	Hs.75752	cytochrome c oxidase subunit VIIb	19.8
	441730	AJ243276	Hs.149017	ESTs	19.8
	420701	N42919	Hs.88630	ESTs, Weakly similar to AC007228.1 R31665.2 [H.sap	19.8
50	403642			predicted exon	19.8
	408987	HS6515		gb:y03811.1 Sources retina N2b:HR Homo sapiens cD	19.8
	446712	AW204789	Hs.209820	ESTs	19.8
	403286			predicted exon	19.8
55	434439	AJ022360	Hs.190583	predicted exon	19.8
	404087			predicted exon	19.7
	455694	BE087300		gb:FM2-BT0349-161299-001-410 BT0349 Homo sapls	19.7
	403287			predicted exon	19.7
	434633	AI183657	Hs.120915	ESTs	19.7
60	409189	AA132837	Hs.13396	ESTs	19.7
	420080	MA0405	Hs.94925	dihydroorotate dehydrogenase	19.7
	408852	AW291435	Hs.254961	ESTs	19.7
	403786			predicted exon	19.7
	416839	H49900	Hs.17882	ESTs	19.7
	434385	AA631946	Hs.259580	ESTs	19.7
65	446845	AD343645	Hs.156108	ESTs	19.7
	425612	BE004257		gb:CM0-BND103-180300-296-c04 BND103 Homo sapl	19.7
	422520			predicted exon	19.6
	436098	R20597	Hs.9739	ESTs	19.6
	438974	AF089916	Hs.6454	chromosome 19 open reading frame 3	19.6
70	447751	AA303541	Hs.24956	hypothetical protein FLJ22056	19.6
	451310	AW205851	Hs.26213	ESTs, Moderately similar to dJ447F3.3 [H.sapiens]	19.6
	435961	BE293127	Hs.283722	GTT1 protein	19.6
	452937	BE410390	Hs.288940	five-span transmembrane protein M83	19.6
	404850			predicted exon	19.6
75	436350	HT4149	Hs.288193	hypothetical protein FLJ10375	19.6
	436508	AW604381	Hs.121211	ESTs	19.6
	430485	BE082109	Hs.241551	chloride channel, calcium activated, family member 2	19.6
	407824	AA147884	Hs.9612	ESTs	19.6
	406388			predicted exon	19.6
80	430204	AA616335	Hs.146137	ESTs, Weakly similar to putative [C.elegans]	19.5
	457560	AB019334	Hs.163909	ESTs	19.5
	429521	BE048708	Hs.50949	ESTs	19.5
	429758	AW137722	Hs.246904	ESTs	19.5
	441473	AA834955	Hs.184846	ESTs, Weakly similar to R28830.1 [H.sapiens]	19.5

	411724	AA770559	Hs.71618	polymerase (RNA) II (DNA directed) polypeptide L (7.	19.5
	450453	AA009883	Hs.50186	ESTs	19.5
	419637	AIS3589	Hs.22769	ESTs, Weakly similar to Yh217p [S.cerevisiae]	19.5
5	442162	AW294965	Hs.150849	ESTs	19.5
	435056	AW023337	Hs.5422	glycoprotein M68	19.5
	417412	X16896	Hs.82112	interleukin 1 receptor, type I	19.5
	413825	BE299181	Hs.75564	CD151 z antigen	19.4
	422637	AW68823	Hs.119206	Insulin-like growth factor binding protein 7	19.4
10	435551	AF12365	Hs.5470	IL-17B receptor	19.4
	440069	BE617892	Hs.6895	actin related protein 2/3 complex, subunit 3 (21 kD)	19.4
	432277	AUG9790	Hs.161825	ESTs	19.4
	426044	AA263322	Hs.182225	RNA binding motif protein 3	19.4
	458064	AA256213	Hs.72010	ESTs	19.4
15	424897	D63216	Hs.153884	frizzled-related protein	19.4
	446734	AA345051	Hs.294092	ESTs	19.4
	403852			predicted exon	19.3
	405699			predicted exon	19.3
	433096	AU076903	Hs.262975	carboxylesterase 2 (intestine, liver)	19.3
20	400344	NM_012368	Hs.258574	olfactory receptor, family 2, subfamily C, member 1	19.3
	417501	AL641219	Hs.82222	sens domain, immunoglobulin domain (Ig), short basic	19.3
	400449			predicted exon	19.3
	453801	AL134761	Hs.23450	mRNA for FLJ00023 protein	19.3
	449498	BE305242	Hs.112442	ESTs, Weakly similar to CLDE_HUMAN CLAUDIN-	19.3
25	454181	AW177377		gb:CM4-CT0129-10089-007+08 CT0129 Homo sapie	19.3
	414807	AT38616	Hs.77348	hydroxyprostaglandin dehydrogenase 15 (NAD)	19.3
	406326			predicted exon	19.3
	421921	H83353	Hs.109571	translocase of inner mitochondrial membrane 10 (yeast)	19.3
	416700	AW498958	Hs.78572	cathespin D (lysosomal aspartyl protease)	19.2
	428857	AIG27342	Hs.224501	ESTs	19.2
30	405501			predicted exon	19.2
	416501	R08652	Hs.20205	hemoglobin, beta pseudogene 1	19.2
	425600	NM_003378	Hs.171014	VGF nerve growth factor inducible	19.2
	425590	AIS5466	Hs.158321	beaded filament structural protein 2, plakodin	19.2
	428151	AA422028		gb:zv26g06.s1 Soares_NhlhMPu_S1 Homo sapiens cDN	19.2
35	426420	BE363808	Hs.168929	KIAA1180 protein	19.2
	414428	BE296936	Hs.182525	VAMP (vesicle-associated membrane protein)-associate	19.2
	404601			predicted exon	19.2
	403861			predicted exon	19.2
40	443863	BE174595	Hs.366	5-pyruvoyl tetrahydropterin synthase	19.2
	405555	BE1523	Hs.181244	major histocompatibility complex, class I, A	19.1
	453572	AA809591	Hs.106486	ESTs, Highly similar to CIGK_HUMAN VOLTAGE-G	19.1
	413154	BE067870		gb:RC0-BT0362-021295-031-b06 BT0362 Homo sapie	19.1
	443021	AA368546	Hs.8504	Ig superfamily protein	19.1
45	412975	T02955	Hs.75106	clustarin (complement lysis inhibitor, SP-40,40, sulfated	19.1
	412633	AF001691	Hs.74304	parietal	19.1
	402071			predicted exon	19.1
	410387	AIZ77367	Hs.47054	ESTs	19.1
	423961	D12666	Hs.136340	osteoblast specific factor 2 (osteoblast 1-like)	19.1
50	407032	U73799		gb:human dynactin mRNA, partial cds.	19.0
	404034			predicted exon	19.0
	456534	XD1195	Hs.100523	phospholipase C, beta 3, neighbor pseudogene	19.0
	446599	Z97832	Hs.15476	differentially expressed in FDCP (mouse homolog) 6	19.0
	426410	BE298446	Hs.180372	8CL2-like 1	19.0
55	419618	AA528235		gb:nh26g06.s1 NCL_CGAP_P3 Homo sapiens cDNA c	19.0
	457632	AW252151	Hs.112689	ESTs	19.0
	417138	AA193546	Hs.65771	Homo sapiens chromosome 19, BAC CIT-HSPC_204F	19.0
	417933	X02308	Hs.82562	thymidylate synthetase	19.0
	458808	AW134832	Hs.246295	ESTs	19.0
60	415860	D50521	Hs.17888	diazepam binding inhibitor (GABA receptor modulator	18.9
	445918	AW291274	Hs.862626	ESTs	18.9
	423725	AJ303108	Hs.132127	hypothetical protein LOC57822	18.9
	401747			predicted exon	18.9
	454209	AW178083		gb:MRA-S70085-270899-006-A37 S70065 Homo sapi	18.9
65	417661	T84155	Hs.15464	Homo sapiens cDNA: FLJ21351 fls, clone COL02762	18.8
	426499	C14937	Hs.11169	Gene 33/Mig-6	18.8
	404240			predicted exon	18.8
	439718	AA307634	Hs.6650	vacuolar protein sorting 45B (yeast homolog)	18.8
	401789			predicted exon	18.8
	456952	AW445081	Hs.301469	ESTs	18.8
70	439739	AI199391	Hs.124464	ESTs	18.8
	437574	T44445		Homo sapiens clone 24416 mRNA sequence	18.8
	427490	Z95152	Hs.176805	mitogen-activated protein kinase 13	18.8
	443482	AW188093	Hs.250395	ESTs	18.8
75	411420	BE390652		gb:501266220F1 NHL_MGC_44 Homo sapiens cDNA	18.8
	435196	F35675	Hs.189128	ESTs, Moderately similar to ALLU_HUMAN III ALLU	18.8
	417022	NM_014737	Hs.80995	Rae association (Raf/GSARF-6) domain family 2	18.7
	413531	AL036358	Hs.75416	DAZ associated protein 2	18.7
	428981	BE313077	Hs.93135	ESTs	18.7
80	421698	AW352042	Hs.106061	RD RNA-binding protein	18.7
	443907	AU076484	Hs.8953	TYRO protein tyrosine kinase binding protein	18.7
	406754	AA477223	Hs.75922	brain protein 13	18.7
	400661			predicted exon	18.7
	442638	AB088742	Hs.134713	ESTs	18.7
	434169	AA863752	Hs.179724	ESTs	18.7

	424126	AA335635	Hs.96917	ESTs	18.7
	408473	BE293039	Hs.129553	Ewing sarcoma breakpoint region 1	18.7
	401952			predicted exon	18.7
5	447326	AW002252	Hs.201395	ESTs	18.7
	459053	AB07052	Hs.210361	ESTs	18.7
	403362			predicted exon	18.7
	427697	T18997	Hs.180372	BCCL2-like 1	18.7
	402051	H83353	Hs.109571	translocase of inner mitochondrial membrane 10 (yeast)	18.7
10	433785	BE044593	Hs.112704	ESTs	18.7
	405423			predicted exon	18.6
	423559	AA420450	Hs.292511	ESTs	18.6
	444071	AB27808	Hs.110524	ESTs	18.6
	410512	AA085603	Hs.250570	ESTs	18.6
15	440376	AB044452	Hs.236816	ESTs	18.6
	427353	X55253	Hs.249144	melanorexin 2 receptor (adrenocorticotrophic hormone)	18.6
	432749	NM_014438	Hs.278509	interleukin-1 Superfamily e	18.6
	415602	F12920	Hs.165575	ESTs	18.6
	407891	AA086620	Hs.41135	endomucin-2	18.6
20	455910	ZAS712		gb:HSCLIA121 normalized infant brain cDNA Homo s	18.6
	426716	NM_006379	Hs.171921	sera domain, immunoglobulin domain (Ig), short basic	18.6
	444246	H53281	Hs.10710	hypothetical protein FLJ120417	18.6
	428125	AA393071	Hs.182579	leucine aminopeptidase	18.6
	405457			predicted exon	18.5
25	446525	AI333070	Hs.156141	ESTs	18.5
	423334	AK000906	Hs.127273	hypothetical protein FLJ10044	18.5
	423103	AA322029		gb:EST14685 Corebellum II Homo sapiens cDNA 5' on	18.5
	443649	T89608	Hs.16501	ESTs	18.5
	419289	AB111085	Hs.62406	Homo sapiens cDNA: FLJ22573 fls, clone HSI02387	18.5
	411942	ABW87015		gb:CV2-PT0010-250300-096-f12 PT0010 Homo sapien	18.5
30	442440	BE464435	Hs.146180	ESTs, Weakly similar to non-receptor protein tyrosine k	18.5
	454574	AB085109		gb:UFA-ST01117-070100-027-004 ST0117 Homo sapie	18.5
	454377	A0076811		gb:TB05C12 Chromosome 7 Fetal Brain cDNA Library	18.5
	422365	AF035537	Hs.115521	REV3 (yeast homolog)-like, catalytic subunit of DNA p	18.5
	421733	AL1119671	Hs.1420	fibroblast growth factor receptor 3 (achondroplasia, th	18.5
35	420603	AB042636	Hs.4775	juncophilin 3	18.4
	401373			predicted exon	18.4
	402292			predicted exon	18.4
	444118	AA458542	Hs.10326	coatamer protein complex, subunit epsilon	18.4
40	408310	AW179023		gb:FM3-ST00038-170659-001-e08 ST00038 Homo sapie	18.4
	411236	ABW53752		gb:QV4-TT00038-130100-077-b07 TT00038 Homo sapie	18.4
	431405	AF470895	Hs.252574	ribosomal protein L10a	18.4
	441408	AF733249	Hs.126897	ESTs	18.4
	433594	BE180394	Hs.165590	ribosomal protein S13	18.4
45	444515	AB160278	Hs.146884	ESTs	18.4
	402407			predicted exon	18.4
	404270			predicted exon	18.4
	409103	AF251237	Hs.112208	XAGE-1 protein	18.4
	415198	AW009480	Hs.943	natural killer cell transcript 4	18.3
50	403771	BE387244	Hs.2664	flavin containing monooxygenase 4	18.3
	426536	AA340864	Hs.278562	claudin 7	18.3
	433504	NM_014574	Hs.3353	GA00274 gene product	18.3
	415506	W70022		gb:zsf1e10.1 Soares_fetal_heart_NbHH19W Homo sa	18.3
	401401	BE047878	Hs.99093	Homo sapiens chromosome 19, contig R28379	18.3
55	420758	AW297536	Hs.33053	ESTs	18.3
	457520	AA553495	Hs.182264	ESTs	18.3
	432323	AK001409	Hs.274396	hypothetical protein FLJ10547	18.3
	404750			predicted exon	18.3
	450845	AL117441	Hs.25364	DKFZP434N126 protein	18.3
60	445160	A029114	Hs.150797	ESTs	18.3
	418461	BE242781	Hs.288037	Homo sapiens cDNA FLJ12993 fls, clone NT2P3000	18.3
	401809			predicted exon	18.3
	458121	S42416	Hs.74547	Human T-cell receptor alpha chain mRNA for	18.3
	435108	AA100847	Hs.193380	ESTs, Highly similar to AFT14650 1 F-box protein Flax	18.3
	446398	AW444655	Hs.170838	ESTs	18.3
65	428145	BE443327	Hs.182626	chromosome 22 open reading frame 5	18.2
	443502	AK001537	Hs.12488	hypothetical protein FLJ10675	18.2
	407352	H47860		ghp7p7h12r1 Soares fetal liver spleen 1NFS Homo s	18.2
	413190	AA151802	Hs.40358	adaptor-related protein complex 1, sigma 2 subunit	18.2
	436371	AB21912	Hs.113912	ESTs	18.2
70	400985			predicted exon	18.2
	433427	AB16449	Hs.171889	cholic acid phosphotransferase 1	18.2
	427504	AA776743	Hs.191589	ESTs	18.2
	426759	AB590401	Hs.21213	ESTs	18.2
75	423792	AW135866	Hs.245854	ESTs	18.2
	406236	AB160105	Hs.84298	CD74 antigen (Invariant polypeptide of major histocom	18.1
	406659	AA663965	Hs.277477	major histocompatibility complex, class I, C	18.1
	437453	AB71350	Hs.181391	hypothetical protein DKFZp761G2113	18.1
	405276	AW372087	Hs.278429	hepatocellular carcinoma-associated antigen 59	18.1
	445628	AB097678	Hs.107713	ESTs	18.1
80	421043	BE379455	Hs.85072	ESTs	18.1
	442344	A022925	Hs.301212	ESTs	18.1
	448744	AL135434	Hs.9469	phosphoinositid 3-phosphate binding protein-1	18.1
	416822	AA724811	Hs.74427	p53-induced protein	18.1
	414500	W24087	Hs.76265	DKFZP564B167 protein	18.1

	427272	NM_001096	Hs.174140	ATP citrate lyase	18.1
	402964			predicted exon	18.1
	433217	AB040914	Hs.278626	KIAA1461 protein	18.1
5	427902	AB092022	Hs.208343	ESTs, Weakly similar to cerebroside sulfotransferase [H	18.1
	445866	AB63918	Hs.195078	ESTs	18.1
	435926	U10051	Hs.248019	POU domain, class 4, transcription factor 3	18.1
	414186	BE263293		gb:601144891.2 NH_MGC_19 Homo sapiens cDNA	18.1
	416305	AJ076628	Hs.79187	coxsackie virus and adenovirus receptor	18.1
10	411088	BE247593	Hs.145053	ESTs	18.1
	179407	AW410377	Hs.14502	Homo sapiens cDNA: FLJ21276, fig. clone COL01629	18.1
	407938	AA096037	Hs.85552	phospholamban	18.1
	443360	AI840623	Hs.252720	ESTs	18.1
	417286	AA122237	Hs.81874	microsomal glutathione S-transferase 2	18.0
15	405515			predicted exon	18.0
	438319	AW016401	Hs.233476	ESTs	18.0
	419387	BE373356	Hs.90107	cell membrane glycoprotein, 110000M(r) (surface anlig	18.0
	414015	AA340987	Hs.75593	prolylcarboxypeptidase (angiotensinase C)	18.0
	447778	BE205092	Hs.71190	ESTs	18.0
20	435523	TG2849	Hs.11090	high affinity immunoglobulin epsilon receptor beta sub	18.0
	429230	AF088991	Hs.195274	NADH dehydrogenase (ubiquinone) 1 beta subcomplex	18.0
	457822	AA970001	Hs.150319	ESTs	18.0
	442424	AI942715	Hs.129589	ESTs, Moderately similar to B34087 hypothetical prot	18.0
	416394	AF132818	Hs.94728	Kruppel-like factor 5 (intestinal)	18.0
	413477	AI815825	Hs.48756	ESTs, Moderately similar to neuronal-STOP protein [M	18.0
25	405277			predicted exon	18.0
	450182	AA263143	Hs.24596	RAD51-interacting protein	18.0
	442181	U95186	Hs.11320	endothelial PAS domain protein 1	18.0
	429490	AI571131	Hs.293684	ESTs, Weakly similar to alternatively spliced product u	18.0
	406744	AA554082	Hs.278860	hypothetical protein FLJ20300	17.9
30	425205	NM_058584	Hs.155106	receptor (calcitonin) activity modifying protein 2	17.9
	414387	AL041148	Hs.186257	ESTs	17.9
	411811	AW964370		gb:PM4-SN0016-100500-004-h9 SN0016 Homo sapie	17.9
	433882	U04441	Hs.3622	procollagen-proline, 2-oxoglutarate 4-dioxygenase [pro	17.9
	414333	BE274897		gb:65112559F1 NIH_MGC_20 Homo sapiens cDNA	17.9
35	403747			predicted exon	17.9
	435542	AA687376	Hs.269533	ESTs	17.9
	403093			predicted exon	17.9
	412088	AI689496	Hs.108932	ESTs	17.9
40	450506	NM_004480	Hs.418	Breast activation protein, alpha	17.9
	404783			predicted exon	17.9
	454633	AW811380		gb:IL3-ST0143-250999-019-DG5 ST0143 Homo sapien	17.9
	440788	AI806894	Hs.128577	ESTs	17.9
	411800	IK3342	Hs.5184	TH1 drosothrips homolog	17.9
45	441381	BE263308	Hs.7797	TERF1 (TRF1)-interacting nuclear factor 2	17.8
	422033	AW245905	Hs.110903	claudin 5 (transmembrane protein deleted in velocardio)	17.8
	403333			predicted exon	17.8
	403297	R17710	Hs.113314	ESTs	17.8
	403036			predicted exon	17.8
50	417524	AJ077231	Hs.82932	cyclin D1 (PRAD1; parathyroid adenomatosis 1)	17.8
	417081	AA193283	Hs.291950	ESTs	17.8
	440789	AB007657	Hs.7416	KIAA0397 gene product	17.8
	438397	AA804978	Hs.123206	ESTs	17.8
	439948	AA702875	Hs.114135	ESTs	17.8
	450273	AW25454	Hs.24743	hypothetical protein FLJ20171	17.8
55	435989	W05773	Hs.191368	ESTs	17.8
	427031	AA397601	Hs.125147	ESTs	17.8
	454505	AW801365		gb:IL5-UIM0067-240300-050-a01 UM0067 Homo sapl	17.8
	403447			predicted exon	17.8
60	433297	AV658581	Hs.282833	ESTs	17.8
	443326	BE195494	Hs.188478	ESTs	17.8
	448283	AI340462	Hs.182879	ribosomal protein L12	17.8
	458057	AA393603	Hs.36752	Homo sapiens cDNA: FLJ22634 fig. clone KIAA4314	17.8
	453269	BE181729	Hs.29206	Homo sapiens clone 24658 mRNA sequence	17.8
	434098	AA625499		gb:af09308.1 Source_NthMMPv_S1 Homo sapiens cDN	17.8
65	450911	AA011586	Hs.272097	ESTs	17.7
	410342	R91350	Hs.743	Fc fragment of IgG, high affinity L, receptor for, gamma	17.7
	407082	ZAT055		gb:Human partial cDNA sequence, farnesyl pyrophosph	17.7
	415271	X94232	Hs.78335	microtubule-associated protein, RP/EB family, member	17.7
70	417413	AA197072	Hs.85082	Human DNA sequence from clone RP11-243115 on chr	17.7
	408937	AA210734	Hs.291366	ESTs	17.7
	433469	AA583498		gb:cnZ005.a1 NC1_CGAP_Gas1 Homo sapiens cDNA	17.7
	459536	AI254723	Hs.145498	ESTs	17.7
	428500	AI815395	Hs.184841	delta-6 fatty acid desaturase	17.7
75	433463	RI41963	Hs.4197	ESTs	17.7
	406537			predicted exon	17.7
	410003	AA079487		gb:zmr708.s1 Stratagene colon HT29 (937221) Homo	17.7
	440857	AA907808	Hs.135556	ESTs	17.7
	451072	AA013451	Hs.117929	ESTs	17.7
80	418853	AT150878	Hs.87429	thrombospondin 1	17.7
	443824	BE161129	Hs.9651	related RAS viral (v-ras) oncogene homolog	17.7
	422826	AA344932	Hs.118788	metallothionein 2A	17.6
	410756	AB003780	Hs.86159	KIAA1399 protein	17.6
	436621	AI86254	Hs.132929	ESTs	17.6
	453317	NM_002277	Hs.41896	keratin, hair, acidic, 1	17.6

5	456628	AF156889	Hs.148427	LIM homeobox protein 3	17.6
	421486	AW438002	Hs.104659	hypothetical protein DKFZp762E1312	17.6
	428634	AW809713	Hs.10338	ESTs	17.6
	451419	R38309	Hs.174389	EST	17.6
10	448413	A745379	Hs.42911	ESTs	17.6
	424323	A4338791	Hs.146763	nascent-polypeptide-associated complex alpha polypept	17.6
	423943	AF163370	Hs.135756	polymerase (DNA-directed) kappa	17.6
	438423	BE536678	Hs.147099	ESTs	17.6
15	434025	AF114264	Hs.216381	Homo sapiens clone HH409 unknown mRNA	17.6
	408246	AS5569	Hs.435946	L13 protein	17.6
	441573	AW468847	Hs.127194	ESTs	17.5
	420867	NM_014183	Hs.100002	HSPC162 protein	17.5
20	453680	AL079547	Hs.14485	ESTs	17.5
	402202			predicted exon	17.5
	410768	AF038185	Hs.66187	Homo sapiens clone 23700 mRNA sequence	17.5
	409932	A1376750	Hs.57600	adaptor-related protein complex 1, sigma 1 subunit	17.5
25	425563	AF084199	Hs.295837	ESTs	17.5
	440475	A087671	Hs.126343	ESTs	17.5
	452767	AW014195	Hs.61472	ESTs, Weakly similar to unknown [S.cerevisiae]	17.5
	416570	A113056	Hs.64593	ATP synthase, H ⁺ -transporting, mitochondrial F1F0, su	17.4
30	419600	AA448958	Hs.91481	NEU1 protein	17.4
	418588	A4347205	Hs.91375	Human clone 23614 mRNA sequence	17.4
	428975	NM_004672	Hs.194694	mitogen-activated protein kinase kinase 6	17.4
	448928	AC050260	Hs.5384	Homo sapiens cDNA FLJ1743 fs, clone HEMBA100	17.4
35	403924			predicted exon	17.4
	419889	AA251600		gbczs10d12.r1NCL CGAP_GCBP_Homo sapiens cDNA	17.4
	402523	AW408600	Hs.104859	hypothetical protein DKFZp76BE1312	17.4
	426065	N32049		gbyw96g06.s1 Soares_placenta_8to9weeks_2NtHPb0	17.4
40	453199	A1382666	Hs.301854	gbyw96g06.s1 Soares_placenta_8to9weeks_2NtHPb0	17.4
	455132	AW857955		gbyw96g06.s1 Soares_placenta_8to9weeks_2NtHPb0	17.4
	442332	AA472111	Hs.8858	gbyw96g06.s1 Soares_placenta_8to9weeks_2NtHPb0	17.4
	432065	AA401039	Hs.2903	protein phosphatase 4 (formerly X), catalytic subunit	17.3
45	444652	BE513613	Hs.11538	actin related protein 2/3 complex, subunit 1A (41 kD)	17.3
	417935	RS3687	Hs.170044	ESTs	17.3
	430350	AA430993	Hs.227913	AP5-like 1	17.3
	446272	BE265912	Hs.14601	hematopoietic cell-specific Lyn substrate 1	17.3
50	425996	WE7330	Hs.81255	S100 calcium-binding protein A4 (calcium protein, calv	17.3
	416954	D67467	Hs.80620	guanine nucleotide exchange factor for Rap1; M-Ras-re	17.3
	437418	AJ478954	Hs.59459	ESTs	17.3
	447256	A084908	Hs.158607	ESTs	17.3
55	402203			predicted exon	17.3
	417611	AW933583		gtrCT1-BN0035-130400-013-s04 BN0035 Homo sapie	17.3
	425560	A338161	Hs.110878	ESTs	17.3
	446163	AA026880	Hs.25252	Homo sapiens cDNA FLJ13603 fs, clone PLACE1010	17.3
60	445017	A1205493	Hs.176860	ESTs	17.3
	438658	A022068	Hs.123571	ESTs	17.3
	442238	AW133374	Hs.270949	ESTs	17.3
	443195	BE148235	Hs.193063	Homo sapiens cDNA FLJ14201 fs, clone NT2RP3002	17.3
65	442609	AL020996	Hs.8518	proteinase (prosome, macropain) 26S subunit, ATPase	17.2
	416591	A0091978	Hs.75387	selenoprotein N	17.2
	403674			predicted exon	17.2
	430514	AA118501	Hs.241587	megakaryocyte-enhanced gene transcript 1 protein	17.2
70	411696	AW857404		gtrCT1-BN0035-130400-013-s04 BN0035 Homo sapie	17.2
	434560	R13052	Hs.3394	Homo sapiens clone 24877 mRNA sequence	17.2
	422827	BE336857	Hs.118787	transforming growth factor, beta-induced, 56kD	17.2
	414364	D38521	Hs.75935	KIAA0077 protein	17.2
75	409119	AA531133	Hs.4253	G protein-coupled receptor 44	17.2
	425640	U04051	Hs.293204	ESTs, Highly similar to COSM_HUMAN CYCLIN-DE	17.2
	436844	BE247871	Hs.15627	Nt protein 2	17.2
	401657			predicted exon	17.2
80	449763	A0822112	Hs.118241	ESTs	17.2
	409501	AF237621	Hs.80828	keratin 1 (epidermolytic hyperkeratosis)	17.2
	449536	A056608	Hs.291328	ESTs	17.2
	444958	AW22643	Hs.167047	ESTs	17.2
85	429978	AA245027	Hs.241507	ribosomal protein S6	17.2
	455304	AW135440		ESTs	17.2
	458840	A294955	Hs.224277	gtrCT1-BN0035-130400-013-s04 BN0035 Homo sapie	17.1
	456329	T41418		gtrCT1-BN0035-130400-013-s04 BN0035 Homo sapie	17.1
90	414839	XS3692	Hs.77462	DNA (cytosine-5-methyltransferase 1	17.1
	402582			predicted exon	17.1
	411651	AW855392		gtrCT1-BN0035-130400-013-s04 BN0035 Homo sapie	17.1
	404097			predicted exon	17.1
95	447252	R50916		gbyw96g06.s1 Soares_adult brain N2b4HBSY Homo sa	17.1
	430224	A080780	Hs.227730	integrin, alpha 6	17.1
	412828	AL133398	Hs.74821	prion protein (p27-30) (Creutzfeldt-Jakob disease, Genet	17.1
	444558	AW181975	Hs.165892	ESTs	17.1
100	420869	XS5964	Hs.123638	regulatory factor X, 1 [Influences HLA class II expressi	17.1
	448812	H50775	Hs.22140	BN0035 antigen	17.0
	431777	AA570225	Hs.105470	found in inflammatory zone 1	17.0
	422007	AF739435	Hs.39168	ESTs	17.0
105	403051			predicted exon	17.0
	402427			predicted exon	17.0
	417408	F17211	Hs.86092	Human DNA sequence from clone RP11-2431/16 on chr	17.0
	450598	AF151078	Hs.25199	hypothetical protein	17.0

	421121	AA459028	Hs.86228	TRIAD3 protein	17.0
	458488	ALD40555	Hs.208544	ESTs	17.0
	417158	AW055223	Hs.110062	ESTs, Weakly similar to ACR3_HUMAN 30 KD ADP	17.0
5	439318	AW837046	Hs.6527	G protein-coupled receptor 56	17.0
	428758	AA433688	Hs.98502	Homo sapiens cDNA FLJ14303 fls, clone PLACE2000	17.0
	447572	AB031546	Hs.103732	ESTs	17.0
	434434	AA633546	Hs.107201	ESTs	17.0
	405994	D65864	Hs.57735	acetyl LDL receptor; SREC	17.0
	408927	AW295650	Hs.265453	ESTs	17.0
10	435093	AA534163	Hs.6476	serine protease inhibitor, Kazal type, 5	17.0
	454468	AA584138	Hs.270895	Homo sapiens mRNA for KIAA1678 protein, partial cd	17.0
	426996	AW936304	Hs.173108	Homo sapiens cDNA: FLJ21897 fls, clone HEP04447,	17.0
	436859	AJ217900	Hs.144464	ESTs	17.0
	422731	AI138411	Hs.103732	gb:CKFZP434A1.229_r1.434 [synonym: htes.3]	17.0
15	422994	AA059071	Hs.198793	KIAA0750 gene product	16.9
	432847	BE265941	Hs.275554	proteasome (prosome, macropain) 26S subunit, non-AT	16.9
	416977	AW130242	Hs.293476	ESTs	16.9
	408927	AA971409	Hs.84295	CD4 antigen [invariant] polypeptide of major histocom	16.9
	453768	U83527	Hs.105423	gb:HU83527 Human fetal brain (MLove2) Homo sap	16.9
20	431314	AJ732204	Hs.105423	ESTs	16.9
	423185	BE296960	Hs.125078	ornithine decarboxylase anlyzyme 1	16.9
	435086	AW975243	Hs.122595	ESTs	16.9
	447383	AJ24231	Hs.21303	glyn:Z2a11r11 Soares melanocyte 2NblHM Homo sapie	16.9
25	456251	R13325	Hs.38774	ESTs	16.9
	456327	H88741	Hs.38774	ESTs	16.9
	450594	N31038	Hs.178113	glyn:5tp04_r17 Soares melanocyte 2NblHM Homo sapie	16.9
	428177	AA423567	Hs.121619	ESTs, Moderately similar to kineasin theta protein B [Mm	16.9
	453250	AJ948200	Hs.83954	protein associated with PRK1	16.9
	418294	AF061739	Hs.156628	ESTs	16.9
30	446546	BE167687	Hs.124650	Homo sapiens cDNA: FLJ21275 fls, clone COLFE967	16.9
	421100	AW551638	Hs.124650	gb:RC1-OT0018-140303-021-408 HT0613 Homo sapie	16.9
	455993	BE179085	Hs.601112470F1 NIH_MGC_16	Homo sapiens cDNA	16.9
	458375	BE251770	Hs.601112470F1 NIH_MGC_16	gb:RC1-OT0379-290100-032-510 CT0379 Homo sapie	16.9
35	454803	AW860148	Hs.255558	ESTs	16.9
	445474	AA40014	Hs.255558	gb:cx049d06.1 Soares_t0tal_t0tal_Nb2Hf8_9w Homo	16.9
	443188	AC039813	Hs.270482	ESTs	16.9
	441557	AW462547	Hs.36558	solute carrier family 2 (facilitated glucose transporter),	16.9
	420206	M91463	Hs.195534	Homo sapiens cDNA FLJ22235 fls, clone H0100009	16.9
40	442202	BE272802	Hs.195534	gb:RC1-OT0001-031299-011-411 DT0001 Homo sapie	16.9
	416913	AW634714	Hs.30051	progesterone binding protein	16.9
	419355	AA428520	Hs.69489	dentritic cell protein	16.9
	452975	M55521	Hs.109414	ESTs	16.8
	432525	AF290298	Hs.120350	phospholipase A2, group VI (cytosolic, calcium-ndepe	16.8
45	453718	AI119317	Hs.11282	ESTs, Weakly similar to cleft lip and palate transmem	16.8
	437270	R18087	Hs.246783	ESTs	16.8
	408007	AW135965	Hs.25691	receptor (coldzinin) activity modifying protein 3	16.8
	405954	AJ904740	Hs.25691	predicted exon	16.8
	429568		Hs.21299	ESTs, Weakly similar to AF151840 1 CGI-82 protein [H	16.8
50	445556	W22050	Hs.170298	ESTs	16.8
	410584	AA038500	Hs.172164	ESTs, Weakly similar to match to ESTs AA667999 [H	16.8
	437659	AJ358106	Hs.164307	ESTs	16.8
	447869	AW139113	Hs.164307	ESTs	16.8
	458025	AJ275406	Hs.110675	gb:q53c10x1 Soares_NHMPu_S1 Homo sapiens cDN	16.8
55	445814	AW607653	Hs.23467	apolipoprotein C-IV	16.8
	454610	AW910224	Hs.202821	gb:AF4-575125-021199-017-407 ST0125 Homo sapie	16.8
	449303	AK001495	Hs.111680	hypothetical protein FLJ10633	16.8
	422105	AJ929700	Hs.202821	endosulfine alpha	16.8
	444788	AJ871122	Hs.102497	ESTs	16.8
	414057	AJ813559	Hs.57079	signal recognition particle receptor [docking protein]	16.8
60	408822	AW500715	Hs.190232	Homo sapiens cDNA FLJ13267 fls, clone CVARC1000	16.8
	433379	AA586358	Hs.190232	ESTs	16.8
	441552	AA337975	Hs.205555	gb:cx08e12a1 NCL_OGAP_GCB1 Homo sapiens cDN	16.8
	403982		Hs.58314	predicted exon	16.8
	433771	W20410	Hs.266175	ESTs	16.8
65	439509	AF086332	Hs.233555	phosphoprotein associated with GEMs	16.8
	431639	AK005880	Hs.233555	hypothetical protein FLJ20401	16.8
	430129	BE301708	Hs.224375	predicted exon	16.8
	401465		Hs.22564	myosin VI	16.8
70	448913	AA194422	Hs.61480	schwannomin interacting protein 1	16.8
	410261	AF145713	Hs.102497	estlin	16.7
	421189	BE244219	Hs.224375	ESTs	16.7
	450489	AJ697990	Hs.224375	gb:RCS-BT0562-260100-011-A02 BT0562 Homo sapi	16.7
	410186	AW602528	Hs.501441684F1 NIH_MGC_63	Homo sapiens cDNA	16.7
75	447224	BE517125	Hs.501441684F1 NIH_MGC_63	predicted exon	16.7
	403010		Hs.189554	predicted exon	16.7
	404681		Hs.90419	ESTs	16.7
	445572	A243445	Hs.14316	KIAA0882 protein	16.7
	419440	AB202689	Hs.250497	ESTs, Highly similar to dJ745C22.1 [H.sapiens]	16.7
80	443406	AB252338	Hs.16561	HSPC141 protein	16.6
	457901	AW207023	Hs.67846	leukocyte immunoglobulin-like receptor, subfamily B (16.6
	448364	T08558	Hs.205280	predicted exon	16.6
	407239	AA076350	Hs.205280	Homo sapiens cDNA FLJ20781 fls, clone COL04235	16.6
	401847				
	429523	AK000788			

	432845	AI989751	Hs.150378	ESTs	16.6
	402246			predicted exon	16.6
	404371			predicted exon	16.6
5	422954	AW998605	Hs.32399	ESTs, Weakly similar to Similar to Ena-VASP like prot	16.6
	415042	NM_005759	Hs.77837	UDP-glucose pyrophosphorylase 2	16.6
	432201	AI536613	Hs.135657	ESTs	16.6
	456993	AL134577	Hs.200302	ESTs	16.6
	456526	AW663597	Hs.100000	S100 calcium-binding protein A8 (calgranulin A)	16.6
10	444060	AA340277	Hs.10248	Homo sapiens cDNA FLJ20167 fs, clone COL09512	16.6
	428926	BE409838	Hs.194657	cacharin 1, type 1, E-cadherin (epithelial)	16.6
	446199	AB53278	Hs.176557	ESTs	16.6
	443422	R10268	Hs.301529	ESTs	16.6
	401117			predicted exon	16.6
	400613			predicted exon	16.6
15	431214	AA284921	Hs.256811	v-viral simian leukemia viral oncogene homolog B (ras re	16.6
	431640	AL133077	Hs.268746	Homo sapiens cDNA: FLJ22615 fs, clone HS05116	16.5
	421335	X99977	Hs.103505	ARS component B	16.5
	427154	AL137262	Hs.288591	Homo sapiens cDNA: FLJ22523 fs, clone HRC12507	16.5
	401010			predicted exon	16.5
20	435878	BE512828	Hs.5273	NADH dehydrogenase (ubiquinone) Fe-S protein 3 (30k	16.5
	401589			predicted exon	16.5
	402538			predicted exon	16.5
	430478	NM_014349	Hs.241535	TNF-inducible protein CG12-1	16.5
	437623	DK3890	Hs.5719	chromosome condensation-related SMC-associated pro	16.5
25	401244			predicted exon	16.5
	415167	AA106764	Hs.264410	ESTs	16.5
	436291	BE514605	Hs.289092	Homo sapiens cDNA: FLJ22380 fs, clone HRC07453,	16.5
	405183			predicted exon	16.5
	438480	AJ271643	Hs.87469	putative acid-sensing ion channel	16.5
30	456691	AA204238	Hs.205696	ESTs	16.5
	415332	R34976	Hs.76293	ESTs	16.5
	445622	AA359760		gb-EST67699 Fetal lung II Homo sapiens cDNA 5' end	16.5
	444859	AW449137	Hs.157487	ESTs	16.5
	437192	AW975788	Hs.75355	ubiquitin-conjugating enzyme E2N (homologous to yea	16.5
35	400691			predicted exon	16.5
	448372	AW445166	Hs.170902	ESTs	16.5
	425798	AA364002		gb-EST74529 Pituitary gland II Homo sapiens cDNA 5' on	16.5
	495253	AL154746	Hs.32913	Homo sapiens mRNA: cDNA DKFZp761C0082 (from c	16.5
	429746	AW196332	Hs.197488	ESTs	16.4
40	414717	BE271039	Hs.77060	proteasome (prosome, macropain) subunit, beta type, 6	16.4
	400727			predicted exon	16.4
	422691	NM_003365	Hs.119251	ubiquitin-cytochrome c reductase core protein I	16.4
	405639			predicted exon	16.4
45	414444	BE286594		gb-601119754F1 NIH_MGC_17 Homo sapiens cDNA	16.4
	456146	AL834349	Hs.79005	protein tyrosine phosphatase, receptor type, K	16.4
	414610	BE388044		gb-601263747F1 NIH_MGC_44 Homo sapiens cDNA	16.4
	414267	AL078459	Hs.289109	dimethylarginine dimethylaminohydrolase 1	16.4
	401269			predicted exon	16.4
	403613			predicted exon	16.4
50	414203	BE262170		gb-601150415F1 NIH_MGC_19 Homo sapiens cDNA	16.4
	454315	AW373554	Hs.261928	nuclear pore complex interacting protein	16.4
	452114	NZ2687	Hs.8235	ESTs	16.4
	404638			predicted exon	16.4
	404600			predicted exon	16.3
55	448855	AF070674	Hs.22316	Homo sapiens clone 24819 mRNA sequence	16.3
	406629	AW277078	Hs.181165	eukaryotic translation elongation factor 1 alpha 1	16.3
	450957	BE515202	Hs.21497	Homo sapiens mRNA for FLJ00042 protein, partial cds	16.3
	494986	H60542	Hs.37848	ESTs	16.3
	402585			predicted exon	16.3
60	436008	AI078428	Hs.58785	ESTs	16.3
	401492			predicted exon	16.3
	412268	NM_003005	Hs.73800	selectin P (granule membrane protein 140kD, antigen C	16.3
	405086			predicted exon	16.3
	437345	BE259522	Hs.5555	NADH dehydrogenase (ubiquinone) 1, alpha/beta subco	16.3
65	432280	BE440142	Hs.2943	signal recognition particle 19kD	16.3
	419596	BE379320	Hs.91448	MKP-1 like protein tyrosine phosphatase	16.3
	428601	AW277121	Hs.254801	ESTs	16.3
	431394	AK000692	Hs.252351	HERV-H LTR-associating 2	16.3
	452998	BE019681	Hs.8019	Homo sapiens cDNA: FLJ21288 fs, clone COL01927	16.3
70	439508	AI147392	Hs.124607	ESTs	16.3
	416844	M2582	Hs.1200	acetylcholine 12-lipoxygenase	16.2
	446081	AA572412	Hs.13795	f-box and WD-40 domain protein 2	16.2
	443334	AI076123		ghoxy2604x1 Soares_fetal_liver_spleen_1NFLS_S1 H	16.2
	459610	AA076708		gb-7801802 Chromosome 7 Fetal Brain cDNA Library	16.2
75	426517	AI532756	Hs.59236	ESTs, Weakly similar to E35049 ubiquitin 1, cytochrome	16.2
	451938	AI354355	Hs.16697	down-regulator of transcription 1, TBP-binding (negativ	16.2
	454476	AW805749		gb-CAV1-UM0105-180400-162410 UM0105 Homo sap	16.2
	407214	AA412048	Hs.279574	CGI-39 protein; cell death-regulatory protein GRIM19	16.2
	405580			predicted exon	16.2
80	409452	BE336714	Hs.289271	cytochrome c-1	16.2
	415841	N13878	Hs.249495	heterogeneous nuclear ribonucleoprotein A1	16.2
	458710	AV660896		gb-AV660896 GLC Homo sapiens cDNA clone GLCG	16.2
	450657	AK001579	Hs.25277	hypothalamic protein FLJ21065	16.2
	404230			predicted exon	16.2

439471	W69839	Ha.58033	ESTs	16.2
408848			predicted exon	16.2
428707	AA496205	Ha.193700	Homo sapiens mRNA; cDNA DKFpZ588I0324 (from c	16.2
418272	AA178882		gb:238029.1 Stratiagene muscle 937209 Homo sapiens	16.2
444465	AZ06592	Ha.143843	ESTs	16.2
431257	AF039397		gb:Homo sapiens Yuh6 autotransmembrane protein 1 (K	16.2
447775	BE119318		gb:RC1-H70615-290300-021-g5 HT0615 Homo sap	16.2
403833			predicted exon	16.2
444140	AV648089	Ha.282383	ESTs	16.2
446102	AW168667	Ha.252956	ESTs	16.2
414745	T70298		gb:Y26202.1 Scars fetal liver spleen 1NfLS Homo s	16.2
430783	AW971248	Ha.291289	ESTs, Weakly similar to ALU1_HUMAN ALU SUBFA	16.2
414070	AW963783		gb:EST375856 MAGE resequences, MAGH Homo sap	16.2
444283	AI139971	Ha.154636	ESTs	16.2
425539	XG2715	Ha.3557	zinc finger protein 74 (Cco52)	16.2
409427	AW383658		gb:RC2-5T0168-071299-013-08 ST0168 Homo sapien	16.2
409417	AA155247	Ha.256906	ESTs, Weakly similar to ALU7_HUMAN ALU SUBFA	16.2
435350	AA679001	Ha.192221	ESTs	16.2
408732	AZ065598	Ha.217493	annexin A2	16.2
406096	P12200	Ha.5811	chromosome 21 open reading frame 59	16.2
417551	AJ816291	Ha.82273	hypothetical protein	16.2
441252	AW360901	Ha.183047	ESTs, Weakly similar to unnamed protein product [Hs	16.2
419806	AL037237	Ha.91585	transmembrane 9 superfamily member 1	16.1
438894	AJ830419	Ha.300431	ESTs	16.1
451287	AK002158	Ha.26194	hypothetical protein FLJ11296	16.1
412499	AW565916	Ha.11238	KIAA0622 protein; Drosophila "multiple esters" (Mast	16.1
433355	AJ808235		gb:W4601.1 rat Scars JHFL_T_GBC_S1 Homo sapien	16.1
416818	AJ884408	Ha.204786	ESTs, Weakly similar to E48013 protein-rich proteoly	16.1
438785	AJ031888	Ha.132594	ESTs	16.1
424470	BE244261	Ha.8615	nuclear RNA export factor 1	16.1
416194	H27114	Ha.301212	ESTs	16.1
446702	R44518	Ha.143496	ESTs	16.1
414222	AL135173	Ha.878	sorbitol dehydrogenase	16.1
443122	AW06656	Ha.209022	ESTs, Weakly similar to Pro-Put-DUTase polypeptin	16.1
448848	BE151545	Ha.159089	ESTs	16.1
458294	W28506		gb:48R1 Human retina cDNA randomly primed subtra	16.1
445887	AJ283105	Ha.145597	ESTs	16.1
412332	AW937661	Ha.288324	Homo sapiens cDNA FLJ13263 fls, clone OVARC1001	16.1
403912			predicted exon	16.1
441448	R66269	Ha.28714	ESTs	16.1
403153			predicted exon	16.0
444907	AW772596	Ha.148598	ESTs	16.0
421946	R93629	Ha.109173	hypothetical protein FLJ20625	16.0
437513	AW410881	Ha.5648	proteasome (prosome, macropain) 28S subunit, non-AT	16.0
407752	AA572581	Ha.13328	ESTs	16.0
447953	AJ804218	Ha.209514	Homo sapiens cDNA: FLJ22343 fls, clone HRC06043	16.0
425788	AJ001342	Ha.14570	Homo sapiens cDNA: FLJ22530 fls, clone HRC12866	16.0
421449	AA173491	Ha.291501	ESTs	16.0
418323	NM_002118	Ha.1162	major histocompatibility complex, class II, DM beta	16.0
447787	BE020108		gb:501483015F1 NH_MGC_69 Homo sapiens cDNA	16.0
422716	AJ703035	Ha.124475	ESTs	16.0
443958	BE241860	Ha.10029	cathelin	16.0
417908	AA207221		gb:255804.1 Stratiagene neuroepithelium (937321) Ho	16.0
438542	AA810131	Ha.123317	ESTs	16.0
420268	XG2625	Ha.149029	integrin, alpha 5 (fibronectin receptor, alpha polypeptid	16.0
458825	H87220	Ha.146408	nitric oxide	16.0
431360	NM_000427	Ha.251680	lozotin	16.0
414266	BE267834		gb:501124426F1 NH_MGC_8 Homo sapiens cDNA c	16.0
405711	AA304461	Ha.130798	ESTs	16.0
426075	AW513591	Ha.270149	ESTs	16.0
413488	BE144017	Ha.184693	transcription elongation factor B (SII), polypeptide 1 (I	16.0
448767	AJ380107	Ha.159954	ESTs	16.0
418098	W55044	Ha.211559	Homo sapiens cDNA: FLJ23378 fls, clone HEP46248	16.0
404239			predicted exon	16.0
458401	AW286939	Ha.172154	ESTs	16.0
412655	BE241949	Ha.75082	ras homolog gene family, member G (rho G)	15.9
423072	AJ762548	Ha.123118	soluble carrier family 12 (sodium/potassium/chloride tran	15.9
444954	AW247076	Ha.12163	eukaryotic translation initiation factor 2, subunit 2 (beta	15.9
449023	AJ523261	Ha.248875	ESTs	15.9
435729	BE048886	Ha.275017	EST	15.9
438575	BE304789	Ha.145350	myosin, heavy polypeptide 9, non-muscle	15.9
413047	H02209		gb:Y380c9.1 Scars placenta N02HP Homo sapiens cD	15.9
425939	AK000086	Ha.165948	hypothetical protein FLJ20079	15.9
446663	AW614370	Ha.254520	ESTs	15.9
448564	AL044952	Ha.21453	Homo sapiens mRNA for Inositol 1,4,5-bisphosphate 3	15.9
455640	BE064059		gb:CV3-8T0296-010300-111-e04 BT0296 Homo sapie	15.9
404345	AA730407	Ha.159156	protocatherin 11	15.9
418512	AW498974	Ha.89981	diacylglycerol kinase, zeta (104K)	15.9
411551	AW851309		gb:1.3-C70229-170200-017-C11 CT0220 Homo sapien	15.9
446726	AW300144	Ha.209209	Homo sapiens cDNA FLJ11629 fls, clone HEMBA100	15.9
410748	BE383816	Ha.136005	ESTs, Highly similar to bG115620.2 [H.sapiens]	15.9
449618	AJ078459	Ha.14366	Homo sapiens cDNA FLJ12919 fls, clone NT2R92002	15.9
428637	AW256451	Ha.24606	ESTs	15.9
424012	AW358377	Ha.137569	tumor protein 63 kDa with strong homology to p53	15.9

	403151			predicted exon	15.8
	432263	A582743	Hs.94953	ESTs, highly similar to C10C_HUMAN COMPLEXE	15.8
	432971	AF135224	Hs.182296	kallikrein 13	15.8
5	432826	X75363	Hs.250770	kallikrein 15	15.8
	431972	A080145	Hs.191711	ESTs	15.8
	400269			predicted exon	15.8
	404703	A504493	Hs.98980	polymerase (DNA directed), delta 1, catalytic subunit (1	15.8
	446335	AW150717	Hs.256176	STAT induced STAT inhibitor 3	15.8
	418443	NM_005239	Hs.85146	v-ets avian erythroblastosis virus E26 oncogene homolog	15.8
10	445773	H73456	Hs.13299	Homo sapiens mRNA: cDNA DKFpZp761M0111 (from	15.8
	433782	AF095945		ghbHomo sapiens clone H03670	15.8
	406473			predicted exon	15.8
	420831	AA280824	Hs.190035	ESTs	15.8
	402939			predicted exon	15.8
15	405196			predicted exon	15.8
	452947	AW130413		ghc:5004.x1 NCL_CGAP_Gas4 Homo sapiens cDNA	15.8
	414170	A4335996	Hs.3743	matrix metalloproteinase 24 (membrane-inserted)	15.8
	437133	AB018319	Hs.5460	KIA0776 protein	15.8
	458356	A024855	Hs.131575	ESTs	15.8
20	407857	A029445	Hs.92254	hypothetical protein FLJ20163	15.8
	405687			predicted exon	15.8
	415189	L34857	Hs.78146	platelet/endothelial cell adhesion molecule (CD31 antig	15.7
	408662	AW247699	Hs.105897	ESTs	15.7
	448338	A462857		gh-b:72h08.x1 Soares_NHMP1.S1 Homo sapiens cDN	15.7
25	402694			predicted exon	15.7
	430224	AW675175	Hs.235975	hypothetical protein DKFpZp434D0412	15.7
	458792	H56666		ghw:76d02.1 Soares_placenta_8to8weeks_2NHFPto	15.7
	402944			predicted exon	15.7
	422675	BE018517	Hs.119140	eukaryotic translation initiation factor 5A	15.7
30	408661	AW247625		ghc:2620094.Sprims NIH_MGC_7 Homo sapiens cDNA	15.7
	423238	A4333569	Hs.280482	ESTs	15.7
	421517	AB018352	Hs.105399	KIA00809 protein	15.7
	428865	AB023217	Hs.225968	KIAA1000 protein	15.7
	440815	AW071945	Hs.7436	putative acyltransferase	15.7
35	400634			predicted exon	15.7
	451034	ALD50341	Hs.25846	zinc metalloproteinase, STE24 (yeast, homolog)	15.7
	457571	A0375726	Hs.279918	hypothetical protein	15.7
	450105	BE281124	Hs.288013	similar to yeast BET3 (S. cerevisiae)	15.7
	407464	AJ276396		ghHomo sapiens mRNA for matrix extracellular phosph	15.7
40	439465	AF080285		ghHomo sapiens full length insert cDNA clone ZD478	15.7
	451837	T92157	Hs.16970	ESTs	15.7
	433013	A778940	Hs.189729	ESTs	15.7
	402738			predicted exon	15.7
45	432686	AA650114		ghc:ns2h09.x1 NCL_CGAP_Pr3 Homo sapiens cDNA c	15.7
	457666	AW470302	Hs.129663	ESTs	15.7
	401269			predicted exon	15.7
	427509	M26205	Hs.2161	complement component 5 receptor 1 (C5a ligand)	15.7
	418846	AB21602	Hs.116127	ESTs	15.6
	448891	A587332	Hs.209115	ESTs	15.6
50	445930	AF055009	Hs.13456	Homo sapiens clone 24747 mRNA sequence	15.6
	421264	AK001724	Hs.102950	coat protein gamma-cop	15.6
	447073	AW044921	Hs.157726	ESTs	15.6
	445438	AB014578	Hs.12707	KIAA0678 protein	15.6
	432126	AA865239	Hs.55144	ESTs	15.6
55	424081	AF236287	Hs.130803	calcium channel, voltage-dependent, alpha 1F subunit	15.6
	440832	A067548	Hs.128224	ESTs	15.6
	449228	AA403107	Hs.148590	ESTs, weakly similar to AF208845 1 BM-004 [Hsaple	15.6
	434263	AJ033345	Hs.116215	ESTs	15.6
	459270	ALD36524		ghc:DKFZ434E2211.r1 434 (synonym: hsa3) Homo s	15.6
60	454425	AW300927	Hs.27192	hypothetical protein d1057820.2	15.6
	412065	AA099907	Hs.271806	ESTs	15.6
	400837			predicted exon	15.6
	458866	BE816694	Hs.288042	Homo sapiens cDNA FLJ14299 fls, clone PLACE1010	15.6
	417124	BE127672	Hs.25338	ESTs	15.6
	414376	BE393856	Hs.66915	ESTs, weakly similar to 16.7kd protein [Hsaplens]	15.6
65	416536	AW749855		ghc:CN4.BT0534-281298-053-055 BT0534 Homo saple	15.6
	454128	ALD31259	Hs.41639	programmed cell death 2	15.6
	441074	AW500001	Hs.4783	Homo sapiens cDNA: FLJ22035 fls, clone HEP08938	15.6
	451742	777609	Hs.117970	ankyrin 2, neuronal	15.6
70	402687			predicted exon	15.6
	431838	AJ097229	Hs.217484	ESTs	15.6
	402855			predicted exon	15.6
	449635	AJ589942	Hs.232150	ESTs	15.6
75	434392	AW983709	Hs.268051	ESTs	15.6
	444301	AK000136	Hs.10790	hypothetical protein FLJ20129	15.5
	414973	C19089		ghc:C19089 Human placenta cDNA (Tfjigawa) Homo	15.5
	428374	AW405195	Hs.183994	protein phosphatase 1, catalytic subunit, alpha isoform	15.5
	415745	AD011107	Hs.150799	ESTs	15.5
	432632	AW084589	Hs.162246	ESTs	15.5
80	417112	AA193439		ghc:z41b09.x1 Soares_Nh3MP1.S1 Homo sapiens cDN	15.5
	418101	ALD47476	Hs.98485	gap junction protein, beta 4 (connexin 30.3)	15.5
	453110	AW384928	Hs.225160	Homo sapiens cDNA FLJ13102 fls, clone NT2RF0002	15.5
	468606	AJ23597		ghc:AJ235977 Uni-ZAP XR retinal pigment epithelium H	15.5
	435689	AJ41028	Hs.256155	ESTs	15.5

407395	AF011757		gb:Homo sapiens RAGE binding protein (P12) mRNA,	15.5
408584	A059167	Hs.207144	ESTs	15.5
454566	AW812994		gb:RC3-ST0185-230300-019-g02 ST0186 Homo sapien	15.5
430492	U15197	Hs.300803	Homo Histo-blood group ABO protein mRNA, partial	15.5
439460	AA836220	Hs.13774	ESTs	15.5
409231	BE103060		gb:601302340F.1 NH ₄ MGC_21 Homo sapiens cDNA	15.5
453360	AW294092	Hs.21594	ESTs	15.5
416981	BE391476	Hs.80617	ribosomal protein S16	15.5
439988	AA801119	Hs.255976	ESTs	15.5
408917			predicted exon	15.5
424395	AA464840		gb:zx3h11.1 J. Scores _{total} Refus _{Nb2HF8_9w} Homo	15.5
431029	BE392725	Hs.248571	Homo sapiens PAC clone RP5-1163J12 from 7q21.2-q3	15.5
441680	AW444598	Hs.7540	RAP1, GTP-GDP dissociation stimulator 1	15.5
437630	AB020656	Hs.5567	KIAA0851 protein	15.5
409475	BE163600	Hs.136912	ESTs	15.5
405885	AW503098		gb:U1-HF-BP0p-aje-g-10-0-U1.r1 NH ₄ MGC_51 Homo	15.4
459090	AA443323	Hs.107812	ESTs, Weakly similar to SPDP [H.sapiens]	15.4
425324	AA488101	Hs.159245	Inactivation escape 1	15.4
403768			predicted exon	15.4
413570	U53309	Hs.76553	sumarate hydratase	15.4
456674	BE266120	Hs.269358	ESTs	15.4
417931	W55642	Hs.82561	trefoil factor 3 (mucin)	15.4
430125	U48118	Hs.233550	serine protease inhibitor, Kunitz type 1	15.4
452164	AW953265	Hs.271277	hypothetical protein from EUROIMAGE 363668	15.4
422984	W28614	Hs.76984	chorionite songlammotropin hormone 2	15.4
408649	BE242232	Hs.26045	protein tyrosine phosphatase, receptor type, A	15.4
417497	AW402482	Hs.82212	CD33 antigen	15.4
404666			predicted exon	15.4
456847	A0360455	Hs.37776	ESTs	15.4
426595	AA406486	Hs.221988	ESTs	15.4
445350	AF029112	Hs.12540	lymphospholipase 1	15.4
450214	BE439763	Hs.227671	regulator of G-protein signaling 4	15.4
447933	R74546	Hs.29438	Homo sapiens cDNA FLJ12094 f1s, clone HEM86100	15.4
411660	AW855718		gb:RC1-CT0279-070100-021-a05 CT0279 Homo sapie	15.4
425653	BE269247	Hs.170226	Homo sapiens clone 23579 mRNA sequence	15.4
447552	A0394125	Hs.160413	ESTs	15.4
448712	W01046	Hs.181634	Homo sapiens cDNA FLJ23602 f1s, clone LNG15735	15.4
420180	A0040355	Hs.25191	ESTs	15.4
440099	AL050058	Hs.6519	DNFZP564G202 protein	15.4
427560	BE242818	Hs.179506	nuclear RNA helicase, DECO variant of DEAD box fam	15.4
432894	AW167668	Hs.279772	brain specific protein	15.3
412113	AW161274	Hs.74427	g3p13-induced protein	15.3
431614	A1598927		gb:qf1907.r1 Scores _{placenta} 8to9weeks_21nbHP8to	15.3
445870	AW410053	Hs.13406	synthase 18	15.3
424347	AA728883	Hs.145513	Homo sapiens mRNA; cDNA DNFXP434L0435 (from	15.3
425132	AW250114		gb:2821154.Sprine NH ₄ MGC_2 Homo sapiens cDNA	15.3
439766	AL350551	Hs.283852	Homo sapiens mRNA full length insert cDNA clone EU	15.3
432946	U60599	Hs.279854	mannosidase, alpha, class 2B, member 1	15.3
406130			predicted exon	15.3
453389	AA448787	Hs.24872	ESTs, Weakly similar to asoric carboxypeptidase-like p	15.3
425491			predicted exon	15.3
436481	AA378597	Hs.5199	HSPC150 protein similar to ubiquitin-conjugating enzy	15.3
446826	A0006028	Hs.16230	hypothetical protein FLJ20619	15.3
441211	AW598155	Hs.17750	hypothetical protein FLJ13326	15.3
418711	AW247977	Hs.87595	translocase of inner mitochondrial membrane 22 (yeast)	15.3
457301	AA469146		gb:bc67003.1 NC1_OGAP_P1 Homo sapiens cDNA c	15.3
449999	A0579421	Hs.231098	ESTs, Highly similar to ALU4_HUMAN ALU SUBFA	15.3
435060	H05724		ESTs	15.3
416686	D44643	Hs.14144	secreted modular calcium-binding protein 1	15.3
411340	AW676686		gb:CM4-PT0031-180206-507-a05 PT0031 Homo sapie	15.3
407639	AW205369	Hs.252936	ESTs	15.3
458012	AK424869	Hs.188211	ESTs	15.3
426480	NM_001621	Hs.170037	aryl hydrocarbon receptor	15.3
408741	M73720	Hs.646	carboxypeptidase A3 (mast cell)	15.3
437371	AK000658	Hs.5370	hypothetical protein FLJ10006	15.3
437134	AA349544	Hs.12915	ARF2 (actin-related protein 2, yeast) homolog	15.3
441890	A0095547	Hs.126075	ESTs	15.3
409442	AA301062	Hs.169248	cytochrome c	15.3
407078	Z26256		gb:H.sapiens isoform 1 gene for L-type calcium channe	15.2
435553	AW407157	Hs.181125	immunoglobulin lambda locus	15.2
443177	BE259461	Hs.202	benzodiazepine receptor (peripheral)	15.2
448771	BE315511	Hs.296244	SNARE protein	15.2
435837	A068248	Hs.187869	ESTs	15.2
423623	AB011117	Hs.129943	KIAA0545 protein	15.2
422651	NM_015570	Hs.118826	DNFXP566G0919 protein	15.2
403221	AL134878	Hs.119500	karyopherin alpha 4 (importin alpha 3)	15.2
431620	AA126109	Hs.264981	Z-5-galactosyltransferase 2	15.2
404794	NM_000078	Hs.89538	ch-usherin/ery ester transfer protein, plasma	15.2
412944	AA394110	Hs.197143	ESTs	15.2
450817	N71597	Hs.29698	ESTs	15.2
418666	AF001434	Hs.155119	E1 domain containing 1	15.2
451636	AW173270	Hs.140444	ESTs	15.2
426302	AA459265	Hs.275163	non-melanistic cells 2, protein (NM235) expressed in	15.2
454485	AW793322		gb:PMO-UM0018-120400-002-b01 UM0018 Homo sap	15.2

	440617	AA894880	Hs.181181	ESTs	15.2
	445718	AA459480	Hs.23956	hypothetical protein FLJ20502	15.2
	405227			predicted exon	15.2
5	431006	BE152871		gb:CM1-IHT0333-101299-064-d12 HT0333 Homo sapi	15.2
	443476	AW058594	Hs.133678	ESTs, Weakly similar to AF151889.1 CG-131 protein	15.2
	438828	AL34275	Hs.6454	hypothetical protein DKFZp611F2014	15.2
	407634	AW015589	Hs.301280	ESTs, Highly similar to AF241831.1 Intracellular hyatu	15.2
	436857	AA732647		gb:nc25801.1 NCL_CGAP_GCB1 Homo sapiens cDN	15.2
10	431526	Y10129	Hs.258742	myosin-binding protein C, cardiac	15.1
	447365	NM_005289	Hs.18482	KIAA1927 protein	15.1
	435373	AA723297	Hs.127138	ESTs	15.1
	432868	BE618609	Hs.279591	Homo sapiens clone 25055 mRNA sequenon	15.1
	437352	AL353957	Hs.284181	hypothetical protein DKFZp434P0531	15.1
	413209	AW063791	Hs.21263	Homo sapiens cDNA FLJ15152.1a, clone NT2P3003	15.1
15	407376	AW051138	Hs.142287	ESTs, Weakly similar to ALUJ_HUMAN III ALU CL	15.1
	430475	BE37420	Hs.241531	peffin	15.1
	446764	AW291276	Hs.285532	ESTs	15.1
	425865	AB017548	Hs.160100	Homo sapiens gene for Septaplatin Reductase, partial c	15.1
	453464	AJ894911	Hs.32389	receptor (calcitonin) activity modifying protein 1	15.1
20	447245	AW449032	Hs.170257	ESTs	15.1
	401780			predicted exon	15.1
	434063	AJ018893	Hs.3727	un-interacting protein	15.1
	418114	AJ85549	Hs.183588	glucuronidase, beta	15.1
25	441018	AB029587	Hs.148782	ESTs	15.1
	425872	BE391583	Hs.165433	ESTs, Highly similar to T17342 hypothetical protein D	15.1
	428062	N57014	Hs.44013	ESTs	15.1
	451234	AJ14901	Hs.24032	ESTs	15.1
	423565	AB020719	Hs.207802	KIAA0912 protein	15.1
	418092	R45154	Hs.105604	ESTs	15.1
30	424550	AJ850541	Hs.115258	ESTs	15.1
	425523	AW065889	Hs.154210	endothelial differentiation, sphingolipid G-protein-cou	15.1
	445213	AW204314	Hs.170784	ESTs	15.1
	418102	R58959	Hs.26608	ESTs	15.0
	425082	AJ908894	Hs.245893	ESTs	15.0
35	446749	NM_015059	Hs.16089	OC-136 protein	15.0
	406124			predicted exon	15.0
	457408	AL137507	Hs.255348	Homo sapiens mRNA; cDNA DKFZp781P211 (from c	15.0
	410051	U25737	Hs.218182	ESTs, Weakly similar to d1042K10.2 [H.sapiens]	15.0
40	440965	AJ239648	Hs.159859	ESTs	15.0
	440190	AW752597		gb:U3-CT0214-161295-045-606 CT0214 Homo sapien	15.0
	417437	U52682	Hs.82132	interferon regulatory factor 4	15.0
	454249	AW249008		gb:2521048.Sprime NIH_MGC_7 Homo sapiens cDNA	15.0
	432276	AF163352	Hs.274255	semaphorin receptor-interacting protein	15.0
45	401116			predicted exon	15.0
	423950	AA164516	Hs.136309	OGI-61 protein	15.0
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	452883	AA303384	Hs.25740	ETOI (5. cerevisiae)-like	15.0
	446187	AK001241	Hs.14229	hypothetical protein FLJ10379	15.0
	404122			predicted exon	15.0
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	403077			predicted exon	15.0
	438000	AJ825880	Hs.5995	non-kinase Cdo42 effector protein SPEC2	15.0
	447118	AB014599	Hs.17411	KIAA0639 protein	15.0
	417878	U50916	Hs.82845	Human clone 238.15 mRNA sequence	15.0
55	444078	H03048	Hs.25026	ESTs	15.0
	458234	BE551408	Hs.127196	ESTs	15.0
	434208	T32641	Hs.127648	hypothetical protein PRO2175	15.0
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TABLE 38:

Phy: Unique Eos probeset Identifier number

CAT number: Gene cluster number

Accession: Genbank accession numbers

Phy	CAT Number	Accession
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	408447	1071855.1
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	409427	1125867.1
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	446852	65989_1	AJ358760 AA158850 AW802737 AW852738 AV656291
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	447775	73665_1	BE179318 BE020344
	447787	73719_1	BE021008 BE312062 AW836316 BE262546
	448218	75525_1	A188489 BE622201
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	448838	78409_1	BE314761 AA263136 W00335 W00327
	449231	80303_1	BE410360 AA442408 AA315540
	450594	83962_1	N31036 NA2915 F07753 AA010329
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	452947	939810_1	AW130413 AJ83262
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	454610	1225643_1	AW809109 AW809112 AW809122 AW809126 AW809128 AW809133 AW809131 AW809113 AW809111 AW809132
40	454633	1227504_1	AW810224 AW810337 AW810295 AW810333 AW810335 AW810296 AW810603
	454636	1228005_1	AW811380 AW811385
	454803	1235520_1	AW812694 AW812722 AW812630
	454961	1246745_1	AW805148 AW806230 AW821887 AW821863 AW821870 AW821894 AW822351 AW823278
45	455132	1254686_1	AW847807 AW847835 AW847636
	455426	1283303_1	AW857955 AW861636 AW857967 AW857958 AW857945 AW857963 AW857968 AW857959 AW857961 AW857956 BE072135
	455640	1348141_1	AW857972 BE071371 AW857952 AW857946 AW857944 AW857947 AW857934
	455694	1360600_1	AW837792 BE072130 BE072251 BE072254
	455910	1362504_1	BE064059 BE063903 BE063838 BE063863 BE064056 BE063974 BE063904 BE063896 BE063896 BE063906 BE063980
	455923	1388665_1	BE067300 BE067293 BE067279
50	456054	1452761_1	Z43712 BE156729 BE156738 BE156731 BE156733 BE156740 BE156672 BE156672 BE156672 BE156642 BE156541
	456239	1785807_1	BE179085 BE179084 BE179088 BE179264
	456304	1843275_2	BE313241 BE383148
	457301	314434_1	T41418 T41320 T41379
55	458025	46409_1	W25505
	458036	65588_1	AA469146 AA469396 AA469216 AA469395
	458940	670072_1	AZ75406 L23206
	458710	69727_1	AJ239397 AV655764
	458792	748294_1	AZ94935 AW409222 BE408182
60	459170	920646_1	AV660855 BE167375
	459270	959232_1	NS6668 AI460076
			AB055518 AB055516 AB055457 AB055515 AW176013 AW176037
			AL039504 AL039497

TABLE 3C:

Pkey: Unique number corresponding to an Exon probelet

Ref: Sequence number. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham I. et al. (1999) Nature" refers to the publication entitled "The DNA sequence of human chromosome 22" Dunham I. et al. (1999) Nature 402:489-495

Strand: Indicates DNA strand from which exons were predicted

NL_position: Indicates nucleotide positions of predicted exons

Pkey	Ref	Strand	NL_position
400449	9887692	Minus	50889-51188
400613	9884507	Plus	92278-92472
400634	8567720	Plus	101102-101223,101886-102018
400642	8117693	Plus	10475-10845
400681	8118474	Plus	84912-85187
400684	8118708	Plus	58189-58323
400685	8118708	Minus	72569-73056,73713-73800
400727	6705687	Plus	106175-107016
400749	7331445	Minus	9162-9293
400807	8567878	Plus	93375-92935
400837	9188531	Plus	144778-144638,145582-145670,146556-146751,147255-147418,147682-147807
400842	1927148	Plus	90462-90673
400848	1927148	Plus	107149-107339,110873-111171
400891	9558279	Minus	140073-140427
400917	7283198	Minus	172358-173631

	400931	7651921	Minus	142145-142353,144311-144721
	400984	7139719	Minus	155282-155403
	400985	7770576	Minus	173043-173584
	400970	7950452	Minus	92744-92895
5	400982	8078794	Minus	119245-119471
	401010	8117391	Minus	83867-84180
	401072	3587273	Plus	64370-64524
	401088	8452704	Plus	194859-195179
10	401116	9966559	Plus	123579-124447
	401117	8570083	Minus	28948-29204
	401167	9436381	Plus	16944-19176
	401204	9743388	Minus	33684-33872
	401220	9529324	Minus	48078-48279
	401244	4827300	Minus	55359-56376
15	401245	4827300	Minus	55373-95531
	401268	9797154	Plus	152277-152483,157312-157416,158025-158205,158838-158974,160716-160592
	401269	8954205	Plus	2259-2591
	401283	9500093	Minus	47256-47456
20	401373	7248205	Minus	84211-84336
	401405	7798126	Minus	69276-69452,69548-69958
	401465	6582292	Plus	25676-25600
	401492	7341778	Plus	171020-171282,171856-172241
	401521	7705251	Plus	9127-9234
25	401556	8459360	Minus	96277-99420,96979-97160
	401575	7229504	Minus	76253-76364
	401589	9966292	Plus	135969-136263
	401628	8575954	Minus	210617-210796
	401657	9100664	Minus	7213-8163
	401747	9789672	Minus	118816-118816,119119-119244,119509-119761,120422-120960,130161-130381,130468-130593,131097-131258,131866-131932,132451-132575,133580-134011
30	401757	7239630	Plus	88641-88751
	401760	7249190	Minus	28397-29917,29920-29045,29135-29296,29411-29567,29705-29787,30224-30673
	401781	7249190	Minus	83215-83435,83531-83656,83740-83901,84237-84393,84555-85037,85290-86814
35	401785	7249190	Minus	165776-165996,166189-166314,166408-166593,167112-167268,167387-167469,168634-168942
	401789	7249213	Minus	70399-70625,70941-71055
	401809	7242191	Minus	107645-108096
	401847	7135731	Plus	85447-85593
	401887	7229381	Plus	93973-94120
40	401913	9365520	Minus	33753-33904
	401952	1767728	Minus	71433-71648,76711-76833,78677-78845,79585-79763,82349-82485
	401991	4156128	Plus	2398-2513
	401994	4153858	Minus	42904-43124,43211-43336,44507-44763,45199-45281,46337-46732
	402023	7528158	Minus	132672-133040
45	402066	6649269	Plus	135643-136031
	402071	8117361	Plus	85924-86039
	402075	8117407	Plus	121907-122035,122904-122921,124019-124161,124455-124610,125672-126076
	402131	7704961	Minus	33114-33209,33496-33678
	402144	7242226	Plus	115425-115977
50	402203	6576119	Minus	8124-8285
	402277	2894631	Plus	16360-17152,17933-18018,18170-18305
	402292	2447720	Plus	33880-34025,34176-34336,34953-35103
	402297	6598824	Plus	35279-35403,35573-35599
	402407	3562498	Minus	115812-116187
55	402421	9796341	Minus	46600-46862,46758-46811,46293-85345,89776-89829,90048-90101,102817-102924
	402427	9798372	Plus	16226-16431
	402430	9796372	Minus	62382-62552
	402520	7596899	Minus	171761-171996
	402538	9801137	Minus	96314-96539
60	402543	9638308	Minus	89684-90833
	402570	9884747	Minus	12649-12865
	402595	9506890	Minus	174893-175050,183210-183435
	402639	9958129	Minus	20167-22383
	402694	8585867	Plus	2218-2440
	402699	8570594	Minus	182775-182883,184551-184732
65	402738	7331557	Minus	8725-8859
	402855	9662953	Minus	59763-59909
	402869	6434643	Minus	136539-139335
	402939	9187334	Minus	18329-18335
	402944	9368420	Plus	110411-110716,111173-111540
70	402948	9368458	Minus	143456-143626,143808-143935
	402958	9368493	Plus	13324-13507
	403010	3132346	Plus	76385-76952
	403036	3132360	Plus	66545-66712
	403051	4827080	Minus	5269-5411
75	403095	8954197	Minus	716157-17773,72930-74144
	403077	8954241	Plus	146923-147221,47326-147628
	403093	8954241	Plus	177083-177373,177464-177751
	403151	7407985	Minus	14055-14264
	403153	9795871	Minus	42232-43369
80	403177	8938213	Minus	142560-142726
	403223	7630968	Plus	81529-81592
	403234	7637801	Plus	180641-180822
	403273	8018055	Plus	133609-134029
	403286	8080320	Plus	118369-118672

	403287	8080320	Minus	126097-126411
	403348	7239527	Plus	13809-13988
	403359	8570207	Minus	108939-109229
	403382	8571772	Plus	64059-64550
5	403447	9837821	Minus	159072-159387
	403508	7630896	Plus	5570-5719
	403582	8101186	Plus	16308-16458
	403613	8493504	Plus	81290-81465
	403642	8699871	Plus	7062-7311
10	403662	5823349	Plus	58627-59062,59222-59548
	403674	7321642	Plus	104980-105623,107394-107590
	403687	7387384	Plus	9009-9034
	403695	3046276	Plus	168272-168514
	403703	4960380	Plus	83681-84042
	403741	7639932	Minus	2633-3468
	403747	7653395	Minus	20453-20621
	403766	7229888	Plus	136283-136830
	403786	8083636	Minus	73028-73217
	403796	8059896	Minus	75073-77654
20	403833	887461	Plus	13522-13684
	403852	7708872	Minus	124007-124202
	403861	7708966	Plus	58363-58649
	403912	7710730	Minus	72000-72250,72431-72700,72929-73199
	403924	7711688	Minus	89309-89692
25	403964	7595976	Plus	178174-178300
	404034	8567780	Minus	44635-47010
	404067	3282182	Plus	1415-2071
	404087	7770701	Plus	65512-65781
	404122	9796270	Plus	90540-92977
30	404230	7981448	Minus	92534-93093
	404239	6002624	Plus	94841-89056
	404240	6302624	Minus	116132-116407,116653-116922
	404270	9828129	Minus	3649-3750,4161-4306,5962-6049,6849-6965
	404356	7630858	Minus	126433-126623
35	404600	8706107	Plus	118354-118444,118648-118792
	404601	8706107	Plus	128449-128603,125085-125249,130525-130733
	404638	9796751	Minus	95433-99528,100035-100161
	404666	7272179	Minus	18877-18993
40	404675	9797204	Minus	46332-46845,49808-49975,51088-51369,54944-55053
	404727	8081050	Plus	115334-115747
	404750	7596836	Plus	181879-182198
	404763	7882612	Plus	50981-51392
	404767	7882827	Minus	23244-23759
	404828	6580415	Minus	26291-27253
45	404850	5420148	Minus	35145-35413,40635-41082
	404881	5931510	Minus	36380-36508
	404890	7325350	Plus	101200-101408
	404971	3212939	Minus	74585-75332
50	405022	7330304	Plus	217163-217439
	405028	7533974	Minus	110588-110847,110933-111115
	405071	7708797	Minus	11115-11552
	405088	8072518	Minus	116580-117621
	405133	8515055	Minus	28127-28288
	405138	8576241	Plus	90033-90516
55	405183	7206940	Plus	12335-12553
	405194	7230072	Plus	159465-159645,193346-193610
	405196	7230083	Minus	135716-135851
	405208	7230142	Plus	8068-8214
	405226	7248966	Plus	53547-54128
60	405227	6731245	Minus	22550-22802
	405256	7323310	Plus	26070-26309
	405277	3980473	Plus	23471-23572
	405307	3638954	Plus	39195-39429
	405311	3638954	Plus	46113-46456
65	405333	3165399	Plus	149905-150215
	405411	3451356	Minus	17933-17778,18021-18290
	405423	4753276	Plus	6162-6983
	405451	5801645	Plus	81857-82045
	405501	9211311	Minus	49085-49400,49565-49678,50117-50262
70	405515	9454624	Plus	37329-37469
	405545	1054740	Plus	11857-118807,119091-119296,121626-121823
	405580	4512867	Plus	188233-188547
	405596	5002511	Plus	38810-39017
	405600	5923640	Plus	25962-27225
75	405610	5757553	Minus	71907-72080
	405639	5931650	Plus	211184-211350
	405687	6249668	Minus	54787-54891,55844-55917
	405699	4165331	Plus	100727-100859
80	405783	5738434	Minus	27238-27885
	405867	6758731	Minus	74553-75173
	406086	7107817	Plus	9418-9573
	406124	9149714	Minus	1331-1774
	406130	9181404	Minus	32394-32498
	406140	9182321	Minus	49887-50219

406160	7144945	Plus	55498-56268
406207	5923650	Minus	162607-162800
406215	7342161	Plus	310-432
406268	6580295	Minus	8505-7072
406277	5686030	Minus	4759-5490
406326	9212385	Plus	84508-84655
406388	9256205	Plus	85153-85277
406457	9755793	Plus	44569-45406
406473	9755566	Minus	109569-109931
406537	7711478	Plus	32394-33017
406571	7711622	Minus	65534-65912,66116-66596
406580	7711638	Minus	98554-97840

15 TABLE 4A lists about 131 genes up-regulated in ovarian cancer compared to normal ovaries that are likely to be extracellular or cell-surface proteins. These were selected as for Table 3A, except that the ratio was greater than or equal to 10, and the predicted protein contained a PFAM domain that is indicative of extracellular localization.

20 TABLE 4A: ABOUT 131 UP-REGULATED GENES ENCODING EXTRACELLULAR/CELL SURFACE PROTEINS, OVARIAN CANCER VERSUS NORMAL OVARY

Play	Ex. Accon	UG ID	Title	PFAM	ratio
403077			predicted exon	fn3	15.0
403535	AJ077012	Hs.289562	ESTs, Weakly similar to ubiquitous TP	Kunitz_RPTI	14.9
403089			predicted exon	fn3	14.9
457148	AF091035	Hs.184627	KIAA0181 protein	srcras	14.8
457176	A026984	Hs.293682	ESTs	lamlnln_EGF_lamlnln_B	14.8
424283	NM_004445	Hs.47786	Epithel	fn3_glycane_EFM_1b	14.8
408482	NM_000676	Hs.45743	adenosine A2b receptor	7tm_1	14.6
428695	AJ355647	Hs.189599	purinergic receptor (family A group 5)	7tm_1	14.5
426125	X27241	Hs.166994	FAT tumor suppressor (Drosophila) ho	EGF	14.4
423732	AF580566	Hs.321163	small carrier family 16 (monocarboxy	sugar_1MCT	14.3
422125	NM_003455	Hs.111867	solute carrier family 30 (zinc transport	Calnexin	14.2
407483	NM_012368		(NONE)	7tm_1	14.2
445689	AW594895	Hs.167046	ESTs	7tm_1	14.1
410164	AV533687	Hs.35545	ring finger protein 15	zf-CRICH-SPRYzf-B_box	14.0
423217	NM_000094	Hs.1640	collagen, type VII, alpha 1 (epidermol	fn3vwv	14.0
405448	A015709	Hs.172089	Homo sapiens mRNA; cDNA, DKFZp5	lypase3ush1;CUB	14.0
450684	AA972605	Hs.25333	interleukin 1 receptor, type II	lg	13.9
406592	L36607		gbl-Homo sapiens (clone Z2) pregnancy	lg	13.8
425549	U64683	Hs.158297	programmed cell death 1	lg	13.0
452755	AW138537	Hs.213436	ESTs	cystatin	13.8
427637	AK000616	Hs.179936	ItfBln 1	Bund_7	13.7
424591	R55704	Hs.150598	hyponectin (ovacin) receptor 1	7tm_1	13.7
405024			predicted exon	TGF-beta2TGFb_propeptide	13.7
405285			predicted exon	A2M/A2M_N	13.7
412116	AW402166	Hs.784	Epstein-Barr virus induced gene 2 (ym,	7tm_1	13.7
402256	U94722	Hs.16206	cadherin 5, type 2, VE-cadherin (vascu	cadherin_Cadherin_C_jam	13.6
420511	AF052682	Hs.98485	gap junction protein, beta 4 (connexin 3	connexin	13.5
448638	R17122	Hs.21639	nuclear protein, marker for differentiat	lg	13.4
431117	AF003322	Hs.259500	delta (Drosophila)-like 1	EGF;DSL	13.4
439285	AL133916	Hs.298038	ESTs	tyrosinase-LRRNT-LRRCT	13.4
424283	AA338246	Hs.301678	ESTs	E1-E2_ATPase_Hydrolase	13.3
436233	A742878	Hs.124116	ESTs	lg	13.3
443859	NM_013409	Hs.9914	folliculin	kazal	13.2
410016	AJ257977	Hs.57807	small inducible cytokine subfamily A (IL8	13.2
414020	NM_002984	Hs.75703	small inducible cytokine A4 (homolog)	IL8	13.2
400242			predicted exon	Ephrin	13.0
429057	AF156557	Hs.194816	elastin-like protein 1	Bund_7SP2	12.9
439294	A093753	Hs.143004	ESTs	E1-E2_ATPase_Hydrolase	12.8
458453	AV649408	Hs.282418	ESTs	RVD_R_TPR	12.8
444181	A0303063	Hs.10491	KIAA1237 protein	fn3lg;PH;RhoGEF	12.8
422357	AF016272	Hs.115418	cadherin 16, KSP-cadherin	cadherin	12.7
429632	W74001	Hs.55279	serine (or cysteine) proteinase inhibitor	serpin	12.6
407000	U12139	Hs.152623	gbl-Human alpha1(X) collagen (COL1	TSPN;Collagen;COLF	12.6
417064	W02903	Hs.15440	ESTs	lectin_c	12.6
439389	AA318940	Hs.86004	ESTs	hemopoietin;Peptidase_M10	12.6
407766	A4657538	Hs.36972	telomerase 1	transmembrane4	12.5
410498	AA355749	Hs.158267	gbl-EST64559 Jarkat T-cells VI Homo	aa_permeases	12.5
422487	AJ010501	Hs.158267	muclin 4, tracheobronchial	vwd	12.5
422300	D30783	Hs.115263	epineurin	EGF	12.5
402425			predicted exon	lon_trans	12.4
414875	H42679	Hs.77522	major histocompatibility complex, clas	lg	12.2
424239	M67439	Hs.143526	dopamine receptor D5	7tm_1	12.2
424262	NM_000435	Hs.8546	Notch (Drosophila) homolog 3	EGFanknotch	12.2
405369			predicted exon	7tm_1	12.1
402406			predicted exon	Gal-bind_lectin	12.1
426514	BE816633	Hs.301122	bone morphogenetic protein 7 (osteoge	TGF-beta2TGFb_propeptide	12.1
406811	U82579	Hs.67846	leukocyte immunoglobulin-like recepto	lg	12.0
416441	BE407197		gbl-301552F1 NH_MGC_21 Homo	SDF	12.0

43321	AB040917	Hs.9760	KIAA1484 protein
442815	AA852875	Hs.8850	a disintegrin and metalloproteinase domain
423613	AF036035	Hs.129910	hyaluronoglucosaminidase 3
411213	AA076359	Hs.63285	neurotrophin
425483	AF291022	Hs.391723	Homo sapiens proteoglycanin Fal2 (FA
421256	AA286731		gb255308.r1 NCL_CGAP_GCB1 Hom
423795	AW849759		gbL3.3_C20216-240200-077-004 CTO
42424	AI186431	Hs.115577	prostate differentiation factor
413296	AF75296	Hs.22791	gb-w7805.r1 NCL_CGAP_K0412 Ho
448999	AF179274	Hs.77541	transmembrane protein with EGF-like
414876	AA341040	Hs.199538	inhibin, beta C
423444	AF94038		predicted exon
402114			smad1 inducible cytokine subfamily B (
1519216	AJ076716	Hs.164021	lythotolin alpha (TNF superfamily, m
430263	D12614	Hs.36	predicted exon
400484			predicted exon
45841	AA875863	Hs.152345	poliovirus receptor-related 1 (herpesv
409420	Z15008	Hs.54461	laminin, gamma 2 (alpha100kD), kal
418043	AW377752	Hs.83341	Hs.sapiens mRNA for tyrosine kinase re
426523	S68616	Hs.170222	solute carrier family 9 (sodium/hydrog
446051	BE048061	Hs.153315	ESTs
439710	AF086543		gb:Homo sapiens full length insert cDN
415602	NM_005159	Hs.79389	nei (chicken)-like 2
181259	AA279530	Hs.83398	integrin, beta 2 (antigen CD18 (p95), ly
425721	AC020115	Hs.158309	uroplakin Ia,
409757	NM_001898	Hs.123114	cystatin SN
430630	AW269920	Hs.2621	cystatin A (afelin A)
429630	M85289	Hs.211573	hspuran sulfate proteoglycan 2 (perleca
427269	A0297346	Hs.174023	solute carrier family 1 (glutamate/chev
401248	AB023889	Hs.85950	mitogen-activated protein kinase 8 inte
412627	BE391939	Hs.74276	chloride intracellular channel 1
420104	U05825	Hs.1287	zinc finger protein 173
405276	AB023889	Hs.85950	mitogen-activated protein kinase 8 inte
425864	U56420	Hs.159903	olfactory receptor, family 5, subfamily
446745	AW118189	Hs.156400	ESTs
441834	AL138034	Hs.7879	KIAA0735 gene product
409096	BE241845	Hs.26744	Novel human gene mapping to chromo
416118	N52773	Hs.167721	ESTs
443071	AL080021	Hs.85986	complement component 1, q subcompo
431247	AL021578	Hs.276869	matrilin 4
431449	AC05994	Hs.62378	tumor necrosis factor receptor superfam
457044	S73999	Hs.21311	arginine vasopressin receptor 1A
416319	AB15601	Hs.79197	CD83 antigen (activated B lymphocyte
402172			predicted exon
424218	AF031824	Hs.143212	cystatin F (leukocystatin)
409208	Y00093	Hs.51077	integrin, alpha X (antigen CD11C (p15
426330	M77235	Hs.169331	sodium channel, voltage-gated, type V,
439758	AA845235	Hs.124470	ESTs
412429	AV050262	Hs.76795	GPO2 oncogene
449867	AW079749	Hs.164719	ESTs, Weakly similar to AF116721 11
432408	N39127	Hs.76381	myxovirus (influenza) resistance 1, hom
406672	M26041	Hs.198523	major histocompatibility complex, class
419749	X73608	Hs.33029	sporadicocystin, cwev and kazal-like
419086	NM_000216	Hs.85591	Kallmann syndrome 1 sequence
425009	X58268	Hs.154151	protein tyrosine phosphatase, receptor I
423869	BE409301	Hs.134012	C1q receptor
430209	AF177941	Hs.233538	Pro-alpha1(V) collagen
400834			predicted exon
424941	AL076728	Hs.8867	cysteine-rich, angiogenic inducer, 61
403891			predicted exon
430776	AJ011021	Hs.247905	potassium voltage-gated channel, subfa
423242	AL036128	Hs.274404	plasminogen activator, tissue
413731	BE243845	Hs.75511	connective tissue growth factor
423309	BE000776	Hs.126782	anti-repeat protein
431726	NM_007351	Hs.268107	medullin
450245	AA007538	Hs.271767	ESTs, Moderately similar to ALU1_HU
446983	AA157484	Hs.57199	complement component C1q receptor
414320		Hs.75893	predicted exon
400253			predicted exon
406594	M94891	Hs.225932	pregnancy specific beta-1-glycoprotein
418793	AW382987	Hs.89474	prostaglandin-endoperoxide synthase 1
410564	NM_006033	Hs.65370	lipase, endothelial
427274	NM_005211	Hs.174142	cotony stimulating factor 1 receptor, fo

fn3gp_LRRC1	11.9
disintegrin:Reprolysin;	11.9
Ig:Semu:Acetyltransf	11.9
CUG:MAAF_F8_type_C	11.9
EGF:cadherin:aminin_G	11.8
7m_3	11.8
sftras	11.7
TGF-beta	11.7
kazal	11.7
sftras	11.5
TGF-beta	11.5
laminin_EGF:aminin_G	11.5
IL6	11.5
TNF	11.4
Peptidase_S9	11.4
Ig	11.4
laminin_EGF:aminin_B	11.4
fn3gp:kinase	11.3
Ns_H_Exchange	11.3
Reprolysin:disintegrin	11.2
Xlnk	11.3
wvc:SPN	11.3
Integrin_B	11.3
transmembrane4_COOX:Elu	11.2
cystatin	11.2
7m_3ANF_receptor	11.2
laminin_EGF:fg:Id_recep_La	11.1
SDF	11.1
wvc:wvc:TL	11.1
G-patch:MuS_C	11.1
zf-C2HC4:SPRYzf-8_box	11.1
wvc:wvc:TL	11.1
7m_1	11.1
vwa	11.0
sugar_3	11.0
PRRhoGAP:Gal-bind_lectin	11.0
hemopexin:Peptidase_M0	11.0
C1q:Collagen	10.9
EGF:vwa	10.9
TNR_r8	10.9
7m_1	10.9
Ig	10.8
Ig	10.7
cystatin	10.6
vwa	10.6
lon_trans:IQ	10.6
transmembrane4	10.6
IL6	10.6
ABC_tran:ABC_membrane	10.6
lon_trans:K_lectra	10.6
Ig:MAHC_H_alpha	10.5
kazal:lyng:gb:ub_L1	10.5
fn3:wap	10.5
fn3:lyp_phosphatase:MAM	10.5
C1q_EFTU:EFQ_C	10.4
Collagen:COL1A1:SPN	10.4
IRK	10.4
Cys_knot:tp_1wvc:GFIP	10.4
tp_1wvc:lyng:lyng	10.4
lon_trans	10.3
EGF:fn1:lyng:lyng	10.3
Cys_knot:tp_1wvc	10.3
anti:lyng	10.3
Ig	10.2
EGF:Xlnk	10.2
disintegrin:ZU5	10.1
7m_1	10.0
Ig	10.0
EGF	10.0
Ribosome_L22	10.0
phnase:ij	10.0

TABLE 4B:

*Play: Unique Eco probe/identifier number

CAT number: Gene cluster number

Accession: Genbank accession numbers

80	Play	CAT Number	Accession
	410498	120611.1	AA355749 AA085520 AW086333 AA340319 BE170536
	416441	159480.1	BE407197 AA182474 AA180369 BE275628 BE276131
	421258	200725.1	AA265731 AA267621 AW186228 AW137774
	423795	230993.1	AW049759 AW849758 T85549 AA331069

439710 47550_1 AF086543 W96291 W96225
443296 55539_2 AT765266 AW297086 BE568658

TABLE 4C:

Play: Unique number corresponding to an Eos processed

Ref: Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham L et al." refers to the publication entitled "The DNA sequence of human chromosome 22" Dunham, et al. (1999) *Nature* 402:489-495

Strand: Indicates DNA strand from which exons were predicted

NL_position: Indicates nucleotide positions of predicted exons

Pkey	Ref	Strand	NL_position
400464	9026970	Plus	22074-22114
400534	8705192	Plus	121953-122288
402114	8318586	Plus	71578-71715
402172	8575911	Minus	143378-143571
402406	3970929	Plus	10872-11123,12632-13048
402425	9786347	Minus	50224-60355
403077	8954241	Plus	146923-147222,147326-147628
403089	8954241	Plus	171954-172239
403591	7387384	Minus	80250-88463
405204	7107727	Plus	89500-86957
405285	6139075	Minus	55744-55903,57080-57170,61478-61560
405368	2104517	Plus	46055-47188

TABLE 5A lists about 685 genes down-regulated in ovarian cancer compared to normal ovaries. These were selected as for Table 3A, except that the numerator and denominator were switched, and the ratio was greater than or equal to 3.0 (i.e. 3-fold down-regulated in tumor vs. normal ovary).

TABLE 5A: 685 DOWN-REGULATED GENES, OVARIAN CANCER VERSUS NORMAL OVARY

Play: Primerkey

Ex. Accn: Exemplar Accession

UG ID: UniGene ID

Title: UniGene Title

ratio: ration normal ovary vs tumor

Pkey	Ex. Accn	UG ID	Title	ratio
421013	M62287	Hs.1345	mutated in colorectal cancers	14.8
439360	AA48468	Hs.55346	ESTs, Weakly similar to Z141_HUMAN ZINC FINGER	12.8
407644	D16815	Hs.37288	nuclear receptor subfamily 1, group D, member 2	12.6
424851	AA576441	Hs.119059	ESTs	11.6
455066	AK933057		gbc-RC1-CT0249-170200-025-h04 CT0249 Homo sapiens	11.5
425077	H75701	Hs.99886	complement component 4-binding protein, beta	11.3
451617	CO1056	Hs.168000	ESTs	10.0
401308			predicted exon	9.9
445987	AA911705	Hs.130229	ESTs	9.7
409725	T40760	Hs.90459	EST	9.7
415782	BE314524	Hs.78776	putative transmembrane protein	9.7
437690	AA84352	Hs.180544	ESTs	9.6
437787	AA90323	Hs.291625	ESTs	9.5
499054	AW798466	Hs.82396	2',5'-oligoadenylate synthetase 1	9.2
435330	R16769	Hs.185689	ESTs	9.2
436642	AA724430	Hs.127950	ESTs	9.1
437302	AL120000		gbc-CKFZp762E152_r1 762 (synonym: hmlc2) Homo sa	9.1
451683	AA08964	Hs.207673	ESTs	9.1
401464	AF039241	Hs.9328	histone deacetylase 5	9.0
436812	AW259057		gbc-UI-4-BW0-01p-e-09-0-UL1 NCL_CGAP_Sub6 Hom	8.7
410758	BE336994		gbc-60106241BF1 NIH_MGC_10 Homo sapiens cDNA	8.7
412637	AA115097	Hs.261313	ESTs	8.4
419166	AA234638	Hs.293584	ESTs	8.3
423738	AA389155	Hs.37600	ESTs	8.1
413613	AA67568	Hs.75561	teratocarcinoma-derived growth factor 1	8.0
416211	R14625		gbc-y45c03.r1 Soares infant brain INIB Homo sapiens	8.0
443131	AK033833	Hs.132689	ESTs	7.9
415866	T10115	Hs.32423	KIAA1566 protein	7.9
410130	AB11007	Hs.163208	ESTs	7.9
439426	AI131502	Hs.143135	ESTs, Weakly similar to FAFY_HUMAN PROBABLE	7.8
408141	U69205	Hs.45152	ESTs, Moderately similar to neurogenic basic-helix-loop	7.7
419015	T7962	Hs.14463	ESTs	7.6
441573	BE533855	Hs.45029	ESTs	7.5
419396	AA238867	Hs.143868	ESTs	7.5
430562	D78260	Hs.285097	ESTs	7.4
434738	AA362665		gbc-oc17e02.a1 NCL_CGAP_GCB1 Homo sapiens cDNA	7.4
403283			predicted exon	7.4
415861	Z43123	Hs.144513	ESTs	7.4
412732	AW993300		gbc-RC2-B00033-180200-015-g08 BN0033 Homo sapie	7.4
412427	AW118681	Hs.128051	ESTs	7.4
428655	NS7859	Hs.114541	ESTs, Weakly similar to neuronal thread protein AD70-	7.3
409699	BE154650		gbc-PM3-HT0344-071299-003-c08 HT0344 Homo sapie	7.3
420352	BE258835		gbc-601117374F1 NIH_MGC_16 Homo sapiens cDNA	7.3
421418	AA805539		gbc-60106241BF1 NIH_MGC_10 Homo sapiens cDNA	7.2
413597	AW820965	Hs.117183	ESTs	7.2
454102	AW752363		gbc-RC0-CT0201-270999-011-03 CT0201 Homo sapie	7.1
454587	AB06287	Hs.201217	ESTs	7.1
457604	A004397	Hs.130558	ESTs, Weakly similar to similar to O-sialoglycoprotein	7.1

400942			predicted exon	6.9
407596	R6913		gb:q3005.1 Soares fetal liver spleen 1NFS Homo sa	6.9
422046	A538562		gb:250410.x1 NCL_CGAP_U11 Homo sapiens cDNA c	6.9
411394	AA527675	Hs.196542	ESTs	6.9
446224	AW450551	Hs.13308	ESTs	6.9
424943	AU077260	Hs.153524	death-associated protein kinase 1	6.9
453967	AW003077	Hs.232947	ESTs	6.9
446863	AA167642	Hs.14632	ESTs	6.8
431877	AA521204	Hs.105507	ESTs	6.8
411337	AW837349		gb:CV2-LT0038-270300-108-d12 LT0038 Homo sapie	6.8
410596	AA374185		gb:EST65290 HSC172 cells 1 Homo sapiens cDNA 5'e	6.8
417762	AA205976		gb:zq40410.r1 Striatum hNT neuron (937233) Homo	6.7
452364			predicted exon	6.7
452238	F01811	Hs.187931	ESTs, Moderately similar to SZ2703 voltage-gated pola	6.7
415288	R15794	Hs.141027	ESTs, Weakly similar to ALU1_HUMAN ALU SUBFA	6.7
407437	AF220284		gb:Homo sapiens MOST-1 mRNA, complete cds.	6.7
439126	AF063584		gb:zq40410.r1 Striatum hNT neuron (937233) Homo	6.6
452453	AB02519		gb:CV-81009-101198-051 BT009 Homo sapiens cDNA	6.6
431800	AW452768	Hs.162045	ESTs	6.5
425380	A291267	Hs.149950	ESTs, Weakly similar to unnamed protein product [Hsa	6.5
443829	AB993559	Hs.223033	ESTs	6.4
437755	AW204256	Hs.291887	ESTs	6.4
448307	AA480289	Hs.211026	ESTs	6.4
439588	AA922936	Hs.110039	ESTs	6.4
420061	K35566	Hs.44745	ESTs	6.4
425506	AS522299	Hs.173369	ESTs	6.4
433923	AB23453	Hs.146625	ESTs	6.4
408159	H53877	Hs.118826	ESTs	6.3
434844	AF157116	Hs.301355	hypothetical protein LOC56757	6.3
430197	AA468888	Hs.187697	ESTs, Weakly similar to ALU5_HUMAN ALU SUBFA	6.3
440332	AJ218517	Hs.188051	ESTs	6.3
450061	AJ797034	Hs.201115	ESTs	6.3
454984	AW850176		gb:U3-CT0219-271099-022-H04 CT0219 Homo sapien	6.3
421095			predicted exon	6.2
409090	W55067	Hs.103105	ESTs	6.2
405752			predicted exon	6.2
408074	R20723	Hs.124764	ESTs	6.1
459200	Y09306	Hs.30148	homeodomain-interacting protein kinase 3	6.1
416310	T81421	Hs.221396	ESTs	6.1
421976	AL138443	Hs.23450	mRNA for FLJ100223 protein	6.1
423755	NM_001364	Hs.215839	discs, large (Drosophila) homolog 2 (chapsyn-110)	6.0
448732	BE614063		gb:801503953F1 NIH_MGC_71 Homo sapiens cDNA	6.0
453909	AW004045	Hs.203365	ESTs	6.0
431178	AA453984	Hs.218908	Homo sapiens cDNA: FLJ21440 fs, clone COL04389	6.0
445671	AW855915	Hs.288906	Homo sapiens cDNA FLJ12877 fs, clone NT2920052	6.0
421349	W01715	Hs.102958	ESTs, Weakly similar to Lys6p [S.cerevisiae]	6.0
453282	AK000043	Hs.32922	hypothetical protein FLJ20036	5.9
423618	AA278781	Hs.286098	ESTs	5.9
411480	BE142354		gb:CMO-HT0143-270999-062-d12 HT0143 Homo sapi	5.9
449588	AW205979	Hs.196065	ESTs	5.9
423884	AL049925	Hs.225984	DNFZP547G0910 protein	5.9
416453	N58968	Hs.114693	ESTs	5.9
459407	AA825742	Hs.87517	ESTs	5.9
433773	AA759293	Hs.112692	ESTs	5.9
455942	AA009547	Hs.8850	a disintegrin and metalloproteinase domain 12 (metlra	5.9
436254	A076282	Hs.119813	ESTs	5.8
410495	N95428		gb:z880409.s1 Soares_sarcomatous_fibroblasts_JNH5F H	5.8
403277			predicted exon	5.8
444302	AL140115	Hs.225130	ESTs	5.8
459334	A754576	Hs.124523	ESTs	5.8
404020			predicted exon	5.8
454338	AW381251	Hs.1050	placozin homolog, Sec7 and coiled/coiled domains 1cy	5.7
430992	AW373747	Hs.183337	ESTs	5.7
422288	N55394	Hs.86398	8-oxoquinoline DNA glycosylase	5.7
428498	AA423575	Hs.243032	ESTs	5.7
445697	H55649		gb:ry72610.r1 Soares fetal liver spleen 1NFS Homo sa	5.7
411543	AW851248		gb:U3-CT0220-160200-066-F01 CT0220 Homo sapien	5.7
406354	AJ382803	Hs.159235	ESTs	5.7
444431	AW513324	Hs.42280	ESTs	5.7
406605			predicted exon	5.7
405541	AF039241	Hs.9028	histone deacetylase 5	5.6
456950	AJ282149	Hs.55213	ESTs, Highly similar to FXD3_HUMAN FORKHEAD	5.6
454629	Z45439	Hs.270425	ESTs	5.6
445832	AJ261545		gb:q30a07.x1 NCL_CGAP_J0d11 Homo sapiens cDNA	5.6
441223	AJ475007	Hs.132499	ESTs	5.6
423652	AJ531170	Hs.173725	ESTs, Weakly similar to ALU8_HUMAN ALU SUBFA	5.6
443690	AJ966330	Hs.151444	ESTs	5.6
403714			predicted exon	5.6
444165	AL137443	Hs.10441	hypothetical protein FLJ11236	5.6
450914	BE327696	Hs.260922	ESTs	5.6
428020	AJ278807	Hs.173343	ESTs	5.5
458228	AA534936	Hs.184846	ESTs, Weakly similar to R28930 1 [H.sapiens]	5.5
448067	R65568	Hs.183373	src homology 3 domain-containing protein HSP-55	5.5
427000	AL181420	Hs.145221	ESTs	5.5

452351	AA025647		gb285601.r1 Soares_fetal_heart_NbH19W Homo sa	5.5
452359	N95645		gb2a40d05.r1 Soares fetal liver spleen INFLS Homo sa	5.5
405385	AF055934	Hs.44553	unc5 (C elegans homolog) c	5.5
452938	AW753734	Hs.272715	ESTs	5.4
431888	H99557	Hs.2864	carly endosome antigen 1, 162KD	5.5
459418	V99550	Hs.26418	ESTs	5.4
416716	R63017	Hs.294628	ESTs	5.4
413236	H16442	Hs.127376	QAM066 gene product	5.3
439063	AF085922	Hs.113986	ESTs	5.4
446361	AI291234	Hs.282241	ESTs	5.4
455253	AW286952	Hs.196802	ESTs	5.4
433862	AA642418	Hs.17381	ESTs	5.4
455780	BE006090		gbrC1-ETD720-280300-011-g02 BT0720 Homo sapi	5.4
445755	AW294870	Hs.223872	ESTs	5.3
438513	AI278110	Hs.125507	DEAD-box protein	5.3
416671	H94087	Hs.25073	ESTs, Moderately similar to HG14_HUMAN NONHS	5.3
440231	AW015420	Hs.163323	ESTs	5.3
425865	AA460104	Hs.99540	ESTs	5.3
437779	AA345232	Hs.21227	ESTs	5.3
424020	AB014594	Hs.157579	XAM0994 gene product	5.3
425514	AI334963	Hs.156256	ESTs	5.3
430553	AW902062	Hs.30280	ESTs	5.2
408955	T83061	Hs.279604	desmin	5.2
410454	AW740041		gbrPC3-BT0319-100100-012-c05 BT0319 Homo sapi	5.2
438116	AI504105	Hs.122016	ESTs	5.2
409138	W73159	Hs.58290	ESTs	5.2
423047	NM_005323	Hs.123054	H1 Histone family, member T (testis-specific)	5.2
440212	AW300959	Hs.128216	ESTs, Weakly similar to good similarity to E. coli hypo predicted exon	5.2
404108			gbrA588F Heart Homo sapiens cDNA clone A588, mRNA	5.2
456253	T12158		Homo sapiens clone 24881 mRNA sequence	5.1
409365	AA702375	Hs.22640	hypothetical protein PR01488	5.1
444013	T65311	Hs.44404	ESTs	5.1
454071	AB041793	Hs.42502	interferon, beta 1, fibroblast	5.1
419761	M17373	Hs.93177	Homo sapiens cDNA FLJ12542 fls, clone NT280M4000	5.1
451250	AA491275	Hs.236940	predicted exon	5.1
403260			gbrPM2-UM0027-230200-002-h02 UM0027 Homo sap	5.1
454487	AW796342		EST, Weakly similar to intrinsic factor-B12 receptor pr	5.1
444131	AB006600	Hs.207119	ESTs	5.1
441679	BE502287	Hs.65956	ESTs	5.1
450077	AA523732	Hs.120855	ESTs	5.1
412109	AJ010230	Hs.102576	ret finger protein-like 1 antisense	5.1
445140	AB505059	Hs.197913	ESTs	5.1
412126	M74587	Hs.102122	insulin-like growth factor binding protein 1	5.1
447037	AJ357658	Hs.157612	ESTs	5.1
407168	R45175		gbrp40101.s1 Soares infant brain 1N6 Homo sapiens	5.0
436196	AK001084	Hs.300513	gbrHomo sapiens cDNA FLJ10222 fls, clone MEMB81	5.0
444138	AT015772	Hs.151153	ESTs, Weakly similar to T1597.2 [C.elegans]	5.0
458989	AV854623	Hs.288141	Homo sapiens cDNA FLJ13016 fls, clone NT2RP30005	5.0
451640	AA185901	Hs.26771	Human DNA sequence from clone 747H23 on chr6mos	5.0
441318	AJ078234	Hs.176130	ESTs	5.0
407490	S79281		gbrpuncratif ribonuclease (human, mRNA Recombinant	4.9
438224	AA333999		gbrnon9104.s1 Soares_NFL_T_GBC_S1 Homo sapiens	4.9
451628	AW799466	Hs.82296	Z, Z'-oligoadenylate synthetase 1	4.9
457356	AA489621	Hs.191670	ESTs	4.9
409579	R44428	Hs.22801	ESTs	4.9
445747	AB20883	Hs.145328	ESTs, Weakly similar to ALU1_HUMAN ALU SUBFA	4.9
409036	T88893	Hs.228410	ESTs	4.9
433382	T64293	Hs.291453	ESTs	4.9
401287			predicted exon	4.9
424188	AW954552	Hs.142634	zinc finger protein	4.9
404868			predicted exon	4.9
410152	AW823104	Hs.23681	ESTs	4.9
444887	AJ204451	Hs.146196	ESTs	4.9
431075	BE267477		gbr601189542F2 NIH_MGC_7 Homo sapiens cDNA d	4.8
429033	NM_007374	Hs.194756	stine oculis homeobox (Drosophila) homolog 6	4.8
414337	BE366636		gbr501273900F1 NIH_MGC_20 Homo sapiens cDNA	4.8
413336	BE351610	Hs.18458	Homo sapiens cDNA FLJ12277 fls, clone MAMMA10	4.8
445283	AW515753	Hs.246872	ESTs	4.8
434792	AA649223	Hs.132458	ESTs	4.8
433403	AF040247		gbrHomo sapiens erythroid differentiation-related factor	4.8
454940	AW946022		gbrCV9-CT0179-011299-05110 CT0179 Homo sapi	4.8
455534	AW991925		gbrPM3-BN0011-130100-002-b07 BN0011 Homo sapi	4.8
418437	AB48990	Hs.37204	ESTs	4.8
433767	AA669245		gbr6113011.s1 Soares_testis_NHT Homo sapiens cDNA	4.8
434077	AT742323	Hs.226142	ESTs, Weakly similar to ALU7_HUMAN ALU SUBFA	4.8
416192	NM_005036	Hs.998	peroxisome proliferator activated receptor, alpha	4.8
459218	AA812533	Hs.10945	ESTs	4.8
402109			predicted exon	4.8
444490	AI151080	Hs.146830	ESTs	4.8
432632	AW973801	Hs.134655	ESTs	4.8
433683	AA813982	Hs.291842	ESTs	4.8
440444			predicted exon	4.8
443862	AI672277	Hs.199475	ESTs	4.8

	419002	T78625	Hs.268594	ESTs	4.7
	425582	AL157686	Hs.293737	ESTs	4.7
	419086	H18252	Hs.227263	ESTs	4.7
5	441133	AA518101	Hs.194457	ESTs	4.7
	448323	AJ285274	Hs.149868	ESTs	4.7
	440347	AJ125590	Hs.142664	ESTs	4.7
	439481	AF066294	Hs.125844	ESTs	4.6
	455388	W25557		gb:4668 Human retina cDNA randomly primed sublibrary	4.6
10	441864	FS41777	Hs.181315	ESTs, Moderately similar to ALU4_HUMAN ALU SJ	4.6
	449910	RS3483	Hs.260273	ESTs	4.6
	435331			predicted exon	4.6
	429773	AJ332482	Hs.218791	proteoglycan 4, (megakaryocyte stimulating factor, aric	4.6
	422953	BE293242	Hs.153446	Homo sapiens cDNA FLJ13191 fs, clone NT2RP00206	4.6
	422990	Z43784	Hs.78713	scd5e carrier family 25 (mitochondrial carrier; phospho	4.6
	453663	AL048907	Hs.180714	cytochrome c oxidase subunit IVa polypeptide 1	4.6
	447839	NP7050	Hs.164144	ESTs	4.5
	415612	F12693	Hs.13391	ESTs	4.5
	433371	T25451		gb:PTH188 HTCCL1 Homo sapiens cDNA 5'UTR simila	4.5
20	410667	AW336099		gb:QVQ-DT0020-210100-095-040 DT0020 Homo sapie	4.5
	410680	AW806575		gb:MT4-S10121-080200-002-012 ST0121 Homo sapie	4.5
	420451			predicted exon	4.5
	441705	A087052	Hs.55993	ESTs	4.5
	439597	W79576	Hs.58552	ESTs	4.5
25	407825	NM_006152	Hs.40202	lymphoid-restricted membrane protein	4.5
	423973	BE325922	Hs.123119	MAO (methylecgonate decarboxylase, Drosophila) ho	4.5
	456278	BE300369	Hs.42643	ESTs, Weakly similar to KIAA1016 protein [Hsapiens	4.5
	424719	H50452		gb:yr1d03.1 Soares fetal liver spleen 1NF15 Homo sa	4.5
	439542	AW297571	Hs.17646	ESTs	4.5
30	444333	AV643844	Hs.232436	ESTs	4.5
	438331	BE263273	Hs.301128	ESTs	4.5
	410065	AW812744		gb:RC3-ST0186-181099-012-c09 ST0186 Homo saplen	4.5
	453855	AA035843	Hs.61948	ESTs	4.5
	453250	AB07239	Hs.152174	ESTs, Weakly similar to Z140_HUMAN ZINC FINGER	4.5
35	423403	AA325483		gb:EST28475 Cerebellum II Homo sapiens cDNA 5' on	4.5
	454679	AW813110		gb:CM4-ST0189-051099-021-05 ST0189 Homo saplen	4.5
	445368	AJ21631	Hs.166788	ESTs	4.5
	401004			predicted exon	4.5
	425837	AF007567	Hs.159609	insulin receptor substrate 4	4.5
40	420457	AW206285	Hs.253548	ESTs	4.5
	449438	AA927317	Hs.176719	ESTs	4.5
	429409	AB944517	Hs.155380	ESTs	4.5
	447959	AA452764	Hs.270270	ESTs	4.4
	407340	AA810168	Hs.232119	ESTs	4.4
45	424326	NM_014479	Hs.145296	disintegrin protease	4.4
	443479	AF027219	Hs.9143	zinc finger protein 202	4.4
	443246	T75157	Hs.285518	ESTs, Weakly similar to hypothetical protein [Hsapien	4.4
	414475	BE302955	Hs.119598	ribosomal protein L3	4.4
	432075	AW972934		gb:EST385030 MAGE resequences, MAGM Homo sap	4.4
50	417806	R24769	Hs.23725	ESTs	4.4
	406518	W28077	Hs.79389	nei (chicken)-like 2	4.4
	441460	AA962478	Hs.226804	ESTs, Moderately similar to ALUIC_HUMAN [H] ALUJ	4.4
	450549	T40427	Hs.181244	major histocompatibility complex, class I, A	4.4
	426528	AA300028		gb:EST38327 Activated T-cells VII Homo sapiens cDN	4.4
55	430635	AW868405		gb:EST380561 MAGE resequences, MAGJ Homo sapl	4.4
	408479	BE047329	Hs.144483	ESTs	4.3
	446836	AS57139	Hs.129179	Homo sapiens cDNA FLJ13551 fs, clone PLACE10090	4.3
	411280	NS6617		gb:gh28b02.1 Soares_multiple_sclerotic_2NH4MSP H	4.3
	440790	AW593050	Hs.126580	ESTs	4.3
	453801	AF003834		gb:AF003834 Clontech H11149x Homo sapiens cDNA	4.3
60	442277	AA944914	Hs.202391	ESTs	4.3
	449463	AW57038	Hs.196109	ESTs	4.3
	433426	H69125	Hs.133525	ESTs	4.3
	410782	AW504860	Hs.288836	Homo sapiens cDNA FLJ12673 fs, clone NT2RM4002	4.3
65	423040	AA320749	Hs.259454	KIAA1604 protein	4.3
	432430	AW078984	Hs.262400	ESTs	4.3
	432072	NS2937	Hs.269109	ESTs	4.3
	452213	AL110237	Hs.28425	Homo sapiens mRNA; cDNA DKFZp566D224 (from c	4.3
	433535			predicted exon	4.3
70	441919	AS553802	Hs.126121	ESTs	4.3
	416717	H79559	Hs.297726	ESTs	4.2
	430995	NM_005092	Hs.248197	tumor necrosis factor (ligand) superfamily, member 18	4.2
	422659	AA449013	Hs.35283	ESTs	4.2
	415840	R15565	Hs.21758	ESTs	4.2
	451300	AA017066	Hs.237696	EST	4.2
75	443565	AJ221511	Hs.298652	ESTs	4.2
	424194	BE245533	Hs.169854	hypothetical protein SP192	4.2
	459105	NM_014617	Hs.29423	upstream binding protein 1 (UBP-1)	4.2
	453587	BE069037		gb:QVQ-BT0379-161299-040-e12 BT0379 Homo sapie	4.2
	410507	AA355288	Hs.271408	ESTs	4.2
80	453823	AL13767		gb:DKFZp761D2315.1 r 761 (synonym: hamy2) Homo	4.2
	450966	AA017245	Hs.32794	ESTs	4.2
	432694	AW991555	Hs.276755	ESTs, Weakly similar to F5381.2 [C.elegans]	4.2
	455108	AW856686		gb:RCO-CT0299-291199-031-G02 CT0299 Homo sapie	4.2
	443609	AW650231	Hs.282941	ESTs	4.2

	427469	AA403084	Hs.289347	ESTs	4.2
	417178	N51635		gbay87b01.1 Soares multiple sclerosis_2N6HMSF H	4.2
	439751	AA196206	Hs.50794	Homo sapiens mRNA full length insert cDNA clone EU	4.2
5	431982	AW418296	Hs.106754	ESTs	4.1
	442641	AI890955	Hs.262983	ESTs	4.1
	421218	AW881145		gb:CV0-OT0033-010400-182-a07 OT0033 Homo sapie	4.1
	445155	AF103307	Hs.171353	prostate cancer antigen 3	4.1
	418668	AI033028	Hs.132777	ESTs	4.1
	418236	AW994005	Hs.172572	hypothetical protein FLJ20093	4.1
10	432653	AI584317	Hs.122589	ESTs	4.1
	444813	BE522486	Hs.121688	Homo sapiens cDNA FLJ13463 fig. clone PLACE10034	4.1
	411279	AW894775		gb:CV4-OT0057-010300-121-d01 OT0057 Homo sapie	4.1
	440652	AJ216751	Hs.143977	ESTs	4.1
	416808	R11489	Hs.189718	ESTs	4.1
15	420405	AA743396	Hs.189023	ESTs	4.1
	402717			predicted exon	4.1
	435267	N23797	Hs.110114	ESTs	4.1
	412228	AW503785	Hs.73792	complement component (3d/Epsilon Barr virus) receptor	4.1
20	403560	AD292721	Hs.5120	dyenin, cytoplasmic, light polypeptide	4.1
	445162	BS32740	Hs.10476	ESTs	4.1
	459157	AI904385		gb:CM-8T054-080399-054 8T054 Homo sapiens cDN	4.1
	432474	AA584042		gb:am55e09.s1 NC1_CGAP_Lar1 Homo sapiens cDNA	4.1
	455388	AW936234		gb:CV0-DT0020-090200-106-g05 DT0020 Homo sapie	4.0
	425455	AA590748	Hs.130658	ESTs	4.0
25	438597	AA811662	Hs.171497	ESTs	4.0
	437934	AW880871	Hs.77496	small nuclear ribonucleoprotein polypeptide G	4.0
	455385	BE380047		gb:601159362P2 NH1_MGC_53 Homo sapiens cDNA	4.0
	438404	AW956556	Hs.137240	Homo sapiens mRNA for partial 3'UTR, sequence 2	4.0
	457740	AW504548		gb:UHF-BNO-akb-4-07-0-U1r1 NH1_MGC_50 Homo	4.0
30	437385	AA575055	Hs.164060	ESTs	4.0
	444530	AV550124	Hs.282435	ESTs	4.0
	405086	AA246214		gb:z470r1.1 Soares retina N2b-4HR Homo sapiens cD	4.0
	411256	AW834039		gb:CV0-TT0010-091199-053-c09 TT0010 Homo sapie	4.0
	433582	BE548749	Hs.148016	ESTs	4.0
35	438637	BE500941	Hs.126730	ESTs, Weakly similar to KIAA1214 protein [Hsapiens	4.0
	414571	BE416747	Hs.22368	cytosine phosphatase, non-receptor type 11	4.0
	446190	AI275299	Hs.259554	ESTs	4.0
	443542	AI827065	Hs.146040	ESTs	4.0
40	430444	AW25421	Hs.121035	ESTs	4.0
	454572	BE145471		gb:CV0-OT0216-011199-043-c09 OT0216 Homo sapie	4.0
	405946	AW501748		gb:UHF-BROp-alm-b-12-9-U1r1 NH1_MGC_52 Hom	4.0
	456141	AT751357	Hs.288741	Homo sapiens cDNA:FLJ22256 fig. clone HRC02850	4.0
	456140	AA165615	Hs.8008	ESTs	4.0
	441585	AI93261	Hs.144481	ESTs	4.0
45	416677	TS3470		gb:y446g06.1 Soares fetal liver spleen INFLS Homo s	4.0
	401740			predicted exon	4.0
	420122	AA255714	Hs.284153	Fanconi anemia, complementation group A	4.0
	442594	AW272467	Hs.254655	Unifed	3.9
50	426294	AA374185		gb:EST86289 HSC172 cells 1 Homo sapiens cDNA 5' e	3.9
	411922	AW876260		gb:PM4-PT0019-131229-006-E04 PT0019 Homo sapie	3.9
	452320	AA042873	Hs.160412	ESTs	3.9
	431644	AW972822	Hs.165248	cytochrome c	3.9
	409892	AW956113		gb:EST388183 MAGE resequences, MAGD Homo sap	3.9
	418132	T82670	Hs.117421	ESTs	3.9
55	414372	AA143654		gb:z055502r1 Stratagene pancreas (937208) Homo sap	3.9
	401196			predicted exon	3.9
	416900	M5964	Hs.1046	KIT ligand	3.9
	445444	AA380876	Hs.270	pleckstrin homology, Sec7 and coiled-coil domains, bld	3.9
60	435957	N30015	Hs.180368	ESTs	3.9
	442299	AW407391	Hs.155561	ESTs	3.9
	419499	AA808136	Hs.177638	ESTs	3.9
	438403	AA806607	Hs.292205	ESTs	3.9
	440386	AA001308	Hs.193213	ESTs	3.9
	443263	BE565610		gb:001342622F1 NH1_MGC_53 Homo sapiens cDNA	3.9
65	406481			predicted exon	3.9
	435330	AW021633		gb:d72602r1 Morton Fetal Cochlea Homo sapiens cDN	3.9
	415558	AA855143	Hs.125719	ESTs	3.9
	416874	H88752	Hs.42258	ESTs	3.9
	454885	AW836922		gb:CV1-LT0035-150200-074-h06 LT0036 Homo sapie	3.9
70	419896	Z29362		gb:HSZ29362 DKFZpharm1 Homo sapiens cDNA clone	3.9
	445262	BE59361	Hs.233477	ESTs, Moderately similar to A Chain A, Scapya compl	3.9
	419401	AW804653		gb:CV4-UM0094-105300-135-c08 UM0094 Homo sap	3.9
	405662			predicted exon	3.8
	405690	BE405855	Hs.808	heteronucleos nuclear ribonucleoprotein F	3.8
75	435282	AA677428	Hs.189731	ESTs	3.8
	424511			predicted exon	3.8
	451577	N59101	Hs.32703	ESTs	3.8
	457141	AA521410	Hs.41371	ESTs	3.8
80	407817	H52553	Hs.40400	ESTs	3.8
	412813	AA653507	Hs.285711	Homo sapiens cDNA FLJ13089 fig. clone NT2P30021	3.8
	418355	LA2653	Hs.11165	ATPase, H ⁺ -K ⁺ -transporting, noncatalytic, alpha polype	3.8
	445357	AW161533	Hs.300866	ESTs	3.8
	407448	AJ001885		gb:Homo sapiens mRNA, partial cDNA sequence for h	3.8
	455363	AI148037		gb:ag91d01r1 Soares testis_NHT Homo sapiens cDNA	3.8

	44651	W58469	Hs.103120	ESTs	3.8
	455067	AW854538		gb:RC3-CT0255-200100-024-b02 CT0255 Homo sapie	3.8
	442657	BE502631	Hs.130645	ESTs	3.8
5	428142	AA385839	Hs.104972	ESTs	3.8
	428274	AI379772	Hs.99206	ESTs	3.8
	437774	AW878199	Hs.291648	ESTs	3.8
	427737	AA35988	Hs.178066	ESTs. Weakly similar to AF068289.5 HOCME31P.H.s	3.8
	425671			predicted exon	3.8
10	413627	BE182082	Hs.246973	ESTs	3.8
	438858	R37529	Hs.269924	ESTs	3.8
	416612	HT6655		gb:yr97c0.x1 NC1_CGAP_Kid11 Homo sapiens cDN	3.8
	423443	AW557472	Hs.301511	ESTs. Highly similar to KP22_HUMAN SERINE/THR	3.7
	455361	AA035197	Hs.107375	ESTs	3.7
	437243	AA747549	Hs.259122	ESTs	3.7
15	437987	AW452022	Hs.122963	ESTs	3.7
	438781	BE145521	Hs.254602	ESTs	3.7
	455995	BE154837		gb:PMI-HT0345-121199-001-c08 HT0345 Homo sapie	3.7
	411492	AW612343		gb:hg97c10.x1 NC1_CGAP_Kid11 Homo sapiens cDN	3.7
	411247	AW963959		gb:EST376402 MAGS: heterologues, MAGS Homo sap	3.7
20	422666	NM_002410	Hs.121502	manuscript (alpha-1,6-glycoprotein beta-1,6-N-acetyl-g	3.7
	431828	AA572994		gb:hm33f12.x1 NC1_CGAP_Lip2 Homo sapiens cDNA	3.7
	438872	R84197	Hs.23559	ESTs	3.7
	438673	AB247177	Hs.123443	ESTs	3.7
	418624	HE3044		gb:yr77f05.s1 Scans: fetal liver spleen 1NFLS Homo sa	3.7
25	401963			predicted exon	3.7
	402867			predicted exon	3.7
	408315	AW179148		gb:MR4-ST0067-200895-002-B07 ST0067 Homo sapie	3.7
	418320	DE6891	Hs.84084	amyloid beta precursor protein (cytoplasmic tail)-bindin	3.7
30	447199	AI393421	Hs.160900	ESTs	3.7
	422590	AA312738	Hs.193945	Homo sapiens cDNA FLJ13962 fs, clone Y78A10012	3.7
	4551996	AW514021	Hs.246510	ESTs	3.7
	412463	AW923444	Hs.70572	laminin, alpha 4	3.7
	440928	AL046575	Hs.130198	ESTs	3.7
35	441951	W31002	Hs.128195	ESTs	3.7
	440705	AA904244	Hs.153205	ESTs	3.7
	434231	AF119201	Hs.205058	hypothetical protein PRO2831	3.7
	411039	AL135674	Hs.163348	ESTs	3.7
	413137	BE068915		gb:PMO-BT0340-231199-001-b07 BT0340 Homo sapie	3.7
40	417970	AA303924	Hs.57760	Homo sapiens cDNA: FLJ23119 fs, clone LNG079/B	3.7
	433785	AW62707	Hs.33736	Homo sapiens mRNA full length insert cDNA clone EU8	3.7
	455955	AL040421		gb:DKFZp434B0714.f1_434 (synonym: htas3) Homo s	3.7
	443601	AI078554	Hs.15682	ESTs	3.7
	404041			predicted exon	3.6
45	405122			predicted exon	3.6
	404582			predicted exon	3.6
	455786	BE050077		gb:RC6-BT0710-300300-021-F02 BT0710 Homo sapie	3.6
	411859	AA370573		gb:EST82238 Prostate gland 1 Homo sapiens cDNA 5' e	3.6
50	425758	AL030430	Hs.197772	ESTs	3.6
	421776	AW301994	Hs.108163	candidate tumor suppressor p33 INGI1 homolog	3.6
	430169	AA465331	Hs.189047	ESTs	3.6
	407695	AB080007	Hs.86450	ESTs	3.6
	454584	AW007673		gb:MR1-ST0088-021299-004-g01 ST0088 Homo sapie	3.6
	425902	X52609	Hs.161640	tyrosine aminotransferase	3.6
55	438328	W07411	Hs.118212	ESTs. Moderately similar to ALU5_HUMAN ALU SU	3.6
	425066	AA083555	Hs.178222	ESTs	3.6
	428850	AB040490	Hs.95765	ESTs	3.6
	437302	AA837146	Hs.180275	ESTs	3.6
	443873	AI580083	Hs.176154	ESTs	3.6
60	453993	AW615224	Hs.252839	ESTs	3.6
	413623	AA052721	Hs.246973	ESTs	3.6
	409196	NM_001874	Hs.169765	carboxypeptidase M	3.6
	424916	AW867440	Hs.23095	ESTs	3.6
	424769	H06469	Hs.142553	rat finger protein	3.6
	409360			predicted exon	3.6
65	421521	AI538760	Hs.161795	ESTs	3.6
	405549			predicted exon	3.6
	446114	AI275715	Hs.145806	ESTs	3.6
	441392	AA451831	Hs.222118	ESTs. Weakly similar to K1CQ_HUMAN KERATIN, T	3.6
70	424025	AI701852	Hs.301296	ESTs	3.5
	448527	AI525606		gb:PT1.3_G05.r tumor1 Homo sapiens cDNA 5', mR	3.5
	437063	AA351109	Hs.5437	Trac (Human T-cell leukemia virus type II binding pro	3.5
	446880	AE73005	Hs.231948	ESTs. Weakly similar to ALU6_HUMAN BI ALU CL	3.5
	449311	AI657014		gb:MR9a12.x1 NC1_CGAP_G06 Homo sapiens cDNA c	3.5
75	442999	AW662889	Hs.132395	ESTs	3.5
	416238	W90448		gb:hg78c08.s1 Scans: fetal liver spleen 1NFLS_S1 H	3.5
	423209	BE278528	Hs.105823	H.sapiens gene from PAC 4296, similar to syntactin 7	3.5
	409654	AW501833		gb:HLHF-BF09-ajp-d-01-0-UI.r1 NIH_MGC_S2 Homo	3.5
	414941	CI4865	Hs.182159	ESTs	3.5
80	458337	AW751661	Hs.85919	ESTs	3.5
	415296	FS0086		gb:SC114011 normalized infant brain cDNA Homo s	3.5
	423338	AB007961	Hs.127338	KIAA0492 protein	3.5
	411618	F12954		gb:HS03G0951 normalized infant brain cDNA Homo s	3.5
	405583			predicted exon	3.5
	435601	AF217509	Hs.283077	centrosomal P4.1-associated protein; uncharacterized bo	3.5

	450867	AA011454	Hs.245122	ESTs	3.5
	431339	AA508294	Hs.257286	ESTs	3.5
	441989	AT733386	Hs.129194	ESTs, Weakly similar to ALU1_HUMAN ALU SUBFA	3.5
	431343	AW970603	Hs.302941	Homo sapiens cDNA FLJ11661 fs, clone HEMBA100	3.5
5	434317	AT674095	Hs.116323	ESTs	3.5
	414741	RS1321	Hs.25780	Homo sapiens cDNA FLJ11252 fs, clone MAMMA10	3.5
	437907	AW297702	Hs.102915	ESTs	3.5
	443178	AJ51241	Hs.47312	ESTs	3.5
	403957	AJ270770	Hs.154485	transcription factor 7-like 2 (T-cell specific, HMG-box)	3.5
10	455887	BE154173		gb:PM1-HT0340-20129-004-12 HT0340 Homo sapie	3.5
	434362	W27081	Hs.295446	ESTs	3.5
	492611	AA078835		gicm24404.1 Striatogene colon HT29 (937221) Homo	3.5
	414390	BE231040		gb:501156234F1 NIH_MGC_21 Homo sapiens cDNA	3.5
15	457142	AJ924353	Hs.290569	EST	3.5
	423006	U29700	Hs.123014	anti-Mullerian hormone receptor, type II	3.5
	453363	AB987776	Hs.232623	ESTs	3.5
	418913	BE044745		gb:380606.x1 NC1_CGAP_F02F2 Homo sapiens cDN	3.4
	440016	AW118114	Hs.137057	ESTs	3.4
	405096			predicted exon	3.4
20	453072	AW582176	Hs.116532	ESTs	3.4
	436535	DS078		gb:Homo sapiens mRNA fragment	3.4
	424001	W67883	Hs.137476	KAA1051 protein	3.4
	428361	NM_015905	Hs.183858	transcriptional intermediary factor 1	3.4
25	410587	AA370706	Hs.11252	ESTs, Weakly similar to Wisk similarity with the Yy6	3.4
	454543	AW026895		gb:QNA-ST0023-16040-172-c56 ST0023 Homo sapien	3.4
	419515	SI9144	Hs.90791	gamma-aminobutyric acid (GABA) A receptor, alpha 6	3.4
	410280	AA063558	Hs.261286	ESTs	3.4
	425714	AW563278		gb:EST375351 IMAGE sequences, MAGH1 Homo sap	3.4
30	416895	AW561600		gb:EST375672 IMAGE sequences, MAGG Homo sap	3.4
	427935	AW503687	Hs.119424	ESTs, Weakly similar to unnamed protein product [Hsa	3.4
	411673	BE064863		gb:RC1-BT031-3-10300-015-006 BT0313 Homo saplen	3.4
	453339	AW592559		ESTs	3.4
	424696	BE429547	Hs.151503	Homo sapiens clone 24706 mRNA sequence	3.4
	436242	AA002187		gb:Homo sapiens cDNA FLJ11325 fs, clone PLACE10	3.4
35	442837	AJ022082	Hs.50492	ESTs	3.4
	452807	AA026933	Hs.162434	ESTs	3.4
	418110	RS4323	Hs.217754	Homo sapiens cDNA: FLJ22202 fs, clone HRC01333	3.4
	433936	AA208072	Hs.123459	ESTs	3.4
40	458177	AJ744955	Hs.267072	ESTs, Moderately similar to ALU4_HUMAN ALU SU	3.4
	401858			predicted exon	3.4
	405237			predicted exon	3.4
	457688	AL110157	Hs.3843	Homo sapiens mRNA: cDNA DKFZp586F2224 (from	3.4
	456914	AW363582	Hs.75323	prohibitin	3.4
45	421916	RS4441	Hs.101807	Homo sapiens cDNA: FLJ23546 fs, clone LING08361	3.4
	418321	N48146	Hs.269069	ESTs	3.4
	447876	AV654978	Hs.19904	cystathionase (cystathionine gamma-lyase)	3.4
	406197			predicted exon	3.4
	443025	AJ027184	Hs.200918	ESTs	3.4
50	459078	AJ681743		gb:bcag10.x1 NC1_CGAP_Lu24 Homo sapiens cDNA	3.4
	431301	AA502384	Hs.151529	ESTs	3.4
	430282	T8575		gb:vg60g02.r1 Soares fetal liver spleen 1NFLS Homo s	3.4
	428559	H24338	Hs.27041	ESTs	3.4
	455731	BE072188		gb:QV4-BT0536-211299-055-b09 BT0536 Homo saplo	3.4
	420735	AW297440	Hs.86653	ESTs	3.3
55	430881	NM_000809	Hs.248112	gamma-aminobutyric acid (GABA) A receptor, alpha 4	3.3
	405206			predicted exon	3.3
	449178	AJ633748	Hs.197597	ESTs	3.3
	453265	U61232	Hs.32575	tubulin-specific chaperone e	3.3
60	430700	AA769302	Hs.247812	H2A histone family, member K, pseudogene	3.3
	424496	AJ733461	Hs.122912	ESTs	3.3
	446963	AJ82668	Hs.178333	ESTs	3.3
	422879	AJ241409	Hs.188092	ESTs	3.3
	419891	AW448930	Hs.5415	ESTs	3.3
	445570	AA501793		gb:zhf6c06.r1 Soares_fetal_liver_spleen_1NFLS_S1 H	3.3
65	406255			predicted exon	3.3
	412319	AW936903		gb:RC1-DT0029-030200-012-d02 DT0029 Homo saplo	3.3
	401350			predicted exon	3.3
	430589	AF065955		gb:Homo sapiens full length insert cDNA clone YR86G	3.3
70	450589	AJ701505	Hs.202526	ESTs	3.3
	430749	AJ242956	Hs.25960	v-myc avian myelocytomatosis viral related oncogene, n	3.3
	430869	AJ695595	Hs.293219	ESTs	3.3
	454753	AJ981812		gb:CAH1-ST0283-071299-051-c07 ST0283 Homo saplo	3.3
	444479	AA194980	Hs.30818	Homo sapiens cDNA FLJ13681 fs, clone PLACE20000	3.3
75	413516	BE145907		gb:MRO-HT0208-221299-204-a12 HT0208 Homo saplo	3.3
	425541	AA359119		gb:EST188172 Fetal lung 11 Homo sapiens cDNA S' end,	3.3
	457107	AA118218	Hs.185796	ESTs, Weakly similar to N3418.1 [H.sapiens]	3.3
	421480	NM_016158	Hs.104671	erythrocyte transmembrane protein	3.3
	444289	BE267080	Hs.76391	myxovirus (influenza) resistance 1, homolog of murine	3.3
80	417725	R25257	Hs.21503	ESTs	3.3
	453631	AL046418		gb:DKFZp434N247_r1 434 (lancey: hbs3) Homo sa	3.3
	450692	HS0603	Hs.94037	hypothetical protein FLJ23053	3.3
	413357	W47611		gb:z35c06.r1 Soares_senescen_tfibroblast_NotHSF H	3.3
	415327	K22769	Hs.1861	membrane protein, palmitoylated 1 (59KD)	3.3
	457569	AW570021	Hs.291120	ESTs, Weakly similar to ALU8_HUMAN ALU SUBFA	3.3

	449601	R61666	Hs.293590	ESTs	3.3
	435256	AW953633	Hs.287681	Homo sapiens cDNA: FLJ21685 fs, clone COL09372	3.3
	440589	BE397763	Hs.194478	Homo sapiens mRNA; cDNA DKFZp434O1572 (from	3.3
	416768	T36310	Hs.1139	cold shock domain protein A	3.3
5	426768	AW303337	Hs.270411	ESTs	3.3
	400394	AF040257	Hs.263818	Homo sapiens TNF receptor homolog mRNA, partial cd	3.3
	433565	AA599763	Hs.112520	ESTs	3.3
	424093	AA335255		gb:EST39921 Epididymus Homo sapiens cDNA 5' end,	3.3
	445852	AA001742	Hs.83722	ESTs	3.3
10	431892	AA521315	Hs.194424	ESTs	3.3
	405512			predicted exon	3.3
	446990	AJ54717	Hs.223968	ESTs	3.3
	457729	AJ821863	Hs.253467	ESTs, Weakly similar to ALU7_HUMAN ALU SUBFA	3.3
15	417333	AL157545	Hs.42179	homeodomain and PHD finger containing, 3	3.2
	456420	AW401361	Hs.91773	protein phosphatase 2 (formerly 2A), catalytic subunit,	3.2
	403497			predicted exon	3.2
	427146	R52635	Hs.25935	ESTs	3.2
	406454			predicted exon	3.2
20	441033	BE562555		gb:601335667F1 NIH_MGC_44 Homo sapiens cDNA	3.2
	408444	AW661899	Hs.253204	ESTs	3.2
	434739	AA594487	Hs.144130	ESTs	3.2
	437060	AA745591	Hs.202053	ESTs	3.2
	423092	BE274837	Hs.123637	putative homeodomain transcription factor	3.2
25	424695	US9331	Hs.151899	sarcoglycan, delta (35kD dystrophin-associated glycopr	3.2
	443352	AJ054944	Hs.165505	ESTs	3.2
	437800	AL330150		gb:Homo sapiens mRNA; cDNA DKFZp547L156 (from	3.2
	425458	H89317	Hs.162899	ESTs	3.2
	439171	AA831133	Hs.294128	ESTs	3.2
30	407647	AW850158		gb:RC3-CT0379-290100-032-004 CT0379 Homo sapie	3.2
	435608	AW183071	Hs.250896	ESTs	3.2
	426743	AA383833	Hs.245022	ESTs	3.2
	457525	AW973800		gb:EST385901 MAGE resequences, MAGM Homo sap	3.2
	413800	AL222236	Hs.192235	ESTs	3.2
35	455565	BE260069		gb:601150964F1 NIH_MGC_19 Homo sapiens cDNA	3.2
	410081	T91029	Hs.15069	gb:RC3-BN0072-240200-011-407 BN0072 Homo sapie	3.2
	450866	T99968	Hs.18799	ESTs	3.2
	458529	AV652120	Hs.213232	ESTs	3.2
	424751	AA769482	Hs.296320	ESTs	3.2
40	442225	A306587	Hs.129192	ESTs	3.2
	410990	AW812928		gb:RC3-ST0186-250200-018-005 ST0186 Homo saplen	3.2
	435644	AA700657	Hs.269659	ESTs	3.2
	405347			predicted exon	3.2
	441292	AV632143	Hs.135853	ESTs	3.2
45	446294	AV655942	Hs.258132	ESTs	3.2
	454652	AW812088		gb:RC4-ST0173-191099-032-007 ST0173 Homo saplen	3.2
	418995	AJ042330	Hs.87128	ESTs, Weakly similar to similar to YB54 YEAST [Cel	3.2
	430118	AJ377255	Hs.163287	ESTs	3.2
	423691	CI4187	Hs.103538	ESTs	3.2
50	419313	H47206	Hs.194109	ESTs, Weakly similar to ALUB_HUMAN [!!!] ALU CL	3.2
	446122	AJ362780	Hs.181801	ESTs	3.2
	453725	VZ8543		gb:48C5 Human retina cDNA randomly primed subclon	3.2
	453554	AV1118336	Hs.75251	DEAD (Asp-Glu-Ala-Asp) box binding protein 1	3.2
55	428166	AA423849	Hs.79530	M5-14 protein	3.2
	447505	R78778	Hs.29808	Homo sapiens cDNA: FLJ21122 fs, clone CAS05917	3.2
	401871			predicted exon	3.2
	442160	AJ337127	Hs.156325	ESTs	3.2
	404708			predicted exon	3.1
60	412588	AW930055	Hs.44024	ESTs	3.1
	431976	AJ719001	Hs.291065	ESTs	3.1
	408864	AW851824	Hs.281172	ESTs	3.1
	433811	AW979015	Hs.123138	ESTs	3.1
	431691	AJ208511	Hs.292510	ESTs	3.1
	418719	AW975590	Hs.161707	ESTs	3.1
65	431740	H75450	Hs.183412	ESTs, Moderately similar to AF116721 67 PRO1777 H	3.1
	435699	AJ911488	Hs.213724	ESTs	3.1
	459344	AW495353	Hs.257976	ESTs	3.1
	431729	AW804714	Hs.162633	ESTs	3.1
	438771	AW975887	Hs.292079	ESTs	3.1
70	434480	AW956268	Hs.59395	Homo sapiens clone IMAGE:112574 mRNA sequence	3.1
	459547	AA00579	Hs.225186	EST	3.1
	427562	AA946562	Hs.133546	Homo sapiens cDNA: FLJ21120 fs, clone CAS05917	3.1
	433743			predicted exon	3.1
	413560	BE148411		gb:MFO-HT0241-131299-002-404 HT0241 Homo sapie	3.1
75	454372	H96843	Hs.283565	FOS-like antigen-1	3.1
	450018	AA421842	Hs.243509	hypothetical protein FLJ11106	3.1
	428839	AJ077756	Hs.82302	ESTs	3.1
	407110	AA018042	Hs.95078	ESTs	3.1
	436133	T77531	Hs.191124	ESTs	3.1
80	418872	R94785	Hs.270063	ESTs	3.1
	404418			predicted exon	3.1
	446877	AJ559472	Hs.270720	ESTs	3.1
	429053	AA443967	Hs.194114	ESTs	3.1
	425189	H16622		gb:ym26807.1 Soares infant brain 1MB Homo sapiens	3.1

5	404134			predicted exon	3.1
	441404	AJ538880	Hs.126555	ESTs	3.1
	400076			predicted exon	3.1
	411076	AW961336	Hs.69705	ESTs, Weakly similar to KIAA0443 [Laspaians]	3.1
	451049	AA013349	Hs.69502	ESTs	3.1
10	447021	AI355564	Hs.161406	ESTs	3.1
	404083			predicted exon	3.0
	415833	H05175	Hs.107510	ESTs	3.0
	402142			predicted exon	3.0
	419820	R53720	Hs.189745	ESTs	3.0
15	441140	AW016534	Hs.226994	ESTs	3.0
	445976	AA001278	Hs.59905	ESTs	3.0
	457953	AT338815	Hs.117323	ESTs	3.0
	411542	AW850767		gb:U3-CT0220-031199-025-A05 CT0220 Homo sapien	3.0
	403375			predicted exon	3.0
20	445951	AJ022240	Hs.17924	ESTs	3.0
	406241			predicted exon	3.0
	420306	AA258318	Hs.219226	ESTs	3.0
	413161	BE088130		gb:CM2-8T0368-171299-056-001 BT0368 Homo sapie	3.0
	448221	BE622615		gb:501407751.1 NH_MGC_72 Homo sapiens cDNA	3.0
25	415920	Z45894		gb:AC2202121 normalized infant brain cDNA Homo	3.0
	459135	AJ028022		gb:RC-8T015-311298-026 BT015 Homo sapiens cDNA	3.0
	425357	AA355842		gb:EST64303 Jurkat T-cells VI Homo sapiens cDNA 9	3.0
	454724	AA091228		gb:scn2t152.2eq.F Human fetal heart, Lambda ZAP Ex	3.0
	423395	AA002071	Hs.201624	hypothetical protein FLJ11209	3.0
30	427607	AA406119	Hs.270479	ESTs	3.0
	443558	AW499970	Hs.14822	ESTs	3.0
	437948	AA772520		gb:aw73009.s1 Stratagene schizo brain S11 Homo saplen	3.0
	418105	AW937468	Hs.178000	ESTs	3.0
	426763	AL042262	Hs.172101	Human DNA sequence from clone RP1-20221 on chro	3.0
35	403473			predicted exon	3.0
	427501	AJ369280	Hs.131743	ESTs	3.0
	453246	NM_002933	Hs.23239	KIAA1264 protein	3.0
	404587	M69587	Hs.104134	homeo box (Hb family) 1	3.0
	433954	AW241987	Hs.197025	ESTs	3.0
40	453472	AL037925		gb:ZNF256A4037_r1 564 (nynonym: hbr2) Homo sa	3.0
	433163	AF231338	Hs.222024	transcription factor BMAL2	3.0
	435899	W89093	Hs.189914	ESTs	3.0
	425626	AJ537538	Hs.173519	ESTs	3.0
	428931	AA594979	Hs.98967	ATPase, H ⁺ -transporting, lysosomal, noncatalytic acc	3.0
45	425593	AW535592		gb:EST370530 MAGE resequencing, MAGE Homo sapl	3.0
	431899	AA521381	Hs.187726	ESTs	3.0
	422406	AF025441	Hs.116206	Opa-interacting protein 5	3.0
	448178	AA79482	Hs.170799	ESTs	3.0
	404227			predicted exon	3.0
50	440575	AA808870	Hs.120006	ESTs	3.0
	431198	AL047634	Hs.231913	ESTs	3.0
	434221	AF119885	Hs.263040	hypothetical protein PR02543	3.0
	459459	AA450445		gb:z65h11.L1 Scams_tatol_fetus_Nb2HFR_8w Homo	3.0

TABLE 5B:

Play: Unique Eas probe identifier number

CAT number: Clone cluster number

Accession: Genbank accession numbers

55	Play	CAT Number	Accession
		407596	1003489_1
		407647	1007366_1
		408066	103549_1
		408315	1051132_1
60		409211	110306_1
		409699	1149033_1
		409846	1165150_1
		409854	1165229_1
		409892	1167659_1
65		410065	1174258_1
		410454	1204154_1
		410495	1205026_1
		410556	121053_1
		410667	1214678_1
70		410758	1219899_1
		410850	1226008_1
		410950	1228649_1
		411256	1236790_1
		411279	1237516_1
75		411280	1237585_1
		411337	1239217_1
		411542	1249095_1
		411543	1249127_1
		411673	1253737_1
80		411869	1264897_1
		411922	1265828_1
		412619	1266602_1
		412630	1266602_1
		412631	1266602_1

	142480	129929_1	BE142364 BE142341 AA112025
	142732	132385_1	AW963300 N23107 R22345
	143137	1350383_1	BE066915 BE069942
5	143161	1351252_1	BE068133 BE068134 BE068183 BE068184 BE068094
	143247	135544_1	AW963369 AW963371 AA127651 AA376726
	143357	1364165_1	W47611 BE087851
	143516	1374535_1	BE145907 BE145796 BE145803 BE145851 BE145923 BE145812 BE145809 BE145852 BE145856
	143550	1376821_1	BE146414 BE146415 H93958
10	144193	1424706_-2	BE260059
	144337	1436706_1	BE386606 BE275195 BE274984
	144372	143999_1	AA143654 AW753140 AA231770 AW970865 AA585075 AA492132
	144390	1441570_1	BE281040
	145296	1533328_1	F05086 F05091 R17158
15	145618	1540651_1	F12954 H10624 R11948 R55623 T75190
	145920	1561733_1	Z45684 H05861 R51265
	146211	1578593_1	R14625 R17352 H12520 R14650
	146328	1590451_1	W00446 H30749
	146612	1603885_1	H70565 N77403 H67949
20	146824	1604694_1	H69044 T47567 H75691 T50292
	146877	1608521_1	T33470 T64283 H74054
	146895	162974_1	AW561600 AA180217 AA321260
	147178	1655965_1	N51636 T51874 T51829
	147762	169750_1	AA205978 AA205930
25	148193	180520_1	BE046745 ADP4875 AB17476 AW572513 AA447586 H28330 AA232486 AA365704 BE271167
	149401	184454_1	AW804653 AW805017 AA236969
	149396	1886662_1	Z99362 Z99363
	1420362	192979_1	BE268835 AW968316 AA258918 AW643305 R14744 AI580388 BE071923 R36280
	142116	202288_1	AA806529 AA351008 AA352374 AW976806
	142046	210744_1	AW38662 T16929 H13401 F07773 R65838
30	142218	211994_1	AW881145 AA490718 H85637 AA304575 T08067 AA331991
	1423403	227842_1	AA325483 AW962169 AW562680
	142493	235233_1	AA330325 AA354596 AW966145
	142719	242889_1	H69452 AA345787 AW564302 H90399
	1425189	247825_1	H16622 R17322 AA351959
35	1425357	250578_-1	AA35842
	142641	252945_1	AA359119 AW963014 D79384
	142714	253333_1	AW963278 AA362266 AA362267
	1426294	263994_1	AA374185 AW956180 H38344
40	1426528	268722_1	AA360828 AW963760 AA360805 AA360830
	1426593	269748_1	AW965850 AA362139 AW446533
	1430202	314322_1	T65775 AW968345 AA468968
	1430635	319643_1	AW968485 AW968670 AA180922 BE350425
	1431075	327638_1	BE267477 AA491488 AW836723
	1431492	333830_1	AW812343 AA922558 AA925925 AA927038 AW972537 AW635554
45	1431828	333291_1	AA572894 AA516248 AA705285
	1432075	341066_1	AW972934 AA525260 AA525266 AA835021 BE000149 BE000148
	1432474	346197_1	AA584042 AW973273 AA584798
	1433771	364430_1	T26451 AA585298 AA585305
50	1433403	365354_1	AF940027
	1433767	374014_1	AA609245 AA724581 AW241989 AI377274 T47300
	1434738	392552_1	AA5836285 AA648286 AW574440
	1435196	41562_1	AK001084 A4078092 AA625049
	1436242	41641_1	AK002187 R66351
	1436812	427323_1	AW298067 AA731645 AA610101 AW154180 AI60673 AW978773
55	1437900	43772_1	AL390150 AW9659182 AA358923
	1437948	445866_1	AA772920 D19570 D61151 AI591331
	1438224	452656_1	AA533959 AA7181191
	1438335	45946_1	L09078 L03145 L09094 L09088 L03165 L09102
60	1439098	46889_1	AF085955 H69158 H69081
	1439128	46987_1	AF085984 H95905 H95906
	1441033	50807_-1	BE562556
	1442803	56492_-1	BE568610
	1445597	644513_1	H69549 AW753545 AI244270
	1445832	651929_1	AI251545 N39134 AW875371 AW875247
65	1448221	75534_-1	BE622615
	1448527	765707_1	AI525606 BE549857
	1448732	77773_-1	BE614063
	1449311	804513_1	AI570114 AW594035 AI657036 AI638390
	1449570	81018_1	AA001793 AA001871
70	1450078	823882_1	AI681743 AW897287 AW897205 AW897284
	1452351	91233_1	AA025647 RW5716 AW753786
	1452453	918300_1	AI922519 AI925918 AI920516
	1453472	96937_1	AL037925 AL037931 AL037957
	1453530	97021_1	AW021633 AA036730 AI866654
75	1453651	975024_1	AL046418 N52738 R33840
	1453725	978760_1	W28543 AI115531
	1453762	979693_1	AL120800 BE376830
	1453823	982526_1	AL137957 BE064160 BE064186
	1454102	1011693_1	AW752363 BE147120 R22346
80	1454487	1216101_1	AW796242 AW795356 BE161430
	1454543	1223775_1	AW606895 AW606874 AW606465 AW606535 AW606523
	1454564	1224407_1	AW807573 AW807566 AW807572
	1454573	1225624_1	BE146471 AW833743 AW833605 AW821469 AW821488 AW821541 AW821531 AW821513 AW821549 AW821384 AW821625 AW821577
			AW821547 AW834577

454652	1228071_1	AWB12088 AWB12105 AWB12082
454679	1228929_1	AWB13110 AWB13113
454724	123128_1	AA091228 HT1860 HT1073
454753	123379_1	AWB15212 AWB191070 BE158474 AWB191172 AWB19213 AWB19200 AWB19256 AWB19254 AWB19178 AWB19214 AWB19215 AWB19233
454885	1238874_1	AWB36922 AWB37718 AWB76688 AWB339119 AWB36997 AWB33908 AWB36912 AWB33993
454940	1245540_1	AWB46202 AWB46174 AWB46532 AWB46181 AWB46458 AWB46206 AWB46432 AWB46553 AWB46533 AWB46197 AWB46198 AWB46189 AWB46435 AWB46533 AWB46552 AWB46472 AWB46470 AWB46466 AWB46192 AWB46479 AWB46350 AWB46204 AWB46439 AWB46187 AWB46533 AWB46462 AWB46151 AWB46548 AWB46553 AWB46557 AWB46557 AWB46551
454994	1246637_1	AWB60176 AWB60531 AWB60412 AWB60451
455056	1250934_1	AWB53057 AWB53038 AWB53042 AWB53050 AWB53114 AWB53105 AWB53102 AWB53111 AWB53121 AWB53109 AWB53125
455067	1252050_1	AWB65438 AWB65418 AWB64412
455108	1253916_1	AWB53865 AWB53865 AWB53865
455387	1287871_1	BE059037 AWB366025 BE059178 AWB366034
455388	1287904_1	AWB36234 AWB36074 AWB36181 AWB36179 AWB36217 AWB36077 AWB36227 AWB363191
455534	1322942_1	AWB91925 AWB91919
455565	132891_1	BE000537 BE180584 BE180540 BE180542 BE180545
455731	1353872_1	BE072188 BE072299 BE072269 BE072317 BE072238
455786	1355510_1	BE090077 BE090079
455790	1355980_1	BE090590 BE090588 BE090681 BE090693 BE090875
455887	1360350_1	BE154173 BE154098 BE154098
455895	1381366_1	BE154837 BE154879 BE154850 BE154877 BE154835 BE154849 BE154902 BE154905 BE154867 BE154901 BE154904 BE154899
456253	1699178_1	T12198 T11583 R15526 R15585 R45878 R15562
456383	184252_1	A148037 AA287178 AA236755
456388	1842359_1	W23537
457525	351732_1	AW973800 AA557589 AA559886
457740	36528_1	AW500458 AW160900 AF161362 AF150327 AW578393 AW360921 AW360920 AW360890 AW360890 AW3732529
458301	345098_1	AF003834 W36292
458135	918515_1	AF022802 A1922783 A1902800
459157	919504_2	A1904385 A1904382

TABLE 5C:

Play: Unique number corresponding to an Eex probe

Ref: Sequences source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham L. et al." refers to the publication entitled "The DNA sequence of human chromosome 22" Dunham, et al. (1999) Nature 402:489-495

Strand: Indicates DNA strand from which exons were predicted

NL_position: Indicates nucleotide positions of predicted exons

Play	Ref	Strand	NL_position
40	402942	Minus	91593-91757,32720-92843,93962-94079,94024-94997
	401004	Plus	62930-62772
	401287	Minus	42287-42431
	401308	Plus	169019-169649
	401350	Plus	14471-14623
45	401740	Plus	145337-146494,148591-148590
	401871	Minus	58158-59585
	401896	Plus	115129-115294
	401963	Plus	51382-51521
	402105	Minus	22856-24255
50	402109	Minus	171722-171859,173197-173303
	402142	Minus	29392-30598
	402451	Minus	47137-48343
	402697	Plus	52906-53108,53500-53918
55	403277	Minus	27494-27642
	403283	Minus	71124-71996
	403375	Minus	92554-92795
	403473	Minus	54241-54437
	403467	Plus	7221-7441
60	403531	Minus	75903-76134
	403635	Minus	157028-157145,157125-157900
	403714	Minus	145556-145973
	403743	Minus	135483-136646
	404020	Minus	174449-174663
65	404041	Minus	1334-1503,2463-2585,5230-5337,19556-19504
	404044	Minus	225707-226939
	404083	Minus	16550-17082
	404108	Minus	63503-64942
	404134	Minus	40533-40911
	404227	Minus	93110-93269
70	404418	Minus	153339-153481,155099-155294
	404451	Minus	105191-105622
	404582	Plus	53230-53424
	404708	Plus	77523-77658
	404858	Plus	39954-40430
75	405096	Plus	148444-140897,148510-148581
	405290	Minus	157028-157145,157125-157900
	405347	Minus	9771-1116
	405512	Plus	17802-17965,18573-18697
	405549	Plus	10878-11048
80	405583	Plus	55211-55353
	405671	Plus	25805-26923
	405717	Plus	11275-11973
	405752	Plus	91392-91528
	405836	Minus	5031-5217

5	406122	9144067	Minus	30940-31386
	406197	7289992	Minus	47520-47961
	406237	7417725	Plus	30032-30501
	406241	7417725	Minus	34351-35752
	406255	7417729	Plus	2599-3209
10	406394	9256114	Minus	50715-50833
	406454	5588380	Minus	91745-91958
	406481	9864741	Minus	91439-91579
	406562	7711584	Plus	37316-37426
	406605	8272595	Minus	23275-23493,23723-23903

TABLE 6A lists about 68 genes highly down-regulated in ovarian cancer compared to normal ovaries. These were selected as for Table 5A, except the "average" ovarian cancer level was set to the maximum value amongst various ovarian cancers and the "average" normal ovary level was set to the minimum value from various non-malignant ovary specimens, and the ratio was greater than or equal to 2.5 (i.e. 2.5-fold down-regulated in the highest tumor vs. the lowest normal ovary). This has the overall effect of increasing stringency, and reducing the number of false-positives.

TABLE 6A: ABOUT 68 HIGHLY DOWN-REGULATED GENES, OVARIAN CANCER VERSUS NORMAL OVARY

Play: Primerkey					
Ex. Acct: Exemplar Accession					
UG ID: UniGene ID					
Title: UniGene Title					
ratio: ration of normal ovary vs. tumor					
25	Play	Ex. Acct	UGID	Title	ratio
	424851	AA678441	Hs.119069	ESTs	7.9
	437890	AA804362	Hs.180544	ESTs	4.7
	433852	AA842418	Hs.17381	ESTs	4.1
	407437	AF220254		gb-Homo sapiens MOST-1 mRNA, complete cds.	4.0
30	437781	AB062631	Hs.291625	ESTs	4.1
	433282	AK000043	Hs.32922	hypothetical protein FLJ20036	4.0
	440987	AA911705	Hs.130229	ESTs	3.8
	443131	A033533	Hs.130689	ESTs	3.6
	431075	BE267477		gb:01189542F2 NIH_MGC_7 Homo sapiens cDNA c	3.8
35	412637	AA115097	Hs.261313	ESTs	3.5
	406141	U69205	Hs.45152	ESTs, Moderately similar to neurogenic basic-helix-loop	3.6
	420122	AA257114	Hs.284153	Fanconi anemia, complementation group A	3.5
	430553	AW502062	Hs.30280	ESTs	3.4
	401308			predicted exon	3.4
40	410758	BE535988		gb:061062418F1 NIH_MGC_10 Homo sapiens cDNA c	3.4
	421418	AA585639		gb:065055.s1 NCI_CGAP_GCB1 Homo sapiens cDNA	3.4
	450061	AT070334	Hs.201115	ESTs	3.3
	409725	T40760	Hs.90459	EST	3.3
	434738	AA835265		gb:0617602.s1 NCI_CGAP_GCB1 Homo sapiens cDNA	3.3
45	431644	AW927622	Hs.169248	cytochrome c	3.3
	450938	AW753734	Hs.277215	ESTs	3.2
	420497	AW206285	Hs.253548	ESTs	3.2
	439426	AJ131502	Hs.143135	ESTs, Weakly similar to FAFY_HUMAN PROBABLE C	3.2
	407898	R86913		gb:030055.s1 Soares fetal liver spleen INFLS Homo sap	3.2
50	446583	AA187642	Hs.14632	ESTs	3.2
	431982	AAW19296	Hs.105754	ESTs	3.1
	452320	AA042673	Hs.160412	ESTs	3.1
	419401	AW804663		gb:0344-UM0094-160300-135-d06 UM0094 Homo saplin	3.1
	402105			predicted exon	3.1
55	444997	AJ204451	Hs.146196	ESTs	3.1
	403283			predicted exon	3.0
	455388	AW836234		gb:0344-OT0020-050200-106-g05 OT0020 Homo sap	2.9
	428559	H24338	Hs.27041	ESTs	2.9
	419002	T78625	Hs.268594	ESTs	2.9
60	404688			predicted exon	2.9
	409290	W56067	Hs.103105	ESTs	2.9
	406905			predicted exon	2.9
	441202	AB32143	Hs.135853	ESTs	2.8
	422046	AB380582		gb:0344at10.x1 NCI_CGAP_UNI Homo sapiens cDNA c	2.8
65	442865	H57659	Hs.114541	ESTs, Weakly similar to neuronal thread protein AD7c-N	2.8
	444431	AW513324	Hs.42280	ESTs	2.8
	426294	AA374105		gb:EST86289.HSC172 cells 1 Homo sapiens cDNA 5' en	2.8
	412480	BE142384		gb:CMC-HIT0143-27099-062-d12 HIT0143 Homo saple	2.8
	445838	AW206979	Hs.190665	ESTs	2.8
70	401464	AF099241	Hs.5028	histone deacetylase 5	2.7
	438126	AF085984		gb-Homo sapiens full length Insert cDNA clone YT99F0	2.7
	403277			predicted exon	2.7
	450078	AS181743		gb:0344at10.x1 NCI_CGAP_Lu24 Homo sapiens cDNA	2.7
	450900	AJ282148	Hs.56213	ESTs, Highly similar to FXD3_HUMAN FORICHEAD D	2.7
75	420620	AA278807	Hs.173343	ESTs	2.7
	450954	AW798466	Hs.82396	2,5'-isopentenylpyrophosphate synthetase 1	2.6
	421373	Y15221	Hs.103852	small inducible cytokine subfamily B (Cys-X-Cys), mem	2.6
	454338	AW381251	Hs.1050	pleckstrin homology, Sec7 and coiled-coil domains 1(cyt	2.6
	454529	Z45439	Hs.270425	ESTs	2.6
80	446877	AI599472	Hs.270720	ESTs	2.6
	412588	AW593965	Hs.44024	ESTs	2.6
	445802	AI672277	Hs.199475	ESTs	2.6
	446694	AW659942	Hs.258132	ESTs	2.6
	424028	AB014594	Hs.137579	KIA00694 gene product	2.6

454102	AW752363		gb:RC9-CT0201-270999-011-03 CT0201 Homo sapien
430822	AW373747	Hs.183337	ESTs
420289	N55394	Hs.96398	8-croguan/ino DNA glycosylase
410495	N95428		gb:2380209.1 Soares_genescan_ctrolabstc_NHHSF_Ho
412130	AW363803		gb:RC1-010029-030200-012-02 CT0202 Homo sapien
405699	BE154650		gb:PM3-HIT0344-071299-003-c08 HT0344 Homo sapien
445832	A261545		gb:q320a07.x1 NCL_CGAP_Kd11 Homo sapiens cDNA
429755	NM_001364	Hs.215839	disct, large (Drosophila) homolog 2 (chapeyrin-110)
445755	AW294870	Hs.223872	ESTs

TABLE 6B:

Play: Unique Eos probe set identifier number

CAT number: Gene cluster number

Accession: Genbank accession numbers

Play	CAT Number	Accession
407596	103349_1	R06913 R06901 H25362 R01370 H43764 AW044451 W21298
408959	114033_1	BE154650 BE154785 AW468343 BE154816 BE154667
410495	1205826_1	N55428 W24040 AW751365 H19187
410758	1219899_1	BE53988 AW801777
412319	1286602_1	AW536903 AW536907 AW536908 AW536914
412480	129329_1	BE142384 BE142341 AA112025
419401	184454_1	AW304663 AW850517 AA236969
421418	202288_1	AA806639 AA251009 AA838274 AW578806
422045	210744_1	AB595827 T16529 H13401 F07773 RS5805
422594	263594_1	AA374185 AW596180 H38344
431075	327638_1	BE25477 AA491488 AW836723
434738	392562_1	AA832855 AA648265 AW974440
439126	46897_1	AF035984 H05905 RS5906
440932	651726_1	A261545 N55034 AW597371 AW875247
450078	823882_1	AB61743 AW897287 AW897205 AW897284
454102	1011603_1	AW572363 BE147120 N22640
455388	1287904_1	AW56234 AW56074 AW536181 AW936179 AW936217 AW936077 AW938227 AW936191

TABLE 6C:

Play: Unique number corresponding to an Eos probe set

Ref: Sequence source. The 7 digit numbers in this column are Genbank identifier (GI) numbers. "Dunham L et al." refers to the publication entitled "The DNA sequence of human chromosome 22" Dunham, et al. (1999) *Nature* 402:489-495

Strand: Indicates DNA strand from which exons were predicted

NL_position: Indicates nucleotide positions of predicted exons

401308	9212516	Plus	169019-169649
402105	8131588	Minus	22856-24055
403277	8072597	Minus	27454-27642
403283	8075905	Minus	71124-71826
404668	8454393	Plus	35564-40430
405605	8272666	Minus	23275-23493,237-23903

Table 7A lists about 770 genes up-regulated in ovarian cancer compared to normal adult tissues. These were selected from 35403 probesets on the Affymetrix/Eos-Hu01 GeneChip array such that the ratio of "average" ovarian cancer to "average" normal adult tissues was greater than or equal to 2.5. The "average" ovarian cancer level was set to the 2nd highest amongst various ovarian cancers. The "average" normal adult tissue level was set to the 7th highest amongst various non-malignant tissues. In order to remove gene-specific background levels of non-specific hybridization, the 15th percentile value amongst the non-malignant tissues was subtracted from both the numerator and the denominator before the ratio was evaluated.

TABLE 7A: ABOUT 770 UP-REGULATED GENES, OVARIAN CANCER VERSUS NORMAL ADULT TISSUES

Play: Primary

Ex. Accn: Exemplar Accession

UG ID: UniGene ID

Title: UniGene Title

ratio: ration tumor vs. normal tissues

Play	Ex. Accn	UG ID	Title	ratio	
	108680	F09255	Hs.4993	ESTs	23.2
119743	W07042	Hs.53086	ESTs	22.0	
132528	AA283006	Hs.50758	chromosome-associated polypeptide C	22.0	
129571	X51630	Hs.1145	Wilms tumor 1	20.0	
102151	U17280	Hs.3132	steroidogenic acute regulatory protein	19.8	
132941	D43594	Hs.2142	5-hydroxytryptamine (serotonin) receptor 3A	17.5	
132624	AA164819	Hs.53631	ESTs	15.9	
102810	U05011	Hs.30743	preferentially expressed antigen in melanoma protein kinase C, iota	15.4	
101249	L33881	Hs.1504	protein kinase C, iota	14.5	
122802	AA406030	Hs.256579	ESTs	14.5	
135242	M74953	Hs.9700	cyclin E1	13.8	
101804	M68699	Hs.169940	TTK protein kinase	12.2	
122005	AA479726	Hs.105577	ESTs	12.0	
114965	AA250737	Hs.72472	ESTs	11.5	
115536	AA347193	Hs.52180	ESTs	11.4	
132191	AA449431	Hs.158668	KIAA0741 gene product	10.9	
121853	AA425887	Hs.98502	ESTs	10.9	
115881	AA435577	Hs.184549	G protein-coupled receptor 54	10.8	
119780	W72367	Hs.191381	ESTs, Weakly similar to hypothetical protein	10.5	
104301	D45332	Hs.8783	ESTs	10.3	
132632	N59764	Hs.5398	guanine-monomophosphate synthetase	10.1	

	105298	AA233459	Hs.26369	ESTs	8.7
	108857	AA133250	Hs.62180	ESTs	9.1
	113168	TS3592	Hs.161586	EST	9.0
5	115892	AA435946	Hs.50831	ESTs	8.9
	125666	AA199856	Hs.110811	ESTs	8.9
	102200	U21551	Hs.157205	branched chain aminotransferase 1; cytosolic	8.8
	108055	AA043562	Hs.62637	ESTs	8.8
	123572	AA446257	Hs.2373525	signal recognition particle 72kD	8.6
10	115909	AA436666	Hs.559761	ESTs	8.5
	109166	AA170845	Hs.73625	RAB6 interacting; kinesin-like (rab1nesin6)	8.3
	121779	AA422036	Hs.98367	ESTs	8.2
	102915	X07820	Hs.2258	modic metalloproteinase 10 (stromelysin 3)	8.0
	105317	AA233926	Hs.23635	ESTs	7.8
15	125250	W87455	Hs.222526	ESTs; Weakly similar to D20922.2 [C.elegans]	7.8
	126960	AA317900	Hs.161756	ESTs	7.8
	123969	AA075539	Hs.104336	ESTs	7.7
	130376	R40873	Hs.155174	KIAA0432 gene product	7.7
	123339	AA504253	Hs.101515	ESTs	7.7
20	134972	M19720	Hs.169252	Human L-myc protein gene; complete cds	7.6
	111234	N69267	Hs.21943	ESTs; Weakly similar to GNF YGLZ21c [S.cerevisiae]	7.5
	123889	AA676536	Hs.256562	ESTs	7.5
	123494	AA597886	Hs.112110	ESTs	7.4
	131965	AA434329	Hs.36553	ESTs	7.4
	105738	AA470145	Hs.25130	ESTs	7.4
25	109769	U127741	Hs.61345	ESTs	7.3
	106474	AA450212	Hs.42484	Homo sapiens mRNA; cDNA DKFZP564C053 (from cd	7.2
	123308	AA496211	Hs.103538	ESTs	7.2
	106124	AA423537	Hs.73567	ESTs	7.2
30	111345	N69820	Hs.14459	ESTs	7.1
	105200	AA195339	Hs.24641	ESTs	7.1
	116416	AA609219	Hs.35952	ESTs	7.1
	118846	N60567	Hs.25095	ESTs	7.1
	134344	AA279852	Hs.250796	ESTs	7.1
35	120472	AA251875	Hs.104472	ESTs; Weakly similar to Gag-Pol polypeptide [6.9
	115291	AA279943	Hs.122579	ESTs	6.9
	111185	N67551	Hs.12844	ECF-like domain; multiple 6	6.9
	106878	AA179848	Hs.58847	general transcription factor IIIc; polypeptide	6.9
	132939	U76189	Hs.81152	exostosins (multiple)-like 2	6.9
40	134520	N21407	Hs.257325	ESTs	6.9
	114724	AA151701	Hs.256267	ESTs; Highly similar to SPERM SURFACE PROTEIN	6.8
	116256	AA489033	Hs.62201	Homo sapiens mRNA; cDNA DKFZP568K1310 (from c	8.8
	102136	U15552	Hs.85769	acidic 82 kDa protein mRNA	6.7
	132725	L41887	Hs.164167	splicing factor; arginine/serine-rich 7 (SKD	6.5
45	109648	R44600	Hs.71154	ESTs	6.4
	116401	AA599963	Hs.59598	ESTs	6.4
	127563	AJ367707	Hs.150587	ESTs	6.4
	104252	AF002246	Hs.210983	cell adhesion molecule with homology to L1CAM	6.4
50	120438	AA243441	Hs.35948	ESTs; Weakly similar to GNF YW074w [S.cerevisiae]	6.2
	131978	D80008	Hs.36232	KIAA0195 gene product	6.2
	134621	L02547	Hs.172865	cleavage stimulation factor; 3' pre-RNA; subu	6.2
	120571	AA260738	Hs.126678	ESTs	6.2
	102627	U60561	Hs.158174	zinc finger protein 184 (Kruppel-like)	6.1
	100561	HG2874-HT3018	Hs.158174	Ribosomal Protein L39 Homolog	6.1
55	118204	N58599	Hs.48443	ESTs	6.0
	131386	AA056412	Hs.173135	dual-specificity tyrosine-(Y)-phosphorylation	6.0
	123007	G50223	Hs.173135	HWR11-Kruppel-like zinc finger protein (barn	5.9
	131228	AA279157	Hs.24485	chondroitin sulfate proteoglycan 6 (barnacle)	5.9
	106369	AA443828	Hs.25324	ESTs	5.9
60	108255	AA053157	Hs.172508	ESTs	5.8
	125370	AA256743	Hs.151791	KIAA0092 gene product	5.8
	130010	N52566	Hs.142838	ESTs	5.8
	131945	M87338	Hs.35120	replication factor C (activator 1) 4 (37kD)	5.7
	116238	AA479362	Hs.47144	ESTs	5.7
	102221	U24576	Hs.47144	LIM domain only 4	5.7
65	130757	R00641	Hs.18925	ESTs; Weakly similar to cDNA EST yk336a7.5 o	5.6
	131278	U81523	Hs.25195	endometrial bleeding associated factor (ell-	5.6
	101383	M14113	Hs.79345	coagulation factor VIIc; procoagulant compon	5.5
	131836	AA451006	Hs.22990	DKFZP566F064 protein	5.5
	129628	U25727	Hs.11774	cyclin-dependent kinase inhibitor 2 (melanom	5.5
70	106523	AA453441	Hs.31511	ESTs	5.5
	111772	R28287	Hs.237146	ESTs	5.5
	101255	L34500	Hs.148894	mitochondrial translocational initiation factor	5.5
	106895	AA489665	Hs.25245	ESTs	5.5
	104943	AA055217	Hs.169674	ESTs	5.5
75	129229	AA211941	Hs.105943	poly(adenylate) binding protein-interacting pro	5.4
	102305	U33286	Hs.30072	chromosome segregation 1 (yeast homolog)-like	5.4
	106553	AA454967	Hs.5687	ESTs; Highly similar to RNA binding motif pro	5.4
	112305	R54822	Hs.26244	ESTs	5.3
80	123972	C14782	Hs.70357	immunoglobulin superfamily; member 4	5.3
	102676	U72514	Hs.12045	putative protein	5.3
	106459	AA449741	Hs.4029	glioma-amplified sequence-41	5.2
	107865	AA025104	Hs.81252	ESTs	5.2
	121121	AA399371	Hs.185095	ESTs; Weakly similar to zinc finger protein S	5.2
	127162	R76339	Hs.21187	ESTs	5.2

131646	AA171695	Hs.30057	Homo sapiens clone 24749 and 24750 mRNA seque	5.2
217770	AA421714	Hs.11465	KIAA0896 protein	5.2
122512	AA445311	Hs.98558	budding uninhibited by benzimidazoles 1 (yeas	5.1
105870	AA399623	Hs.23505	ESTs	5.1
100341	D53506	Hs.8313	synixin binding protein 3	5.1
118948	H61187	Hs.35201	ESTs	5.1
120821	AA347419	Hs.98870	Homo sapiens mRNA full length insert cDNA do	5.1
130690	AA084286	Hs.130933	paternally expressed gene 3	5.1
122661	AA454535	Hs.245641	ESTs	5.1
124169	AA458862	Hs.104472	ESTs; Weakly similar to Gag-Pol polypeptide [5.1
108610	AA130596	Hs.71331	ESTs; Weakly similar to POTENT HEAT-STABLE PR	5.0
110799	N26101	Hs.7838	Human ring zinc-finger protein (ZNF127-Xp) ge	5.0
120619	AA284372	Hs.111471	ESTs	5.0
122732	AA461225	Hs.95519	ESTs	5.0
129512	AA047344	Hs.107213	ESTs; Highly similar to NY-REN-6 antigen [Hs	5.0
102823	U50914	Hs.5057	carboxypeptidase D	4.9
126950	MI3659	Hs.111461	Homo sapiens autoantigen mRNA; complete cds	4.9
101084	U52425		KIAA0007 protein	4.9
134859	D87716	Hs.90315	Homo sapiens BAC clone RG054D04 from 7q31.	4.9
115955	AA446121	Hs.44199	ESTs	4.9
105516	AA257971	Hs.21214	ESTs	4.9
114332	AA424751	Hs.16219	KIAA0903 protein	4.9
106672	AA461300	Hs.30643	ESTs	4.8
105126	AA424005	Hs.22972	ESTs; Moderately similar to HSAR [Musculus]	4.8
110695	H33453	Hs.124777	ESTs	4.8
102325	U39311	Hs.78534	musE (E. coli) homolog 2 (colon cancer; nonpo	4.8
133262	U52960	Hs.250855	SRB7 (suppressor of RNA polymerase B; yeast)	4.8
119708	W67810	Hs.57904	mugo-nachi (Orosophila) homolog; proliferato	4.7
120695	AA291468		ESTs	4.7
126551	AA446990	Hs.103135	Homo sapiens autoantigen mRNA; complete cds	4.7
103152	X65533	Hs.77890	guanylate cyclase 1; soluble; beta 3	4.7
108699	AA121514	Hs.70832	ESTs	4.7
115054	AA255921	Hs.86035	ESTs	4.7
121423	AA402293	Hs.153498	ESTs	4.7
123203	AA489671	Hs.89709	glutamate-cysteine ligase (gamma-glutamylcyst	4.7
126802	AA947601	Hs.97056	ESTs	4.7
130827	C17384	Hs.194227	F-box protein 21	4.7
134470	X54942	Hs.87358	CDC20 protein kinase 2	4.7
100449	D87470	Hs.75400	KIAA0280 protein	4.7
110970	N51374	Hs.96870	Homo sapiens mRNA full length insert cDNA do	4.7
115901	AA435403	Hs.89509	ESTs; Moderately similar to Fritzed-6 [Hsae	4.7
108739	F10770	Hs.130378	Homo sapiens clone 655 unknown mRNA; comple	4.6
116195	AA465148	Hs.72402	ESTs	4.6
132122	U50592	Hs.40403	Ctbp300-interacting transactivator; with Glu	4.6
108990	AA152236	Hs.72045	ESTs	4.6
109355	AA160529	Hs.46524	ESTs	4.6
115937	AA443269	Hs.305991	KIAA0957 protein	4.6
133520	X74331	Hs.74519	primase; polypeptide 2A (59kD)	4.6
131200	AA689427	Hs.210708	ESTs; Moderately similar to E11 ALU SUBFAMIL	4.6
121369	AA405657	Hs.128791	Human DNA sequence from clone 957N21 on chro	4.5
132880	AA444369	Hs.177537	ESTs	4.5
127386	AA574111	Hs.106728	ESTs	4.5
120067	W53592	Hs.47543	ESTs	4.5
122906	AA477063	Hs.102947	ESTs	4.5
135286	AA401269	Hs.97849	ESTs	4.5
130155	L33404	Hs.151254	kallikrein 7 (chymotrypsin; stratum corneum)	4.5
106163	AA421104	Hs.12094	ESTs	4.5
102634	U69494	Hs.74395	Human hbc547 mRNA sequences	4.4
107876	AA025315	Hs.81184	Novel human gene mapping to chromosomes X	4.4
109454	AA232255	Hs.46912	ESTs	4.4
125960	D53367	Hs.145968	ESTs	4.4
126592	AA160190	Hs.76127	heat homologous to the E6-AP (UBE3A) carboxy	4.4
100269	D36550	Hs.1189	E2F transcription factor 3	4.4
134161	U97168	Hs.79440	IGF-II mRNA-binding protein 3	4.3
100502	H51495-HT1495		Adrenal-Specific Protein Pp2	4.3
105542	AA351838	Hs.8241	ESTs; Weakly similar to heat shock protein h	4.3
109787	F10610	Hs.34853	inhibitor of DNA binding 4; dominant negative	4.3
110759	N21671	Hs.19025	ESTs	4.3
129570	AA476975	Hs.200434	ESTs	4.3
134666	AA482319	Hs.8752	putative type II membrane protein	4.3
117693	N40939	Hs.44162	ESTs; Weakly similar to cDNA EST yk342h12.5 c	4.3
111008	N53389	Hs.7222	ESTs	4.3
120277	AA338155	Hs.97890	ESTs	4.3
103609	AA333808	Hs.21490	KIAA0438 gene product	4.2
121381	AA405747	Hs.97865	ESTs; Weakly similar to WASP-family protein [4.2
100893	HG4557-HT4962		Small Nuclear Ribonucleoprotein U1, 16np	4.2
107176	AA621762	Hs.7576	ESTs	4.2
118976	N33629	Hs.93391	ESTs	4.2
130703	N63295	Hs.16103	ESTs	4.2
106540	AA454607	Hs.38114	ESTs; Weakly similar to coded for by C. eleg	4.2
119367	T76324	Hs.90505	ESTs	4.2
133633	D21262	Hs.75337	nuclear phosphoprotein p130	4.2
105520	AA258068	Hs.33085	WD repeat domain 3	4.2
114264	Z40074	Hs.27595	ESTs	4.1

131046	X02530	Hs.2248	IP10; small inducible cytokine subfamily B (4.1
105220	AA210695	Hs.17121	ESTs	4.1
103111	X63187	Hs.2719	epididymis-specific; whey-acidic protein type	4.1
125640	R37700	Hs.208261	ESTs	4.1
119501	H59617	Hs.5199	ESTs; Weakly similar to UBQUITIN-CONJUGATING	4.1
118052	NS4915	Hs.82719	Homo sapiens mRNA; cDNA DKFZp96F1822 (from o	4.1
134891	F03517	Hs.90787	ESTs	4.1
112364	R59312	Hs.187642	ESTs; Weakly similar to DNA-DIRECTED RNA POLY	4.1
125958	AA291716	Hs.97258	ESTs	4.1
106272	AA432074	Hs.32538	ESTs	4.1
112041	R43300	Hs.22929	ESTs	4.1
131569	AA595653	Hs.30696	transcription factor-like 5 (basic helix-loop	4.1
116134	AA450246	Hs.5199	ESTs; Highly similar to CG1-04 protein [H.sapi	3.9
107638	AA00628	Hs.4743	ESTs; Weakly similar to predicted using Genef	4.0
131941	D62657	Hs.35086	ubiquitin-specific protease 1	4.0
106154	AA425304	Hs.6994	ESTs	4.0
105546	AA252032	Hs.26089	ESTs; Weakly similar to S209.9 [D.melanogaste	4.0
105319	AA435666	Hs.7392	ESTs; Weakly similar to Gu protein [H.sapiens	4.0
121816	AA424814	Hs.187509	ESTs	4.0
122851	AA463627	Hs.99598	ESTs	4.0
123337	AA504153	Hs.132797	ESTs; Weakly similar to ORF YGL050w [S.cerevi	4.0
128443	M0212	Hs.102868	ESTs	4.0
125011	S72869	Hs.107932	DNA segment; single copy; probe p14 (transfer	4.0
133895	AA608628	Hs.21015	ESTs; Highly similar to tetracycline transpor	4.0
132323	AA456102	Hs.256559	ESTs	4.0
134265	H5052	Hs.80768	separin-RNA synthetase	4.0
102827	U91327	Hs.6456	chaperonin containing TCP1; subunit 2 (beta)	4.0
102123	U14518	Hs.1594	centromere protein A (17kD)	3.9
102813	U90551	Hs.151461	embryonic ectoderm development protein	3.9
113970	H98748	Hs.6105	ESTs	3.9
107145	AA621108	Hs.173001	ESTs	3.9
114212	Z29338	Hs.21201	DKFZP566G0846 protein	3.9
106814	AA458934	Hs.179912	ESTs	3.9
132742	AA490882	Hs.65901	ESTs; Weakly similar to C43H8.1 [C.elegans]	3.9
120948	AA397822	Hs.104650	ESTs; Highly similar to similar to mago nashi	3.9
129337	H63542	Hs.110488	KIAA0690 protein	3.9
103835	AA172215	Hs.104848	ESTs; Moderately similar to TRANSCRIPTION FAC	3.9
133330	U42360	Hs.71119	Pituitary prostate cancer tumor suppressor	3.9
133928	N34096	Hs.7766	ubiquitin-conjugating enzyme E2E: 1 (homologous	3.9
133640	H03004	Hs.75356	ubiquitin-conjugating enzyme E2E: 1 (homologous	3.9
133350	AA135469	Hs.71573	ESTs	3.9
115623	AA401476	Hs.38733	postsynaptic protein CRPT	3.9
101973	S82297	Hs.80120	UDP-N-acetyl-alpha-D-galactosamine:polypeptid	3.9
102669	U71207	Hs.29279	eyes absent (Drosophila) homolog 2	3.9
134248	AA262677	Hs.30624	ESTs	3.9
102330	U40434	Hs.155581	mesothelin	3.9
116157	AA461063	Hs.44298	ESTs; Highly similar to HSPC011 [H.sapiens]	3.8
106691	AA463453	Hs.23259	ESTs; Weakly similar to ACTIN; CYTOPLASMIC 2	3.8
115844	AA430124	Hs.234607	ESTs	3.8
107159	AA621340	Hs.10600	ESTs; Weakly similar to ORF YKR081c [S.cerevi	3.8
106498	AA452141	Hs.7171	ESTs	3.8
134405	J04177	Hs.82772	collagen; type XI; alpha 1	3.8
106260	AA451448	Hs.5230	ESTs; Weakly similar to BACR37P7.g [D.melanog	3.8
109864	H02554	Hs.30323	ESTs	3.8
124848	N91948	Hs.125034	ESTs	3.8
134719	U07515	Hs.89232	chromobox homolog 5 (Drosophila HP1 alpha)	3.8
113702	T97307	Hs.161720	ESTs; Moderately similar to III ALU SUBFAMIL	3.8
128639	N91245	Hs.102897	ESTs	3.8
111259	N73808	Hs.24336	ESTs	3.7
129351	AA167268	Hs.62349	Human sac inhibitor mRNA; 3' end	3.7
119741	N70205	Hs.43670	insulin family member 3A	3.7
105012	AA116038	Hs.5329	chromosome 20 open reading frame 1	3.7
128734	AA343629	Hs.104570	kallitren 8 (neurophysin/vasin)	3.7
130567	U07493	Hs.1608	replication protein A3 (14kd)	3.7
114253	Z2699	Hs.14631	ESTs	3.7
103169	H98560	Hs.44450	Sp3 transcription factor	3.7
111259	N70711	Hs.18885	ESTs; Highly similar to CG1-116 protein [H.sapi	3.7
112876	T03488	Hs.4842	ESTs	3.7
112621	H62780	Hs.84122	ESTs	3.7
130385	AA126474	Hs.155223	stanniocalcin 2	3.7
129300	C20976	Hs.110165	ESTs; Highly similar to ribosomal protein L26	3.7
134398	M15841	Hs.82575	small nuclear ribonucleoprotein polypeptide B	3.7
106968	AA504321	Hs.29813	ESTs; Weakly similar to hypothetical 43.2 kDa	3.7
100906	HG4716-HT5168	Hs.155223	Guanosine 5'-monophosphate Synthase	3.7
100418	D66978	Hs.84790	KIAA0225 protein	3.7
101484	M02494	Hs.20315	Interferon-induced protein 56	3.7
102547	U57311	Hs.45838	chromosome 11 open reading frame 8	3.7
103587	Z25063	Hs.82128	ST4 oncofetal trophoblast glycoprotein	3.7
130600	AA478601	Hs.258737	ESTs	3.7
128733	AA328993	Hs.104558	ESTs	3.7
134376	AA412720	Hs.82240	ESTs; Highly similar to CG1-116 protein [H.sapi	3.6
134098	X03323	Hs.79086	ribosomal protein; mitochondrion; L3	3.6
101188	L20320	Hs.184298	cyclin-dependent kinase 7 (homolog of Xenopus	3.6
132149	T10822	Hs.4096	ESTs	3.6

	116200	AA465358	Hs.118793	ESTc; Highly similar to p621 [L-asplena]	3.6
	121920	AA428300	Hs.161841	ESTs	3.6
	126809	AA234365	Hs.102456	survival of motor neuron protein interacting	3.6
5	101070	U04510	Hs.789	ADP-ribosylation factor domain protein t; 64k	3.6
	106693	AA121289	Hs.49597	ESTc; Highly similar to retinoic acid-induced	3.6
	109139	AA176121	Hs.59757	zinc finger protein 281	3.6
	111870	R37778	Hs.18865	ESTc; Weakly similar to hypothetical protein	3.6
	113843	W00080	Hs.27099	DKFZP564J0863 protein	3.6
10	127947	AI432475	Hs.146327	ESTs	3.6
	128055	AI379480	Hs.125449	ESTs; Weakly similar to MaxiK channel beta 2	3.6
	129914	U23277	Hs.13321	rearranged L-myc fusion sequence	3.6
	132145	AA263588	Hs.4094	ESTs	3.6
	134644	S83308	Hs.87224	SRY (sex-determining region Y)-box 5	3.6
15	115047	AA252627	Hs.22554	homeo box B5	3.6
	102399	U42369	Hs.179729	Human N33 protein form 1 (N33) gene, exon 1 a	3.6
	127479	AA513722	Hs.10929	collagen; type X, alpha 1 (Schmid metaphylase)	3.6
	105645	AA262030	Hs.5152	ESTs; Weakly similar to katanin p80 subunit 1	3.6
	101483	M24486	Hs.76768	procollagen-proline; 2-oxoglutarate 4-dioxyge	3.6
20	105709	AA291288	Hs.26761	DKFZP568L0724 protein	3.6
	122636	AA541003	Hs.110031	ESTs	3.6
	124792	R44357	Hs.132784	ESTs; Weakly similar to cDNA EST EMBL701421	3.8
	103621	Z47727	Hs.150675	polymerase (RNA) II (DNA directed) polypeptid	3.5
	105427	AA251330	Hs.28246	ESTs	3.5
	121553	AA412468	Hs.48820	ESTs	3.5
25	116167	AA258421	Hs.43728	hypothetical protein	3.5
	134570	U66615	Hs.172280	GW/SNF related; matrix associated; actin dep	3.5
	110787	N24716	Hs.12244	ESTs; Weakly similar to C44B9.1 [C-epsilon]	3.5
	131621	U77665	Hs.138128	ribonuclease P (30kD)	3.5
	132813	N72118	Hs.57435	solute carrier family 11 (proton-coupled diva	3.5
30	116370	AA521256	Hs.236204	ESTs; Moderately similar to NUCLEAR PORE COMP	3.5
	131965	W90146	Hs.35952	ESTs	3.5
	115221	AA252942	Hs.77941	ESTs	3.5
	115293	AA456020	Hs.50848	ESTs; Weakly similar to KIAA0382 protein [Ls	3.5
35	123507	AA600176	Hs.112345	ESTs	3.5
	129801	F11087	Hs.239566	ESTs	3.5
	115084	AA255586	Hs.2471	Homo sapiens mRNA; cDNA DKFZp564C053 (from cl	3.5
	123442	AA558803	Hs.111496	ESTs	3.5
	115061	AA253217	Hs.41271	ESTs	3.5
40	100146	D13645	Hs.2471	KIAA0020 gene product	3.5
	115140	AA258030	Hs.43536	ESTs; Weakly similar to supported by GENSCAN	3.5
	115360	AA281950	Hs.5057	carboxypeptidase D	3.5
	130261	D63767	Hs.153678	reproduction 8	3.4
	106824	HC4058-HT4326		Oncogene Aml1-Ev1-1, Fusion Activated	3.4
45	102287	U31814	Hs.3352	histone deacetylase 2	3.4
	102738	U89502	Hs.74407	nucleolar protein p40	3.4
	118836	N79820	Hs.50554	ESTs	3.4
	102423	U41754	Hs.170312	small nuclear RNA activating complex; polypep	3.4
	106300	AA435840	Hs.15114	high-mobility group (nonhistone chromosomal)	3.4
50	106156	AA425354	Hs.4210	ESTs	3.4
	106483	AA451676	Hs.30299	IGF-II mRNA-binding protein 2	3.4
	107868	AA025234	Hs.61250	ESTs	3.4
	108187	AA066538	Hs.27642	ESTs; Weakly similar to similar to 1-acylgly	3.4
	116123	AA459282	Hs.43756	ESTs	3.4
55	119501	W07721	Hs.151363	ESTs	3.4
	129121	AA127459	Hs.108788	ESTs; Weakly similar to zelin [D.melanogaster	3.4
	131638	D87120	Hs.25882	predicted osteoblast protein	3.4
	132982	N4893	Hs.6153	ESTs; Highly similar to CG1-48 protein P-Luap	3.4
	133767	D63875	Hs.173288	KIAA0155 gene product	3.4
60	111823	R32583	Hs.24944	ESTs	3.4
	134372	D63877	Hs.82324	KIAA0157 protein	3.4
	130938	AA013250	Hs.21398	ESTs; Moderately similar to PUTATIVE GLUCOSAM	3.4
	115169	AA258427	Hs.58427	ESTs	3.4
	123978	C20853	Hs.170278	ESTs	3.4
65	108807	AA129568	Hs.6376	ESTc; Weakly similar to PROTEIN PHOSPHATASE P	3.4
	132581	R42266	Hs.52256	ESTc; Weakly similar to beta-TCP protein E3R	3.4
	134654	W23625	Hs.8738	ESTc; Weakly similar to ORF YGR200c [S.cerevi	3.4
	106730	AA259701	Hs.5354	DKFZP564052 protein	3.4
70	111295	N73276	Hs.12175	ESTc; Weakly similar to ubiquitin-conjugating	3.3
	102009	U02690	Hs.82643	protein tyrosine kinase 9	3.3
	114161	Z38904	Hs.22385	ESTs; Weakly similar to KIAA0970 protein [Ls	3.3
	130604	X03535	Hs.1657	estrogen receptor 1	3.3
	100103	A7070375	Hs.5395	deichyl-phosphate mannosyltransferase polype	3.3
	121748	AA421171	Hs.234545	ESTs	3.3
	106698	AA463745	Hs.29403	ESTs; Weakly similar to PROBABLE ATP-DEPENDENT	3.3
75	134353	S77154	Hs.82120	nuclear receptor subfamily 4; group A; member	3.3
	134154	AA121320	Hs.79404	neuron-specific protein	3.3
	133142	F03321	Hs.65974	ESTs	3.3
	124461	N50641	Hs.80285	Homo sapiens mRNA; cDNA DKFZp568C1723 (from c	3.3
	140903	AA255534	Hs.124134	ESTs	3.3
80	106772	AA476106	Hs.12892	ESTc; Weakly similar to protein phosphatase-1	3.3
	109704	F09597	Hs.12876	ESTs	3.3
	111131	N64267	Hs.10177	ESTs	3.3
	115019	AA251906	Hs.48473	ESTs	3.3
	116019	AA450312	Hs.237480	Homo sapiens mRNA; cDNA DKFZp434E102 (from cl	3.3

	118528	N67889	Ha.49397	ESTs	3.3
	124027	F03625	Ha.107537	ESTs	3.3
	131699	R86657	Ha.90421	ESTs; Moderately similar to IIII ALU SUBFAMIL	3.3
	111044	N55433	Ha.23025	ESTs	3.3
5	103768	AA089997	Ha.100320	ESTs; Weakly similar to GOLGI 4-TRANSMEMBRANE	3.3
	131982	N49091	Ha.3385	ESTs; Highly similar to CGI-134 protein [Laa	3.3
	123673	AA609471	Ha.112712	ESTs	3.3
	132936	AB002305	Ha.61111	KIAA0307 gene product	3.3
10	103923	X53793	Ha.117050	multifunctional polypeptide similar to SAICAR	3.3
	120572	AA280734	Ha.258787	ESTs	3.3
	132384	AA479933	Ha.46967	Human DNA sequence from clone 167A19 on chrom	3.3
	105656	AA282914	Ha.101176	ESTs	3.3
	105386	AA141719	Ha.155441	ESTs	3.2
15	118995	N71781	Ha.55003	Homo sapiens mRNA full length insert cDNA clo	3.2
	112092	R44538	Ha.140889	ESTs	3.2
	125154	W08419	Ha.24355	ESTs	3.2
	102640	AQ41551	Ha.48544	ESTs	3.2
	133453	M68941	Ha.73826	protein tyrosine phosphatase; non-receptor ty	3.2
20	124006	D60302	Ha.108977	ESTs	3.2
	116083	AA455653	Ha.44581	ESTs; Weakly similar to HEAT SHOCK 70 KD PROT	3.2
	105763	AA470844	Ha.73311	ESTs	3.2
	102621	U50075	Ha.50924	GATA-binding protein 6	3.2
	103330	X85373	Ha.77496	small nuclear ribonucleoprotein polypeptide G	3.2
25	128926	AA481403	Ha.107213	ESTs; Highly similar to NY-REN-6 antigen [Ls	3.2
	101167	L53209	Ha.133677	zinc finger protein 141 (clone p12-44)	3.2
	104065	AA393755	Ha.117211	ESTs; Highly similar to CGI-62 protein [Lasp	3.2
	112917	T10196	Ha.4263	ESTs; Weakly similar to [prediction	3.2
30	120358	AA213459	Ha.100592	transcription factor 17	3.2
	121857	AA420517	Ha.50294	ESTs; Highly similar to DNA-REPAIR PROTEIN CO	3.2
	122124	AA434257	Ha.186579	ESTs; Moderately similar to IIII ALU SUBFAMIL	3.2
	132231	H99131	Ha.42635	ESTs	3.2
	134272	X76540	Ha.223014	protease; serine; 15	3.2
35	116860	AA431719	Ha.51809	ESTs	3.2
	115278	AA279757	Ha.67466	ESTs; Weakly similar to BACN32G1.1 [D;melano	3.2
	134125	R38102	Ha.50421	KIAA0203 gene product	3.2
	129160	AA131252	Ha.103007	ESTs	3.2
	121740	AA149011	Ha.167444	DKFZP586D0823 protein	3.2
40	102242	U27185	Ha.32943	retinoic acid receptor responder [tazarotene	3.2
	104956	AA074880	Ha.120975	ESTs; Weakly similar to hypothetical protein	3.2
	113047	T25857	Ha.7349	ESTs	3.2
	115017	AA251880	Ha.175982	tumor protein p53-binding protein	3.2
	133780	M14219	Ha.76152	decorin	3.1
	129453	AA421213	Ha.111632	Lem3 protein	3.1
45	133553	X66918	Ha.172210	MUP1 protein	3.1
	105036	AA412505	Ha.10553	ESTs	3.1
	102234	U26312	Ha.8123	chromobox homolog 3 (Drosophila HP1 gamma)	3.1
	106133	AA424346	Ha.107573	sialyltransferase	3.1
	116903	H47357		ESTs; Moderately similar to weak similarity t	3.1
50	105721	AA465164	Ha.6670	ESTs	3.1
	107115	AA610108	Ha.27693	ESTs; Highly similar to CGI-124 protein [Laa	3.1
	133228	N90029	Ha.6831	Homo sapiens clone 1400 unknown protein mRNA;	3.1
	104733	AA019498	Ha.23071	ESTs	3.1
	103879	AA228148	Ha.50252	ESTs; Weakly similar to putative [Calegans	3.1
55	103038	X54941	Ha.77550	CDC28 protein kinase 1	3.1
	135154	AA126433	Ha.173242	sorting nexin 4	3.1
	114860	AA255112	Ha.106227	ESTs; Moderately similar to similar to murine	3.1
	102437	U46569	Ha.221956	neuropilin 5	3.1
	100352	D64159		Homo sapiens mRNA for 3-7 gene product, part	3.1
60	103631	Z48570		H.sapiens Sp17 gene	3.1
	104238	AB002364	Ha.27916	a diacylglycerol- and metalloprotease (neuro	3.1
	108613	AA100967	Ha.69165	ESTs	3.1
	115915	AA438894	Ha.48926	ESTs	3.1
	120640	AA286945	Ha.163933	ESTs	3.1
65	124058	H03099	Ha.101618	ESTs	3.1
	136376	U81931	Ha.155172	adaptor-related protein complex 3; beta 1 sub	3.1
	131632	AA443871	Ha.25826	ESTs	3.1
	131523	H89801	Ha.201676	M phase phosphoprotein 10 (U3 small nuclear	3.1
	113827	AA427890	Ha.44426	ESTs; Weakly similar to PHOSPHOLIPID HYDROPER	3.1
70	103828	AA131654	Ha.71435	DKFZP564C0463 protein	3.1
	121198	R45483	Ha.22159	ESTs; Weakly similar to ZINC FINGER PROTEIN H	3.1
	123950	AA621785	Ha.170008	methylmalonate-semialdehyde dehydrogenase	3.1
	131538	Z26331	Ha.26505	ubiquitin-conjugating enzyme E2H (homologous	3.1
	105616	AA280870	Ha.24568	ESTs	3.1
75	101228	L27706	Ha.82916	chaperonin containing TCP1; subunit 6A [zeta	3.1
	100280	D42085	Ha.155314	KIAA0095 gene product	3.1
	132744	X54326	Ha.55921	glutamyl-prolyl-4RNA synthetase	3.1
	103105	X51970	Ha.76913	prolactinase (prolactin, macroprotein) subunit; alpha	3.1
	106984	AA521201	Ha.7129	ESTs	3.1
80	105127	AA158132	Ha.11817	ESTs; Weakly similar to contains similarity t	3.1
	102302	U33052	Ha.69171	protein kinase C-beta 2	3.1
	117708	N45114	Ha.46476	ESTs	3.1
	111314	N74574	Ha.33922	H.sapiens novel gene from PAC 117P20; chromos	3.0
	132902	AA490969	Ha.169147	ESTs	3.0
	130356	X94373	Ha.155017	nuclear receptor interacting protein 1	3.0

	128420	A0268155	Hs.14146	ESTs; Weakly similar to unknown [H.sapiens]	3.0
	108746	AA126974	Hs.43388	ESTs	3.0
	127236	A0341818	Hs.98655	budding uninhibited by benzimidazoles 1 (yeas)	3.0
5	114208	Z35301	Hs.7859	ESTs	3.0
	107071	AA609053	Hs.35188	ESTs	3.0
	104957	AA074919	Hs.10026	ESTs; Weakly similar to ORF YJL063c [S.cerevi	3.0
	124073	H03594	Hs.127376	KIAA0266 gene product	3.0
	133695	AA128100	Hs.2057	uridine monophosphate synthetase (crotale pho	3.0
	101332	L28997	Hs.242894	ADP-ribosylation factor-like 1	3.0
10	104276	C02193	Hs.85222	ESTs; Weakly similar to RZ709_02 [H.sapiens]	3.0
	126160	N09600	Hs.247277	ESTs; Weakly similar to transformation-related	3.0
	125584	M11433	Hs.101850	retinoid-binding protein 1; cellular	3.0
	100405	D85425	Hs.82733	nidogen 2	3.0
15	101335	L49054		Homo sapiens U(3-5)(c25.1p34) fusion gene NP	3.0
	108761	AA127514	Hs.61603	ESTs	3.0
	111346	N89629	Hs.13259	ESTs	3.0
	114988	AA251089	Hs.94557	ESTs; Weakly similar to phosducin; retinal [H	3.0
	116000	AA443338	Hs.48589	ESTs; Weakly similar to finger protein HZF6;	3.0
20	116545	D20313	Hs.74899	ESTs	3.0
	117873	NA9967	Hs.46624	ESTs	3.0
	121463	AA411745	Hs.223691	ESTs; Weakly similar to KIAA0554 protein [H.s	3.0
	128525	AA242816	Hs.102552	ESTs; Weakly similar to KIAA0437 [H.sapiens]	3.0
	131185	M25753	Hs.23950	cyclin B1	3.0
25	134380	D38073	Hs.179555	minichromosome maintenance deficient (S. cere	3.0
	105740	AA253236	Hs.10552	ESTs	3.0
	130919	AA291710	Hs.21276	collagen; type IV; alpha 3 (Goodpasture antiq	3.0
	134423	W56151	Hs.83006	ESTs; Highly similar to CGI-130 protein [H.s	3.0
	104896	AA054228	Hs.23165	ESTs	3.0
	134407	X72954	Hs.82794	calreticulin (20kD calcium-binding protein)	3.0
30	105378	AA446894	Hs.21331	ESTs	3.0
	112283	R35345	Hs.20952	Homo sapiens clone 24411 mRNA sequence	3.0
	109018	AA156950	Hs.114982	ESTs	3.0
	114329	Z39742	Hs.222478	ESTs	3.0
	114869	AA250775	Hs.87747	ESTs	3.0
35	116408	AA608752	Hs.71969	Homo sapiens mRNA; cDNA DKFZp564P08.23 (fcom	3.0
	115286	AA273803	Hs.82204	ESTs	2.9
	105809	AA338827	Hs.26104	ESTs	2.9
	113811	W44528	Hs.46878	ESTs	2.9
	107248	D59894	Hs.34782	ESTs	2.9
40	134489	U09294	Hs.112378	LM and senescent cell antigen-like domains 1	2.9
	134064	D67885	Hs.76895	KIAA0244 protein	2.9
	127370	A024352	Hs.70337	immunoglobulin superfamily; member 4	2.9
	113277	T65797	Hs.11774	protein (peptidyl-prolyl co-trans isomerase)	2.9
45	132783	N74859	Hs.55683	DEAD-box (Asp-Glu-Ala-Asp-His) box polypeptide	2.9
	102010	AA156460	Hs.44229	dual specificity phosphatase 12	2.9
	130095	P01831	Hs.14838	ESTs	2.9
	106618	AA459249	Hs.8715	ESTs; Weakly similar to Similarity with snail	2.9
	103427	X97303		H.sapiens mRNA for Plg-12 protein	2.9
50	133980	D00760	Hs.181309	prolactosome (prosome; macropain) subunit; alpha	2.9
	111353	N30430	Hs.6616	ESTs	2.9
	105344	AA235303	Hs.8545	ESTs	2.9
	134498	M53180	Hs.84131	theophylline synthetase	2.9
	117910	N50528	Hs.12940	zinc-finger and homeoboxes 1	2.9
55	118903	N60774	Hs.132207	ESTs; Moderately similar to IIII ALU SUBFAMIL	2.9
	121713	AA419198	Hs.105577	ESTs	2.9
	129080	H19307	Hs.108507	ESTs	2.9
	129404	AA1172256	Hs.111126	ESTs	2.9
	129457	X55330	Hs.207776	aspartylglucosaminidase	2.9
60	130352	D87450	Hs.154978	KIAA0251 protein	2.9
	133415	X69599	Hs.73149	paired box gene 8	2.9
	120949	AA287115	Hs.36987	ESTs	2.9
	131257	AA259042	Hs.24908	ESTs	2.9
	134480	AA024664	Hs.83916	NADH dehydrogenase (ubiquinone) 1 alpha subco	2.9
65	116734	P13789	Hs.53798	DKFZP586D2223 protein	2.9
	105038	AA126719	Hs.25382	ESTs	2.9
	114986	AA251010	Hs.87807	ESTs	2.9
	105651	AA262481	Hs.18439	ESTs	2.9
	107174	M68874		Human phosphatidylcholine 2-acylhydrolase (cP	2.9
70	123398	AA521855	Hs.105514	ESTs	2.9
	106007	AA411482	Hs.11042	ESTs; Weakly similar to vef1 [H.sapiens]	2.9
	109450	AA232183	Hs.173042	ESTs; Weakly similar to IIII ALU SUBFAMILY J	2.9
	104885	AA010530	Hs.9598	Human BAC clone GS025M02 from 7q21-q22	2.9
	106877	AA1156229	Hs.118331	ESTs	2.9
	116028	AA452112	Hs.42644	thioredoxin-like	2.9
75	105404	AA243303	Hs.21187	ESTs	2.9
	132385	AA598994	Hs.46541	Homo sapiens PAC clone DJ089A10 from 7q32-q3	2.9
	119828	W52480	Hs.56148	ESTs; Moderately similar to NY-REN-58 antigen	2.9
	124637	N80716	Hs.75798	Human DNA sequence from clone 118321 on chro	2.9
	130588	AA287735	Hs.16411	Human DNA sequence from clone 1189524 on chro	2.9
80	105640	AA281623	Hs.7525	ESTs; Weakly similar to KIAA0742 protein [H.s	2.9
	131818	Z35297	Hs.5281	neuronal pentraxin II	2.9
	119298	T23820	Hs.155478	cyclin T2	2.9
	128742	D00763	Hs.251531	prolactosome (prosome; macropain) subunit; alpha	2.9
	115069	AA255876	Hs.86919	ESTs; Weakly similar to IIII ALU SUBFAMILY J	2.9

5	100468	D89289	Ha.118722	lucosyltransferase 8 (alpha 1-6) fucosyltran	2.8
	132920	L66133	Ha.606	ATPase; Cu ⁺ transporting; alpha polypeptide	2.8
	113490	T88700	Ha.173374	ESTs	2.8
	133451	Y07054	Ha.73616	ubiquitin-cytochrome c reductase hinge protei	2.8
	128770	H95645	Ha.143460	protein kinase C, α	2.8
10	129122	N52515	Ha.108790	ESTs	2.8
	104827	AA035630	Ha.8551	PRP4/STK/WD splicing factor	2.8
	111348	N50041	Ha.9585	ESTs	2.8
	130987	R45898	Ha.21853	ESTs; Weakly similar to cAMP inducible 2 prot	2.8
	102139	U15932	Ha.2128	dual specificity phosphatase 5	2.8
15	114902	AA236359	Ha.39504	ESTs	2.8
	106594	AA415461	Ha.18127	ESTs	2.8
	129438	N53125	Ha.107300	ESTs	2.8
	107129	AA620553	Ha.4756	flap structure-specific endonuclease 1	2.8
	104491	N71513	Ha.39328	ESTs	2.8
20	105043	AA132239	Ha.11810	ESTs; Weakly similar to CD4L2 [C.elegans]	2.8
	100885	AA45182	Ha.17875	ESTs	2.8
	109695	F09530	Ha.180591	ESTs; Weakly similar to R06F5.5b [C.elegans]	2.8
	120455	AA251083	Ha.104347	ESTs	2.8
	130861	N23383	Ha.20569	ESTs	2.8
25	131649	AA41254	Ha.30120	ESTs	2.8
	128517	AA280517	Ha.103861	ESTs; Weakly similar to p60 katanin [H.sapien]	2.8
	100486	HG1112-HT1112	Ha.118823	Ras-Like Protein To4	2.8
	116729	F13700	Ha.115823	ribonuclease P; 40SD subunit	2.8
	101051	H42550	Ha.82045	midline (neurite growth-promoting factor 2)	2.8
30	115465	AA256941	Ha.43691	ESTs	2.8
	100137	D13627	Ha.15071	chaperonin containing TCP1; subunit 8 (beta)	2.8
	129837	H05323	Ha.146401	endothelial monocyte-activating polypeptide	2.8
	131582	UB0551	Ha.28777	H2A histone family; member L	2.8
	129445	AA306121	Ha.111515	ESTs; Weakly similar to predicted using Genef	2.8
35	129239	D31544	Ha.109701	ESTs; Moderately similar to weak similarity I	2.8
	106507	AA452584	Ha.31585	protein phosphatase 1; regulatory (inhibitor)	2.8
	101664	H60752	Ha.12120	H2A histone family; member A	2.8
	129426	AA412087	Ha.168272	ESTs; Highly similar to protein inhibitor of a	2.8
	103437	X98260	Ha.82254	M-phase phosphoprotein 11	2.8
40	129821	F11019	Ha.12696	cortactin SH3 domain-binding protein	2.8
	130160	Z35228	Ha.15130	UDP-Galactose 4-epimerase	2.8
	104257	AF006285	Ha.5222	estrogen receptor-binding fragment-associated	2.8
	116204	AA465701	Ha.108646	ESTs	2.8
	125914	AA262925	Ha.190034	cleavage stimulation factor; 7' pre-RNA; subu	2.8
45	131510	AA302114	Ha.27842	ESTs; Weakly similar to similar to 1-acyl-gly	2.8
	106291	AA435551	Ha.30824	ESTs	2.8
	122761	AA458296	Ha.105039	ESTs; Weakly similar to III ALU SUBFAMILY J	2.8
	107056	AA600310	Ha.18720	programmed cell death 8 (apoptosis-inducing 1	2.8
	106535	AA094565	Ha.226440	Human caplin clone 24B61 mRNA sequence	2.8
50	116226	AA478729	Ha.76450	ESTs	2.8
	120266	AA173939	Ha.193902	ESTs; Weakly similar to inner centromere prot	2.8
	128654	H20689	Ha.163180	actin-like 6	2.8
	116726	F13581	Ha.42309	ESTs	2.7
	132540	U33821	Ha.69469	Tax1 (human T-cell leukemia virus type I) bin	2.7
55	133273	AA147725	Ha.69469	dendritic cell protein	2.7
	108846	AA132983	Ha.41155	DKFZP556G151T protein	2.7
	105621	AA203655	Ha.5376	Human caplin mRNA; cDNA DKFZp564K0222 (from c	2.7
	129164	AA282183	Ha.109045	ESTs	2.7
	133618	UT8524	Ha.75251	DEADH (Asp-Glu-Ala-Asp(His)) box binding prot	2.7
60	129521	AA258765	Ha.107476	ATP synthase; H ⁺ transporting; mitochondrial	2.7
	116429	AA609710	Ha.80120	Human chromosome 3p21.1 gene sequence	2.7
	110984	N52006	Ha.80120	UMP-N-acetyl-alpha-D-glucosamine:polypeptid	2.7
	100372	D79997	Ha.184339	KIAA0176 gene product	2.7
	125134	W19228	Ha.100748	ESTs	2.7
65	129254	AA453624	Ha.1058	deoxynucleosyltransferase; terminal	2.7
	102339	U37022	Ha.95577	cyclin-dependent kinase 4	2.7
	108599	AA456646	Ha.28661	ESTs	2.7
	119118	RA4122	Ha.42743	ESTs; Weakly similar to predicted using Genef	2.7
	105913	AA405320	Ha.21291	Human caplin mRNA; cDNA DKFZp564K0222 (from c	2.7
70	106317	AA436568	Ha.172140	ESTs	2.7
	115551	AA365527	Ha.177861	ESTs; Highly similar to CGH-110 protein [H.sapien]	2.7
	103769	AA456176	Ha.70337	immunoglobulin superfamily; member 4	2.7
	105079	AA143189	Ha.12617	ESTs; Highly similar to cDNA DKFZp564K0222 (from c	2.7
	102929	AA205649	Ha.86371	zinc finger protein 254	2.7
75	122089	AA432136	Ha.88682	ESTs	2.7
	129108	L20321	Ha.1087	serine/threonine kinase 2	2.7
	123385	D82075	Ha.110569	Human caplin clone 25007 mRNA sequence	2.7
	131412	U34044	Ha.124027	SELENOPHOSPHATE SYNTHETASE; Human selenium D	2.7
	104052	AA383164	Ha.97644	mammaglobin 2	2.7
80	116254	AA461146	Ha.41086	ESTs; Weakly similar to OXYSTEROL-BINDING PRO	2.7
	105878	AA458872	Ha.123114	Home chromosome 3p21.1 gene sequence	2.7
	114652	AA101416	Ha.107149	ESTs; Weakly similar to PTB-ASSOCIATED SP/UCI	2.7
	105831	AA482014	Ha.23463	centrin; EF-hand protein; 3 COG31 yeast home	2.7
	101445	M21259	Ha.1066	small nuclear ribonucleoprotein polypeptide E	2.7
	124028	X36881	Ha.82302	ribosomal protein L17	2.7
	114471	AA028074	Ha.103387	ESTs	2.7
	102051	U07550	Ha.1197	heat shock 100D protein 1 (chaperonin 10)	2.7
	106916	AA490814	Ha.24170	ESTs; Weakly similar to ribosomal S1 protein	2.7

	116142	AA460649	Hs.39457	ESTs	2.7
	109912	H05509	Hs.24639	ESTs	2.7
	103193	X70476	Hs.75724	cofactor protein complex; subunit beta 2 (bet	2.7
	102046	U07151	Hs.182215	ADP-acylation factor-like 3	2.7
5	104587	R64534	Hs.101469	ESTs	2.7
	112996	T23539	Hs.7165	zinc finger protein 259	2.7
	118138	NS7773	Hs.93560	ESTs; Weakly similar to Ig [R.norvegicus]	2.7
	123056	AA85724	Hs.192119	ESTs	2.7
10	124315	H94892	Hs.6590	viral similar leukemia viral oncogene homolog	2.7
	124447	N48000	Hs.140945	Homo sapiens mRNA; cDNA DKFZp568L141 (from d	2.7
	132834	H77546	Hs.57898	ESTs; Highly similar to NY-REN-49 antigen p1.	2.7
	107529	Y12065	Hs.5592	nucleolar protein (N0650 repeat)	2.7
	130648	AA075427	Hs.17296	ESTs; Weakly similar to Irfendion	2.7
15	106865	AA61551	Hs.16251	ESTs; Highly similar to 73 kDa subunit of cle	2.6
	133848	AA053287	Hs.76728	ESTs	2.6
	134880	AA052376	Hs.93056	15 kDa selenoprotein	2.6
	128871	AA402271	Hs.106776	Homo sapiens mRNA for putative Ca2+-transport	2.6
	106946	AA485223	Hs.34892	ESTs	2.6
20	119892	W84548	Hs.94896	ESTs	2.6
	132309	AA450917	Hs.2780	Jun D proto-oncogene	2.6
	123923	U21558	Hs.50678	TATA box binding protein (TBP)-associated fac	2.6
	114365	Z41588	Hs.18553	ESTs	2.6
	114162	Z38309	Hs.22265	ESTs	2.6
25	133370	AA155897	Hs.71257	DKFZP564I1922 protein	2.6
	105916	AA403890	Hs.3542	ESTs	2.6
	133501	W16684	Hs.74284	ESTs; Moderately similar to Similar to S.cere	2.6
	100530	HG1869-HT1904		Male Enhanced Antigen	2.6
30	130553	AA430032	Hs.25287	pituitary tumor-transforming 1	2.6
	108917	AA137078	Hs.173648	ESTs	2.6
	122249	AA439579	Hs.258543	ESTs; Highly similar to CGI-07 protein [H.sapi	2.6
	119598	W45531	Hs.94642	ESTs	2.6
	119902	W64865	Hs.40094	Human DNA sequence from clone 167A19 on chrom	2.6
35	133272	AA465018	Hs.69423	kallidin 10	2.6
	132575	AA043565	Hs.5188	ESTs; Weakly similar to 60S RIBOSOMAL PROTEIN	2.6
	130459	AA60264	Hs.155983	KAA0677 gene product	2.6
	130363	H07633	Hs.6456	chaperonin containing TCP1; subunit 2 (beta)	2.6
	131130	T19289	Hs.22320	nucleoprotein 150LD	2.6
	112043	R63317	Hs.26312	glioma amplified on chromosome 1 protein (fou	2.6
40	116146	AA460701	Hs.193200	ESTs	2.6
	122378	AA446100	Hs.103817	ESTs	2.6
	103154	A05724	Hs.2639	Norrie disease (pseudoglioma)	2.6
	133555	AA491296	Hs.72005	ESTs	2.6
	115652	AA405098	Hs.38178	ESTs	2.6
45	104975	AA086071	Hs.50758	chromosome-associated polypeptide C	2.6
	134681	A05978	Hs.86474	prostaglandin-endoperoxide synthase 1 (prost	2.6
	112659	T03313	Hs.4747	dykerkesia congenita 1; dykerkin	2.6
	100092	A0002231	Hs.75618	RAB11A; member RAS oncogene family	2.6
	102636	U96838	Hs.79378	cystin A1	2.6
50	104490	N71503	Hs.43087	ESTs; Weakly similar to dyforin [H.sapiens]	2.6
	105813	AA479922	Hs.161022	ESTs	2.6
	105872	AA487907	Hs.18282	ESTs; Highly similar to unknown [H.sapiens]	2.6
	107022	AA259041	Hs.28866	programmed cell death 10	2.6
	107113	AA010073	Hs.23920	ESTs; Weakly similar to oligophrenin-1 [H.sapi	2.6
55	113281	T66300	Hs.112356	Homo sapiens mRNA for lipoyltransferase; comp	2.6
	115586	AA399218	Hs.52423	ESTs	2.6
	115779	AA424183	Hs.70345	ESTs	2.6
	122895	AA428946	Hs.105325	ESTs	2.6
	124726	R15740	Hs.104578	carbohydrate (keratan sulfate Gal-6) sulfat	2.6
60	129775	R94659	Hs.12420	ESTs	2.6
	131991	AA251909	Hs.36708	budding uninhibited by benzimidazoles 1 (yeas	2.6
	132818	D07975	Hs.5064	ESTs	2.6
	134612	AA451712	Hs.171581	ESTs; Highly similar to ubiquitin C-terminal	2.6
	130313	AA620323	Hs.154320	ubiquitin-activating enzyme E1C (homologous t	2.6
65	131971	R070167	Hs.3611	ESTs	2.6
	133175	AA134767	Hs.66666	ESTs	2.6
	102083	U10323	Hs.75117	interferon enhancer binding factor 2, 45KD	2.6
	125670	AA328221	Hs.82855	CD47 antigen (Rb-related antigen; Integrin-as	2.6
	121822	AA425107	Hs.97018	ESTs; Moderately similar to SH3 domain-binding	2.6
70	106719	AA465171	Hs.238944	ESTs	2.6
	130029	AA236412	Hs.236510	ESTs; Moderately similar to PFT27 [M.musculus]	2.6
	124328	H97781	Hs.14415	ESTs; Highly similar to CGI-108 protein [H.sapi	2.8
	105387	AA238551	Hs.108536	chromosome 1 open reading frame 9	2.6
	103073	X59417	Hs.74977	proteasome (prosome; macropain) subunit; alph	2.6
75	116294	AA489000	Hs.93748	ESTs; Moderately similar to TRANSCRIPTION FAC	2.6
	135339	D59269	Hs.127842	Homo sapiens mRNA full length insert cDNA do	2.6
	125390	H95094	Hs.75187	translocase of outer mitochondrial membrane 2	2.6
	102554	U52077	Hs.247848	Human merlin transposase gene; complete con	2.6
	131076	H44386	Hs.22566	ESTs	2.6
80	114096	Z38342	Hs.27007	chromosome condensation 1-like	2.6
	126402	AA234339	Hs.50282	GTP-binding protein ragB	2.6
	102125	U14550	Hs.107573	siRNA transferase	2.6
	134653	AA452818	Hs.87355	ESTs	2.6
	101959	S80343	Hs.180832	angryRNA synthetase	2.6
	116766	H13280	Hs.95097	ESTs	2.6

	104954	AA074514	Hs.26213	ESTs; Weakly similar to protein [H.sapiens]	2.5
	108771	AA127924	Hs.71034	ESTs	2.5
	116439	AA610068	Hs.43913	PIBF1 gene product	2.5
5	133859	U86762	Hs.178761	26S proteasome-associated pad1 homolog	2.5
	137792	AA401893	Hs.242985	hemoglobin; gamma G	2.5
	123620	AA010686	Hs.235720	ESTs; Weakly similar to KIAA0991 protein [H.s]	2.5
	120286	AA191353	Hs.22385	ESTs; Weakly similar to KIAA0970 protein [H.s]	2.5
	115615	AA404186	Hs.48617	ESTs	2.5
10	105203	XT7620	Hs.119838	non-malignant cells 1; protein (NM23A) expe	2.5
	105288	AA435536	Hs.24336	ESTs	2.5
	107444	W28391	Hs.5181	proliferation-associated 2G4; 38kD	2.5
	104625	R16007	Hs.75358	ubiquitin-conjugating enzyme E2N (homologous	2.5
	128917	AA204876	Hs.205097	oncogene TCS1	2.5
15	102259	US2907	Hs.155545	37 kDa leucine-rich repeat (LRR) protein	2.5
	115363	AA282071	Hs.152759	activator of S phase kinase	2.5
	130399	AA449417	Hs.155356	Human sapiens mRNA for putative glucosyltransf	2.5
	130752	D50927	Hs.18696	luciferase kinase 1	2.5
20	132724	AA417952	Hs.55498	geranylgeranyl diphosphate synthase 1	2.5
	106743	AA476352	Hs.21933	ESTs; Weakly similar to KIAA0704 protein [H.s]	2.5
	128949	AA190993	Hs.8850	a disintegrin and metalloproteinase domain 12	2.5
	125685	AA045348	Hs.4943	hyaluronidase carcinoma associated protein;	2.5
	105826	AA368243	Hs.21806	ESTs; Moderately similar to similar to NEDD-4	2.5
	110841	N31610	Hs.18645	ESTs; Weakly similar to partial CDS [C.elegans]	2.5
25	111987	R42036	Hs.6763	KIAA0942 protein	2.5
	132669	AA118379	Hs.54802	ESTs; Weakly similar to S65 RIBOSOMAL PROTEIN	2.5
	104358	D84557	Hs.154562	mitochondrion maintenance deficient (mif); S	2.5
	130800	AA223386	Hs.19574	ESTs; Weakly similar to katanin p80 subunit [2.5
	114481	AA033562	Hs.151572	ESTs	2.5
	113404	T22323	Hs.70337	immunoglobulin superfamily; member 4	2.5
30	102680	D38491	Hs.174135	KIAA0117 protein	2.5
	103563	Z22534	Hs.150402	activin A receptor; type I	2.5
	104573	R89552	Hs.29780	ESTs	2.5
	105025	AA125336	Hs.22744	ESTs; Weakly similar to ZINC FINGER PROTEIN 1	2.5
35	106524	AA258158	Hs.22153	ESTs; Weakly similar to KIAA0352 [H.sapiens]	2.5
	106157	AA425367	Hs.32094	ESTs	2.5
	107243	D59489	Hs.34727	ESTs	2.5
	105920	H05733	Hs.30558	ESTs	2.5
40	105961	H05552	Hs.26090	ESTs; Weakly similar to T20812.1 [C.elegans]	2.5
	114518	AA046407	Hs.106469	suppressor of var1 (S.overvision) 3-like 1	2.5
	114768	AA149007	Hs.182339	Ets homologous factor	2.5
	116906	H91000	Hs.34433	ESTs	2.5
	119025	N98926	Hs.55209	ESTs; Weakly similar to OMR-N9 PROTEIN [H.sap	2.5
45	131712	N29502	Hs.30991	KIAA0957 protein	2.5
	132253	X04705	Hs.53574	homo box D3	2.5
	132740	AA227751	Hs.58556	ESTs	2.5
	115239	AA278550	Hs.73231	ESTs; Weakly similar to similar to the beta 1	2.5
	128820	F10338	Hs.105309	Filand of GATA2	2.5
	124049	F10523	Hs.74519	primase; polypeptide 2A (58kD)	2.5
50	128781	X53372	Hs.105405	small nuclear ribonucleoprotein polypeptide F	2.5
	121351	AA405494	Hs.183052	ESTs	2.5
	134133	X93920	Hs.180383	dual specificity phosphatase 5	2.5
	102502	U51678	Hs.78020	small acidic protein	2.5
	115875	AA433943	Hs.43946	ESTs; Weakly similar to Weak similarity to Ye	2.5
55	132874	AA425776	Hs.58609	ESTs	2.5
	109646	F04543	Hs.5028	DKFZP564C0423 protein	2.5
	111197	H68093	Hs.22509	ESTs	2.5
	102968	X16356	Hs.154672	methylene tetrahydrofolate dehydrogenase (NAD	2.5
	124911	R89892	Hs.123645	ESTs	2.5
60	106628	AA459557	Hs.12311	Human sapiens clone Z3570 mRNA sequence	2.5
	116988	H62527	Hs.2265	yc59612a11 Scarsa retina N2b-4R Homo sapiens	2.5
	131075	X00767	Hs.75066	secretory granule; neuroendocrine protein 1 (2.5
	133578	X78627	Hs.15066	translin	2.5
	100420	D86983	Hs.118893	p53-responsive gene 2	2.5
65	130743	W87710	Hs.18724	Human sapiens mRNA; cDNA DKFZP564F053 (from cl	2.5
	122465	AA448164	Hs.59153	ESTs; Highly similar to CGI-73 protein [H.sap	2.5
	115117	AA256482	Hs.49007	poly(A) polymerase	2.5
	124582	N68477	Hs.108408	ESTs; Highly similar to CGI-78 protein [H.sap	2.5
	104771	AA625911	Hs.249394	ESTs; Highly similar to CGI-S3 protein [H.sap	2.5
	106039	AA043944	Hs.62663	ESTs	2.5
70	105028	AA381251	Hs.35636	ESTs; Weakly similar to putative zinc finger	2.5
	109261	AA195255	Hs.61779	ESTs	2.5
	119789	W73140	Hs.50515	kallikrein 5	2.5
	135612	AA045304	Hs.181671	ESTs; Highly similar to CGI-120 protein [H.sap	2.5
75	134402	U25165	Hs.82712	fragile X mental retardation; autosomal homol	2.5
	104769	AA025987	Hs.114774	ESTs; Weakly similar to IIII ALU SUBFAMILY J	2.5
	125787	AA744748	Hs.23943	ESTs; Weakly similar to PROBABLE ATP-DEPENDEN	2.5
	131775	AA435535	Hs.31321	KIAA0548 protein	2.5

TABLE 7B:

Phy: Unique Ecos probe/seq identifier number
 CAT number: Gene cluster number
 Accession: Genbank accession numbers

100352	37768_1	AL133867 D64159 AF112218 AF176633 AL030303 AL133868 BE620604 AW597629 AW262792 AW591383 AI365413 N36552 AA807027
		AI472041 BE520065
101084	13883_1	AI400934 AW245655 AI077157 AW163245 AW161434 AW250083 AA316055 BE621134 AA171883 BE272484 L05425 BE250310
		NM_013285 BE311494 AA584936 AA308223 AW362588 AA373618 BE394454 AA126101 AA581348 AA303227 AA658438 AA126544
		AL133359 AW995947 AA400201 AA446822 W70616 AW245249 AW577763 AW002316 AA320225 AW703913 AT98554 AW703650
		BE250413 AW250035 BE076336 AB255558 AI057634 AW604193 AW604270 AA023237 AW042432 AW042435 AW057711 AI090114
		AW157242 AA334590 AI628821 AA70650 AW409935 AW172793 AA401208 AW162279 AA688016 BE206452 AB267422 AA857353
		AA483614 AA126418 AA722289 AA780182 AW768894 AW133614 AW159569 AI244063 AA836491 AI376281 AA582480 AA464248
		AA474084 AW246802 AA446657 AA126030 AI092054 AT02210 AI253092 AA171554 AA831455 AW118394 AI954511 AT760439 AI870001
		AA453881 W61287 AAS15586 AA659297 AA635130 AA559293 AA766044 AA196109 N32659 AI907635
100502	26409_1	UI5979 X17544 W52755 NM_003836 Z12172 AW370136 BE282584 I49116 AA333753 BE282238 BE313737 H36153 AW583656 R28800
		BE289332 D16887 AA858610 AA911289 AA319627 R94472 R29022 AA443405 R96397 W04904 W01746 W01204 M74203 N58621
		AA701995 AW416723 N53220 AA020261 Hs_374143 Hs_374143 AA578577 AI149135 AW130598 A472955 AI188018 AI270625
		AA579333 W60010 A004475 AI311266 AA319845 T50070 AL335742 AA235245 W32706 AA447472 R95355 N55573 AA504616 AI291224
		BE467454 T49117 D268620 AA822845 AA449494 AA316817 T492929 R44473 H38154 AW66649 AW935307 AW050112 AW935343
		AW935342 AW935310 AW935345 AA298308 AW9353384 AI164857 AA319871 T29465 C21134 Z19785 AA329107 T52079
		AW935346 C06234 AI951555 T49928 AA371745 AA389296 AA346673 R62547 T50006
102398	entrez_U42359	U42359

Table 8A lists about 54 genes up-regulated in ovarian cancer compared to normal adult tissues. These were selected from 35403 probesets on the Affymetrix/Exon-Hu1 GeneChip array such that the ratio of "average" ovarian cancer to "average" normal adult tissues was greater than or equal to 4.0. The "average" ovarian cancer level was set to the 3rd highest amongst various ovarian cancers. The "average" normal adult tissue level was set to the 4th highest amongst various non-malignant tissues. In order to remove gene-specific background levels of non-specific hybridization, the 15th percentile value amongst the non-malignant tissues was subtracted from both the numerator and the denominator before the ratio was evaluated.

TABLE 8A: ABOUT 54 UP-REGULATED GENES, OVARIAN CANCER VERSUS NORMAL ADULT TISSUES

Play: Primkey

Ex. Accn: Exemplar Accession

UG ID: UniGene ID

Title: UniGene Title

ratio: ration tumor vs. normal tissues

Play	Ex. Accn	UG ID	Title	ratio
35	130941	D49394	Hs.2142	12.1
	101249	L33861	Hs.1904	11.8
	132528	AA283006	Hs.50758	11.5
	102610	U55011	Hs.374143	11.0
	115536	AA347193	Hs.62180	10.0
40	128571	X51630	Hs.1145	9.3
	106298	AA234359	Hs.26359	7.8
	121779	AA422036	Hs.98387	7.3
	104301	D45332	Hs.6783	6.9
	132191	AA449431	Hs.159588	8.7
45	102136	UI5552	Hs.67679	6.6
	101604	AA60598	Hs.169840	6.5
	132672	AA448267	Hs.237625	6.9
	105738	AA470145	Hs.25130	5.8
	106857	AA133250	Hs.62160	5.6
50	115201	A2789443	Hs.122579	5.7
	126232	N59764	Hs.5398	5.8
	116401	AA509963	Hs.53698	5.7
	132725	L11897	Hs.184167	5.7
	128007	S60223	Hs.257325	5.6
55	134520	N21407	Hs.257325	5.5
	108778	AA128548	Hs.90947	6.4
	131228	AA279167	Hs.14485	6.2
	116298	AA479362	Hs.47144	6.2
	108055	AA043562	Hs.62637	5.1
60	132939	U76189	Hs.61182	5.1
	115929	AA405668	Hs.59761	5.0
	120438	AA243441	Hs.99488	5.0
	123494	AA599796	Hs.112110	5.0
	109648	P04600	Hs.7154	4.9
	132624	AA164819	Hs.53831	4.9
65	112334	N63627	Hs.21943	4.9
	135242	M74093	Hs.9700	4.9
	123005	AA479726	Hs.105577	4.8
	116296	AA463053	Hs.62601	4.7
70	106061	HG22747-H73018	Hs.52601	4.6
	111345	N89820	Hs.14559	4.6
	102627	U65561	Hs.158174	4.5
	106450	AA449741	Hs.40225	4.5
	102355	U33285	Hs.90073	4.5
75	129229	AA211941	Hs.109643	4.5
	130376	R04073	Hs.155174	4.4
	120519	AA284372	Hs.111471	4.4
	122002	AA660530	Hs.256579	4.4
	116416	AA609219	Hs.39982	4.3
80	115094	AA259921	Hs.89095	4.2
	126862	AA478091	Hs.97066	4.2
	119602	AI160190	Hs.12172	4.2
	105516	AA257871	Hs.21214	4.1
	131985	AA434329	Hs.36563	4.1

114955	AA250737	Hs.72.472	ESTs	4.0
120821	AA347419	Hs.56870	Human sapiens mRNA full length insert cDNA cl	4.0
134821	L02547	Hs.17285	cleavage stimulation factor; 3' pre-RNA subu	4.0
134161	U97198	Hs.79440	IGF-II mRNA-binding protein 3	4.0

TABLE 8B:

Play: Unique Eos probe/ Identifier number

CAT number: Gene cluster number

Accession: Genbank accession numbers

10	101249	CAT Number 2520_1	Accession L18954 NM_002740 133881 AA095249 BC090871 AW065320 MH5571 AA179776 AA160650 AW117327 BE467131 AA088338 AA0973631 AW076154 AA140090 AB73147 T57875 AT127404 AB277196 AT279471 AA961093 AA815168 AA88896 AB746523 T28044 AA059302 AW050234 AC031293 AB53686 AB630583 AA062633 BE354135 AA180493 AW015748 AA259551 15 106661 23182_1 119401 95955_1 AW083300 LG0596 AA36304 AW966416 H53295 AA468213 AW571519 AA033555 AW083939 AW078851 AA042440 AW63323 AT076533 AA829515 AA053533 AA373691 W92807 AK261669 AA835698 AA447166 AB232448 Z71891 AA435700 AA055965 T00152 AAC53167 161616 373899_1 AW753676 T11789 AW001896 AA059219 AW704020 AB060567 AT280331 A3334300 AA288770 AA663543 N2919 BE537700 AA934687 1797075 W42970 R63752 20 132191 54683_4 AA057576 AB10269 AB30079 R40309 AT203632 AC342128 AC342578 RA3110 AW583268 AB375234 AC029728 RS2802 AQ2642 AQ106092 AB18144 AW16891 W55515 AA551452 AA049431 T10046 AA424059 NG2822 AW197701 AA465242 AA189893 AB94233 AB91151 AC302316 AB473978 AT283341 AW340338 AA744643 AW104778 AW780220 N21497 H97562 AA870003 BE327945 FQ3880 FQ3885 AA076099 AT288468 AB380330 AB747787 AT770467 AC200154 AW089863 AB089890 AB695738 W86524 AT471010 AA700191 AA778937 BE440182 RT9225 AA338263 AA546984 AA047652 N21250 AW1594736 AB95337 AB877776 AW595228 AT148372 AA554044 AC039597 AA871360 AA94291 AB8211 N28672 AA455984 AC321185 AW134062 AB274478 AB29292 25 130941 2774_1 NM_006693 D44394 BE252343 AW429320 AW249140 AW250535 S82612 AC030793 A005640 AW174807 AA811360 AW076407 AW076708 AW048903 AW373173 AB041893 AW301369 AA354922 AW994417 AW994426 AW994431 AA516147 AA516147 AA516147 AA516147 AA516147 AW952527 AA443863 AA043475 AF086541 AA368501 AB925375 AW151631 AT272393 W96131 AA349666 AA453779 AA365504 AW959717 AW763317 AA355553 AB32902 AA651896 AA655907 C00366 AA389369 30 108778 18565_1 AF131233 NM_012088 AA128292 S81493 AL137453 BE614005 AC307628 AB060521 BE080555 BE080552 BE080551 AL120564 R13165 AA230208 R13465 RS5236 AW954182 W00383 AW994417 AW994426 AW994431 AA516147 AA516147 AA516147 AA516147 AA516147 AL126554 AA049431 AA291327 H78763 AW770855 AW250221 AQ25487 AB211411 AW53320 AA056180 AW533205 A25129 AW295143 AC336661 AW638191 AW734622 Z717453 AB553548 AG24243 AA929455 AA72369 AB167211 AW303961 AA229045 AT026330 AA242828 AC01932 AT335550 A951307 AW1766807 S81492 AA918976 R03939 AA460965 T03304 AA477615 AA478070 AW017743 AW089833 AB358324 AB186008 AA741312 AC040184 H67656 AA528221 AA731316 AB381233 AC298473 RS5237 R33736 AB78014 AA128548 AB260775 AB78827 R64193 35 102136 17647_1 AA207616 U1552 NM_014597 AT223318 AA171806 BE269461 AW578439 AW604398 AW531937 AT77816 AW604383 AW577551 BE169672 AW117711 AA366303 AA536302 AC063308 AW365300 AC063304 AC063303 AW591937 AS136420 AW277622 C75087 AT526471 AW022666 BE064697 BE064722 T10372 AW033681 AB11119 AW262088 AA589347 AB918666 AA40033 AB07150 F24260 AA512819 40 108557 61_1 N553411 AB047878 AC024545 AA024545 AA024545 AA024545 AA024545 AA024545 AA024545 AA024545 AA024545 AA024545 AA024545 AW747536 AW6481 AA59306 AA090265 AA480959 AA023220 AW515936 AW068395 AW394407 BE540776 AB036762 AB504020 AA217481 AK001468 AA190315 AA347980 AW961175 AA307782 AA315295 AC347194 AW95307 AW368190 AW368192 AA280772 AA251747 N65676 AT215222 AD126398 N8735 R12281 RS7694 AB600405 AA347193 R15712 AW11906 NS5955 N87768 AW500167 AB341261 AA189874 D20285 AA745165 AA300768 R40628 AT122827 AA132520 AB264568 AW470372 AA489946 AW009517 AB24385 AA19314 AA75339 AB7449 45 102305 18424_1 AS11088 AB787769 AB919056 AB112116 AK001472 BE568761 AA561004 AL043202 U33236 NM_013116 AF053541 AL048759 N99830 AA263091 AW408174 N90467 R84305 AA317882 BE351944 AA030738 T10722 AA027027 AA315580 AA113938 AW083617 AV1038316 L44546 AW083636 AA0243317 AT713388 AA192541 AA545038 AC030037 AW152491 50 108254 AA092534 AA092532 BE030403 AA251221 AC342754 AA331512 AC342616 H56600 W67010 T70379 T82109 D6164 D0375 H8903 BE057572 AA471242 H17730 F11801 T84903 R78705 BE514358 R16380 R16395 AA876127 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5	132632	4312_1	AW50264 AA033658 AA593216 A4307426 AW113369 AW50264 AA033658 AA593216 A4307426 AW113369 AW50264 AA033658 AA593216 A4307426
			AW507616 N208110 N207393 AW672700 NML 030875 U02680 A1660751 V555 C30386 A7195876 AW646165 T33600 AW302852
			AA445421 AW081866 A1463428 BE548103 T96204 R94457 T8225 A554545 AW004084 AW70423 AW675448 AW087890 A4971454
			AA345698 AA597433 AA533069 A0394371 A332803 A1373637 N37964 A331265 N81090 AW674567 AW674987 AA897396
			AW675412 BE368157 AW674408 A2202011 R00723 A7573799 AW65016 A1075785 AW6275744 AW871252 AW6275744 AW871252 AW6275744
10	102610	9336_1	U05011 NML 008115 AW185203 BE363830 BE407339 BE408326 AW3070292 A3112659 A4135204 AW365822 AW365725
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			AW662222 AA669491 A244152 AW611553 BE503285 AA211023 A3383016 A1686174 AW195381 AA842925 A767845 A1690437 A33025
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25			AW507434 A727878 AW490338 AW495072 A4778071 AW236753 A933033 A930458 A270691 AW676235 A525118 A4425156 A330750
			W73583 AA24153 W6034 A1048872 A523878 AW08781 A1333591 A98983 A920911 W4885 A164620 A214485 A732302 A151589
			W68738 A214467 A334640 AW581710 A527525 A58158 W56283 A3635470 A1411919 AW611488 A241834 A3165198 A56356
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			H18989 F13487 D19688 AA45207 BE205942 AW304533 A3327274 A755246 AW070440 A3639155 H100836 A330750
			A723303 AA422691 A330925 AA429642 R59185 AA42959 A281741 N8502 A44206 A70699 AW11807 A4411202 A852692
			W00640 A2414405 AA044744 A505017 BE467493 AW47113 A4446310 BE328705 A911573 A234368 A682862 A6173020 AW079958
			A1140387 AW51989 AW299438 A1127170 AW789164 A424235 A307116 BE543510 A3171116 A6281748 A4710703 A74896 BE551197
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			A101010 A351642 AW76504 A275864 A275864 A1053331 A3359507 A95238 A187531 A7107684 A447520 A447520 A447520
			AW001238 A513452 AW512809 BE2057163 R33171 A1061628 A375569 F10356 A428628 A2511609 A702698 AW13010 A4456417
			AW439150 A271407 AA181033 A440338 A1043887 BE569015 BE22280 A5666618 AW507342 R52629
			AW523158 A189193 A73078 H51510 W06794 A332484 A947438 A354358 A363424 A202712 A508161 A318763 A16558 A352580
40			A112946 A1456870 A104089 A27707 A721178 A434162 A442708 A442708 A442708 A442708 A442708 A442708 A442708 A442708
			A090567 A335556 A379256 A503301 A1095234 A3490973 A5216070 A127237 A525958 A32383 A505290 AW26820 AW182995
			A252084 A48979 A2042457 A424626 A534031 A3369270 A3369270 A3369270 A3369270 A3369270 A3369270 A3369270 A3369270
			A252084 A48979 A2042457 A424626 A534031 A3369270 A3369270 A3369270 A3369270 A3369270 A3369270 A3369270 A3369270
45	134161	10674_1	A506096 AW081421 A442026 A855317 A140635 A434704 A020567 A6166707 A4872656 A4872656 A4872656 A4872656 A4872656
			A51819132 A450143 H84120 A140722 A5061438 A5061438 A5061438 A5061438 A5061438 A5061438 A5061438 A5061438
			BE308976 BE310190 A1025475 A747446 BE275234 H51210 AW35767
			A345453 A062259 AF111708 BE396917 NML 006547 U91759 U76705 BE560799 BE366918 BE269613 BE366928 BE503346 A80818
			A122375 BE545338 A270870 C10804 D58001 A130333 A162118 BE56704 A118796 A25254 A2611621 D33107 A82140 A808047
			A424633 A808738 A4411476 A1446832 A16165 A1058921 A4127428 AW513570 A4201672 A1371038 A243584 A804511
			AW514709 A3435733 A4505002 A905172 AA4471196 A4320258 AW673438 A332004 A5511295 A2427134 W81035 A427292 AW652471
			R54432 AW5046518 A1086619 AW0643682 AA425750 A747038 A368723 A181743 A373688 A1803976 A275537 A441347
			AW1164077 AA155454 W51072 AW197351 AA532674 A335240 A1434998 R53822 AW50583 A240272 W5706 A44731 H50428 A47885
50	132939	11857_1	R23223
			A800928 AF000146 A0022636 BE082610 AW367397 AA451410 A337471 W36526 A622631 A4713385 A4800780 T66134
			AA847838 AA022647 AW547427 A5818001 A431956 A252396 A804298 AW463414 U76189 AW179001 A4525945 A402327 A81774730
			AA410350 A4021450 A4504353 A408343 D16116 A453365 W19390 A333445 A5555767 H47771 A483784 A442816 A552062
			A3329703 A11732 A452031 A708791 A9189636 A22045 A239513 A122021 A23975 A876731 A317049 A103173 A797538 N50076
			AW263562 BE440048 A4400113 A574783 A4038774 AW024592 AA46580 A501952 A4342058 A505925 D61700 W3175 A809499
55	111345	6692_1	A956969 AA526628 A1828717 T61918
			A725335 A9014512 AW408152 A336413 BE308274 A3001402 A347065 AW554678 W39078 AW069236 A3639115 A15630996
			AW375335 AW368072 A3061194 AW369125 AW364187 H42425 T79302 A4131908 BE071359 A5653103 AW091517 A302132 A751643
			AA861077 A73656 A305195 AW118577 A748995 A588497 H52995 AW083479 AW570625 A5613124 A531224 A554210 A569847
			A2523422 AA131905 A406630 A4065158 AW502520 R50559 A431923 A502823 A67489 A960972 A994666 A290346 A485498
			AA565363 A200022 N89620 AW76732 C01145 R5654 A7916
60	104301	145390_1	A739451 A447323 A808748 A186289 A42944 A377929 BE50341 A451185 A215376 A215385 A441710 A772156 AW181980
			A1511168 A479270 A8167569 A1001778 A4757335 A4148511 A1138378 A5044167 A420617 A80281930 A522797 H1575 AW611403
			A896033 A50731308 H64830 A893732 A436159 BE501089 A431613 A937145 A26384 A3035358 A727066 AW039789 A5813437
			A871154 A16738 A705923 A968016 A4474728 BE594985 A4743769 A476407 A4156618 A768535 R14532 D6332 A70632 N51177
65	134520	13368_3	AW074066 A4425184 R20987 AA041668 Z43296
			BE091005 BE545179 A5387738 AW386083 H13769 AW3737820 AW069180 AW752329 AW672595 BE379572 A421732 AW691450
			AW581416 BE091398 N40375 BE091354 BE091351 BE091351 BE091351 A433865 AA445010 A21407 AW707981 A463577
			AW582414 A4336554 R54127 A436101 R26495 A255327 A717728 A238543 A354563 A442754 A442754 A442754 A442754 A442754
			BE544186 A337570 A695940 AW140656 A4065778 A446761 A446761 A446761 A446761 A446761 A446761 A446761 A446761
			A5535056 BE150744 A5930468 AW380546 BE150713 D60209 H88095 BE546301 BE150731 A5930467 BE091348
70	135242	5782_1	AW507616 N208110 N207393 AW672700 NML 030875 U02680 A1660751 V555 C30386 A7195876 AW646165 T33600 AW302852
			AA445421 AW081866 A1463428 BE548103 T96204 R94457 T8225 A554545 AW004084 AW70423 AW675448 AW087890 A4971454
			AA345698 AA597433 AA533069 A0394371 A332803 A1373637 N37964 A331265 N81090 AW674567 AW674987 AA897396
			AW675412 BE368157 AW674408 A2202011 R00723 A7573799 AW65016 A1075785 AW6275744 AW871252 AW6275744 AW871252 AW6275744
			U05011 NML 008115 AW185203 BE363830 BE407339 BE408326 AW3070292 A3112659 A4135204 AW365822 AW365725
			BE662273 AW393295 AA817195 A1071284 AW375329 AW375366 AW178334 AW178333 AW178334 AW367526 A702540 AW172852
			AW70598 AW117792 AB85489 BE465516 BE204747 AW130943 A55113316 AW710852 BE204745 AW173383 A1568252 AW173385
			A1510101 A1744853 A1819174 A442921 A442921 A442921 A442921 A442921 A442921 A442921 A442921 A442921 A442921
			AW151270 BE207425 AW13844 A442921 A442921 A442921 A442921 A442921 A442921 A442921 A442921 A442921 A442921
			AW55014 A5501225 AA508542 AA508541 AA546738 T19428 A5517170 AW166726 AW064220 A10018773 A4617526 A918664 A1831473
			AW15433 A5488577 AW058942 AW050423 A332502 AB680036 A1687500 BE327636 C20455 BE410282 BE254766 BE256014 A3357423
			A1201914 A162638 U06361 A231623 U5098 AW114543 AA455712 N08090 N46559 W07223 N7923 W05057 AW115774 AA56567
			A127549 A139121 A1927558 A1927562 A139471 A1160473 H78795 A711993 A7119928 A7119928 A7119928 A7119928 A7119928
75	135421	27351_1	AB364812 A7323027 N74467 AB83239 H89600 A19925 A54833
			NML 006275 NML 006276 N141887 L22253 BE375959 BE357870 BE274265 BE353818 AW123552 A7323027 A1993518 AW048545 A5800279
			AA454841 BE440161 AW178028 A435960 D55985 AA52235 A553020 W7795 A4278193 R10565 A969201 A739336 BE1174301
			AW662222 AA669491 A244152 AW611553 BE503285 AA211023 A3383016 A1686174 AW195381 AA842925 A767845 A1690437 A33025
			A718952 A553572 BE464509 AW77315 A1337221 AW071091 A593488 AW674551 H54177 AW51080 AW07869 A436178 A500739
			AW507434 A727878 AW490338 AW495072 A4778071 AW236753 A933033 A930458 A270691 AW676235 A525118 A4425156 A330750
			W73583 AA24153 W6034 A1048872 A523878 AW08781 A1333591 A98983 A920911 W4885 A164620 A214485 A732302 A151589
			W68738 A214467 A334640 AW581710 A527525 A58158 W56283 A3635470 A1411919 AW611488 A241834 A3165198 A56356
			AW002038 AA507624 W69150 AA446480 A448025 AA852400 A362221 A3138378 R35093 A3200812 R10397 A449589 AW238462 Z43032
			H18989 F13487 D19688 AA45207 BE205942 AW304533 A3327274 A755246 AW070440 A3639155 H100836 A330750
			A723303 AA422691 A330925 AA429642 R59185 AA42959 A281741 N8502 A44206 A70699 AW11807 A4411202 A852692
			W00640 A2414405 AA044744 A505017 BE467493 AW47113 A4446310 BE328705 A911573 A234368 A682862 A6173020 AW079958
			A1140387 AW51989 AW299438 A1127170 AW789164 A424235 A307116 BE543510 A3171116 A6281748 A4710703 A74896 BE551197
			N50345 AW533776 BE326801 A142882 AW470687 A98568 AA411241 A7594522 A174414 A446336 A040404 A7271934 A565943
			A101010 A351642 AW76504 A275864 A275864 A1053331 A3359507 A95238 A187531 A7107684 A447520 A447520 A447520
			AW001238 A513452 AW512809 BE2057163 R33171 A1061628 A375569 F10356 A428628 A2511609 A702698 AW13010 A4456417
			AW439150 A271407 AA181033 A440338 A1043887 BE569015 BE22280 A5666618 AW507342 R52629
			AW523158 A189193 A73078 H51510 W06794 A332484 A947438 A354358 A363424 A202712 A508161 A318763 A16558 A352580
			A112946 A1456870 A104089 A27707 A721178 A434162 A442708 A442708 A442708 A442708 A442708 A442708 A442708 A442708
			A090567 A335556 A379256 A503301 A1095234 A3490973 A5216070 A127237 A525958 A32383 A505290 AW26820 AW182995
			A252084 A48979 A2042457 A424626 A534031 A3369270 A3369270 A3369270 A3369270 A3369270 A3369270 A3369270 A3369270
			A252084 A48979 A2042457 A424626 A534031 A3369270 A3369270 A3369270 A3369270 A3369270 A3369270 A3369270 A3369270
80	126802	116647_4	A506096 AW081421 A442026 A855317 A140635 A434704 A020567 A6166707 A4872656 A4872656 A4872656 A4872656 A4872656
			A51819132 A450143 H84120 A140722 A5061438 A5061438 A5061438 A5061438 A5061438 A5061438 A5061438 A5061438
			BE308976 BE310190 A1025475 A747446 BE275234 H51210 AW35767
			A345453 A062259 AF111708 BE396917 NML 006547 U91759 U76705 BE560799 BE366918 BE269613 BE366928 BE503346 A80818
			A122375 BE545338 A270870 C10804 D58001 A130333 A162118 BE56704 A1

122802	287993_1	AT87813 AT19315 AT74309 AT815645 AA478473 C21435 NS0944 NS0902 AW1878102 H23837 BE087538 AA316516 AT897303 AW571681 AA554465 AA584252 AA581055 AA604098 AA628160 AA859843 AA42021 AA665030 BE042778 AW273200 AW372223 AW167728 AW063347 AA654306 AW517496 AW104705 AW273214 BE139512 AW189487 AW130825 AW167419 A2289485 AW150010 HB8004 AT743745 AW088710
5	123494	AW175019 AW176011 AF135160 NM_014060 AF178660 BE018005 AK000205 AF151038 BE245156 AW179007 AA345114 BE619758 BE519208 W25509 AA314339 AA335674 AA337056 AW594843 AW302412 N46706 AA316235 AA314286 R15566 BE535633 NM7314 R46463 AW036462 AA923517 AA655223 AA185133 AA837523 A3359320 A3309273 A522276 N40539 AA904977 AA336272 N30240 AA88765 A5171972 A028109 A0094652 AA83262 AA87781 AT74447 AW592944 AW148657 N88861 AA57195 A191824 AA33166 AT171970 AA430389 AA30656 AA303076 AA536025 AW675033 AA284395 AW086987 AW76335 A332320 BE301513 AA452920 AW674302 A255463 AW170412 AB381717 A377585 BE22635 AB68151 AW514809 AW652345 AA597786 BE350848 AA023075 AA664875 AA166871 AB07947 AW514579 AB178602 AA893040 AA83086 A3374788 A283362 AA65152 AA43159 A3379332 AA42056 A128904 AW150433 N38909
10	116296	11967_2
15		AW19502 Z43342 AW002825 AL049382 AA42545 AW971471 BE220243 AW668652 AA343607 AW255245 AA659892 A338788 H26330 BE465333 AW628252 AA538119 A2772791 AA489033 AA741235 A203954 A330253 A275761 Z38417 C01835

Table 9A lists about 382 genes up-regulated in ovarian cancer compared to normal ovaries. These were selected from 35403 probesets on the Affymetrix/Hu61 GeneChip array such that the ratio of "ovarian" ovarian cancer to "average" normal adult ovaries was greater than or equal to 10. The "average" ovarian cancer level was set to the 2nd highest amongst various ovarian cancers. The "average" normal adult ovaries level was set to the arithmetic mean amongst various non-malignant ovaries. In order to remove gene-specific background levels of non-specific hybridization, the 15th percentile value amongst the non-malignant tissues (see Table 7A) was subtracted from both the numerator and the denominator before the ratio was evaluated.

TABLE 9A: 382 UP-REGULATED GENES, OVARIAN CANCER VERSUS NORMAL OVARY

Phylo	Ex. Accn	UG ID	Title	ratio
134454	L33930	HS.173996	CD24 antigen (small cell lung carcinoma clust	86.2
102927	L12876	HS.65114	keratin 18	84.7
115909	AA436556	HS.59761	ESTs	72.3
123165	AA468892	HS.14472	ESTs; Weakly similar to Gag-Pol polyprotein [65.8
116074	AA405542	HS.71520	ESTs	65.4
102193	U20758	HS.313	secreted phosphoprotein 1 (osteopontin; bone	63.1
101839	M63036	HS.692	membrane component; chromosomal 4; surface ma	56.8
115221	AA262942	HS.79741	ESTs	56.1
108958	AA043944	HS.62693	ESTs	52.3
121853	AA425887	HS.95802	ESTs	47.8
133504	W56070	HS.74316	desmoplakin (DP; DPK)	47.0
103546	Z14344	HS.75752	cytochrome c oxidase subunit VIb	46.5
100147	D13655	HS.136348	osteoblast specific factor 2 (osteocalcin-like	45.5
102979	T17042	HS.1908	proteoglycan 1; secretory granule	44.6
130367	AA134138	HS.182579	Homo sapiens leucine aminopeptidase mRNA; com	44.5
102009	U02580	HS.82643	protein tyrosine kinase 9	40.4
126960	AA317900	HS.181756	ESTs	39.6
103111	X63187	HS.2719	epididymis-specific; whey-acid protein type	39.1
133829	AA453783	HS.76550	Homo sapiens mRNA; cDNA DKFZP56461264 (from c	39.0
111223	H89521	HS.34935	ESTs; Weakly similar to myogenin (H.sapiens)	38.9
102803	U89916	HS.26126	claudin 10	38.8
104943	AA055217	HS.169574	ESTs	38.7
106695	AA577718	HS.21103	Homo sapiens mRNA; cDNA DKFZP5649076 (from d	38.4
120555	A037247	HS.230205	ESTs	38.1
102968	H16396	HS.154672	methylene tetrahydrofolate dehydrogenase (NAD	36.3
104052	AA393164	HS.97644	mammaglobin 2	36.0
109166	AA179545	HS.73625	RAB8 interacting; thapsin-like (rabkinase)	35.9
101332	L47276	HS.72256	Homo sapiens (cell line HL-60) alpha topoisome	35.0
106167	AA425906	HS.7856	ESTs	34.5
101042	J05428	HS.10319	UDP glycosyltransferase 2 family; polypeptide	34.3
125852	H02520	HS.76550	Homo sapiens mRNA; cDNA DKFZP56461264 (from c	33.7
101201	L22534	HS.22536	mucin metalloproteinase 7 (matrilysin; uter	32.2
126410	R51912	HS.12409	somatostatin	32.1
134326	U16306	HS.81800	chondroin sulfate proteoglycan 2 (versican)	32.0
125739	AA426557	HS.92137	v-myc avian myelocytomatosis viral oncogene h	31.6
122554	L20826	HS.430	p19in 1 (I isoform)	31.4
112610	R79392	HS.23643	ESTs	30.9
101441	M21005	HS.100000	S100 calcium-binding protein A8 (calgranulin	30.6
116345	AA469881	HS.195057	HER3 receptor tyrosine kinase (c-erbB3, ERBB3	30.1
108860	AA133334	HS.129911	ESTs	29.8
133859	U56782	HS.178761	26S proteasome-associated pad1 homolog	29.2
107255	T34527	HS.80120	UDP-N-acetyl-alpha-D-galactosamine polyepid	28.9
106210	AA426239	HS.10338	ESTs	28.9
134711	X04011	HS.88574	cytochrome b-245; beta polypeptide (cytochrome g	28.9
125769	A032972	HS.82128	ST4 oncofetal trophoblast glycoprotein	27.5
107222	O51235	HS.82689	tumor rejection antigen (gp96)	27.4
102260	U26396	HS.159557	karyopherin alpha 2 (RAG subunit 1; importin a	26.9
124891	M69179	HS.88471	prostaglandin-endoperoxide synthase 1 (prosta	26.8
105588	AA279215	HS.10867	ESTs	26.3
130718	N01916	HS.18376	ESTs	26.3
111185	N07651	HS.12844	EGF-like domain; multiple 6	25.5
131865	W01046	HS.32692	ESTs	25.5
132503	AA235404	HS.5985	Homo sapiens clone 25186 mRNA sequence	25.6
114359	Z41589	HS.153483	ESTs; Moderately similar to H1 chloride chan	25.5

101185	L19872	Hs.170087	aryl hydrocarbon receptor	25.2
128742	D00763	Hs.251531	proteasome (prosome; macropain) subunit; alpha	25.1
116724	F13665	Hs.65641	ESTs	24.9
111929	R40507	Hs.112550	perlemin (mouse)-like 1	24.9
102915	U01620	Hs.2235	matrix metalloproteinase 10 (stromelysin 2)	24.9
131210	AA430047	Hs.24248	ESTs	24.7
101714	M68874	Hs.61882	Human phosphatidylcholine 2-acylhydrolase (cP	24.6
100154	C14557	Hs.81892	KIAAD101 gene product	24.6
134566	U14787	Hs.87409	thrombospondin 1	24.3
100294	D45396	Hs.75454	antioxidant protein 1	23.9
104080	AA402971	Hs.57771	kallikrein 11	23.7
107055	AA500310	Hs.16720	programmed cell death 8 (apoptosis-inducing f	23.7
115697	AA111502	Hs.63325	ESTs; Weakly similar to siway hypox-like p	23.7
130350	U02020	Hs.239138	pre-B-cell colony-enhancing factor	23.7
105870	AA399623	Hs.23505	ESTs	23.6
116528	N67685	Hs.45357	ESTs	23.4
105309	AA233790	Hs.41004	ESTs; Weakly similar to cDNA EST yk3867.5 co	23.2
109680	F09255	Hs.4993	ESTs	23.2
131501	AA121127	Hs.181307	H3 histone; family 3A	23.2
100824	HG4058-H14328	Hs.12365	Oncogene Ant1-Ev1, Fusion Activated	23.1
111680	F38578	Hs.12365	ESTs	23.0
101543	M01166	Hs.2050	pentactin-related gene; rapidly induced by IL-	22.8
102095	U11313	Hs.75760	steroid carrier protein 2	22.8
114988	AA251089	Hs.94576	ESTs; Weakly similar to phospholipid; retinal [H	22.8
120693	AA591408	Hs.2142	ESTs	22.8
130941	D49394	Hs.3784	5-hydroxytryptamine (serotonin) receptor 3A	22.8
106654	AA460449	Hs.193380	ESTs; Highly similar to phosphoserine aminotr	22.7
109141	AA176428	Hs.58892	ESTs	22.6
102345	U37263	Hs.38178	Microfilament-associated glycoprotein-2	22.6
115652	AA405058	Hs.5085	ESTs	22.4
100103	AF007875	Hs.32846	duclchyl-phosphate mannoseyltransferase polype	22.3
105463	AA253370	Hs.53831	ESTs	22.2
132524	AA164019	Hs.58086	ESTs	22.2
119743	W70242	Hs.50758	chromosome-associated polypeptide C	22.0
132528	AA283006	Hs.25338	ESTs	21.8
107174	AA251714	Hs.84087	KIAAD143 protein	21.8
134495	D63477	Hs.35553	ESTs	21.5
131985	AA434329	Hs.21989	ESTs	21.2
105832	AA398346	Hs.24727	ESTs; Weakly similar to transformation-relate	21.2
126160	N95960	Hs.44343	ESTs	20.9
114846	AA234329	Hs.24792	ESTs; Weakly similar to ORF YOR283w (S.severi	20.9
109703	F05964	Hs.173242	sorting nexin 4	20.8
135154	AA129433	Hs.22650	cyclin B1	20.7
131165	M25753	Hs.24958	ESTs	20.5
105616	AA262670	Hs.23579	ESTs	20.2
131148	C00038	Hs.110498	KIAA0990 protein	20.2
129337	R63542	Hs.75355	ubiquitin-conjugating enzyme E2N (homologous	20.1
133640	D83004	Hs.178729	collagen; type X; alpha 1 (Schmid metaphyseal	19.9
127479	AA513722	Hs.75703	small inducible cytokine A4 (homologous to mo	19.8
133711	J04130	Hs.3281	neuronal pentraxin II	19.7
131818	Z38297	Hs.107295	ESTs	19.5
125303	Z38271	Hs.72855	ESTs	19.5
109112	AA169379	Hs.8768	ESTs; Weakly similar to III ALU SUBFAMILY SQ	19.2
105376	AA235559	Hs.194657	cadherin 1; E-cadherin (epithelial)	19.1
103605	Z35402	Hs.194657	Ribosomal Protein L29 Homolog	19.1
105661	H02674-H73018	Hs.1145	Wilms tumor 1	19.0
129571	X51630	Hs.73291	ESTs; Weakly similar to similar to the beta 1	18.9
115239	AA278650	Hs.28777	H2A histone family; member L	18.9
131562	U93551	Hs.423584	paternally expressed gene 3	18.9
131272	AA423584	Hs.15485	ESTs; Weakly similar to APICAL-LIKE PROTEIN [18.7
130343	AA490262	Hs.28988	glutaredoxin (thioltransferase)	18.6
103245	U76648	Hs.8645	Homo sapiens connexin 26 (GJB2) mRNA, complet	18.6
101809	M85949	Hs.9657	ESTs	18.4
105344	AA235333	Hs.83429	butyrobetaine (gamma); 2-oxoglutarate dioxyge	18.4
135225	AA455988	Hs.27942	tumor necrosis factor (ligand) superfamily, m	18.3
116786	H25836	Hs.90769	ESTs; Weakly similar to similar to 1-acyl-gly	18.2
131510	AA207114	Hs.78853	uracil-DNA glycosylase	18.0
124029	F15671	Hs.55301	ESTs; Weakly similar to C43H8.1 (C.elegans)	17.9
103352	X29398	Hs.97100	cystin E1	17.9
132742	AA490862	Hs.112110	ESTs	17.8
135242	M74093	Hs.105052	chromosome 14 open reading frame 2	17.7
123404	AA509786	Hs.100861	ESTs; Weakly similar to p60 katanin [H.sapien	17.6
129168	T50621	Hs.151394	UDP-Gal-beta(1-6)Gal-beta 1,3-galactosyltransfe	17.6
128517	AA280617	Hs.294328	Rpoon2 2 (zeonogene 24p3)	17.5
130160	Z32228	Hs.57904	mago-nashi (Drosophila) homolog; proliferation	17.5
103448	X59113	Hs.105341	ESTs	17.5
119708	W67810	Hs.251871	CTP synthase	17.5
122946	AA477445	Hs.30596	transcription factor-like 5 (basic helix-loop	17.3
125819	AA44840	Hs.41271	ESTs	17.3
131689	AA59553	Hs.161720	ESTs; Moderately similar to III ALU SUBFAMIL	17.3
115061	AA253217	Hs.125759	ESTs	17.3
113702	T97307	Hs.146947	TRAF family member-associated NFkB activator	17.2
115291	AA278943			
102587	U59863			

	129229	AA211941	Hs.105643	polyadenylate binding protein-interacting pro	17.2
	129351	AA167268	Hs.62349	Human ras inhibitor mRNA; 3' end	17.2
	110769	N22222		yw3406.61 Morton Fetal Cootless Homo sapiens	17.1
5	113182	T55234	Hs.9676	Human DNA sequence from clone 30M3 on chromo	17.0
	115892	AA435948	Hs.50851	ESTs	17.0
	123114	AA486407	Hs.105235	ESTs; Moderately similar to KIAA0454 protein	17.0
	123442	AA598803	Hs.111496	ESTs	17.0
	123339	AA504253	Hs.101515	ESTs	16.9
	123689	AA599556	Hs.255582	ESTs	16.9
10	131941	D62657	Hs.35088	ubiquitin-specific protease 1	16.8
	120649	AA287115	Hs.99697	ESTs	16.8
	102139	U19332	Hs.2128	dual specificity phosphatase 5	16.8
	115522	AA331393	Hs.472378	ESTs	16.7
15	132543	AA215333	Hs.97101	putative G protein-coupled receptor	16.6
	131257	AA256042	Hs.24908	ESTs	16.5
	103508	AA233892	Hs.55902	ESTs; Weakly similar to IIII ALU SUBFAMILY SX	16.3
	123701	AA279359	Hs.35220	BCL-2-associated si-napogene 2	16.3
	134449	L34155	Hs.83450	laminin; alpha 3 (laminin (150KD); laminin (16	16.3
20	126180	R18070	Hs.3712	ubiquitin-cytochrome c reductase; Rieske iron	16.3
	106124	AA423987	Hs.7597	ESTs	16.2
	115363	AA282071	Hs.157259	activator of S phase kinase	16.2
	117588	N34896	Hs.44548	ESTs	16.1
	131245	AA620599	Hs.24766	DKFZP564E1962 protein	16.1
	106174	M61916	Hs.82124	luminin; beta 1	16.0
25	126819	AA305536	Hs.161489	ESTs	16.0
	134039	S76569	Hs.78572	laminin; alpha 4	16.0
	130648	AA075427	Hs.17296	ESTs; Weakly similar to /prediction	15.9
	108223	U90914	Hs.5057	carboxypeptidase D	15.8
	128470	AA447504	Hs.100281	Homo sapiens mRNA; cDNA DKFZP564B222 (from d	15.8
30	115844	AA430124	Hs.234607	ESTs	15.7
	132543	AA417152	Hs.5101	protein regulator of cytokinesis 1	15.7
	130155	L34304	Hs.1151254	kalikrein 7 (chymotrypsin; stratum corneum)	15.7
	101098	J04162	Hs.763	Fr fragment of IgG; low affinity ligase, recall	15.7
	122472	AA251875	Hs.104472	ESTs; Weakly similar to Gag-Pol polypeptide [15.6
35	116844	H54938	Hs.38331	ESTs	15.6
	106753	AA476944	Hs.7331	ESTs	15.6
	114767	AA148885	Hs.154443	minichromosome maintenance deficient (S. cere	15.5
	114768	AA149007	Hs.162339	Est homologous factor	15.5
	127370	AI024352	Hs.70337	immunoglobulin superfamily; member 4	15.5
40	101597	M27492	Hs.82112	interleukin 1 receptor; type 1	15.4
	102519	U52569	Hs.60626	Purkinje cell protein 4	15.4
	102510	U52011	Hs.30743	preferentially expressed antigen in melanoma	15.4
	111244	N65556	Hs.24724	MIFH-amplified sequences with leucine-rich tan	15.4
	120404	AA234921	Hs.96427	KIAA1013 protein	15.3
45	130455	X17059	Hs.153556	N-acetyltransferase 1 (arylamine N-acetyltran	15.2
	129519	AA260785	Hs.112242	ESTs	15.1
	106553	AA454967	Hs.5887	ESTs; Highly similar to RNA binding motif pro	15.0
	109502	AA233837	Hs.44755	ESTs; Weakly similar to membrane glycoprotein	14.9
	115867	AA443887	Hs.42911	ESTs	14.9
50	104636	AA004415	Hs.108106	ESTs	14.8
	134133	X33920	Hs.180383	dual specificity phosphatase 6	14.9
	134444	X04470	Hs.251754	secretory leukocyte protease inhibitor (anti	14.8
	132598	Y02052	Hs.170121	protein protein phosphatase; receptor type; c	14.8
55	131987	D82399	Hs.135644	Homo sapiens clone 23714 mRNA sequence	14.6
	134056	R27358	Hs.7886	ESTs; Weakly similar to Palle associated prot	14.6
	101249	L33681	Hs.1904	protein kinase C; iota	14.5
	105298	AA233459	Hs.26369	ESTs	14.5
	107119	AA620307	Hs.27379	ESTs	14.5
	115839	AA429038	Hs.40541	ESTs	14.5
60	122802	AA460530	Hs.256579	ESTs	14.5
	123856	AA043021	Hs.13225	UDP-Gal-beta-GlcNAc beta 1-4-galactosyltransf	14.3
	130269	AA284694	Hs.168352	nucleoporin-like protein 1	14.3
	134374	D62633	Hs.8236	ESTs	14.3
	106370	AA443841	Hs.18676	apomy (Drosophila) homolog 2	14.2
65	130219	AA291710	Hs.21270	collagen; type IV; alpha 3 (Goodpasture anti	14.1
	132523	U21858	Hs.60679	TATA box binding protein (TBP)-associated fac	14.1
	107968	AA034020	Hs.61539	ESTs	14.1
	125390	H55094	Hs.75187	translocase of outer mitochondrial membrane 2	14.1
	107148	AA621131	Hs.58989	ESTs; Weakly similar to W91A11.2 gene product	14.1
70	110786	N97430	Hs.15420	ESTs	14.0
	109481	AA233342	Hs.90680	ESTs; Weakly similar to WD40 protein Clao 1 (13.9
	105646	AA282147	Hs.8868	ESTs	13.9
	106030	AA4112251	Hs.12682	development and differentiation enhancing fac	13.8
	132618	AA253330	Hs.5344	adaptor-related protein complex 1; gamma 1 su	13.7
75	132230	S82240	Hs.6838	ras homolog gene family; member E	13.7
	124803	R45480	Hs.164866	cyclin K	13.6
	121381	AA405747	Hs.97865	ESTs; Weakly similar to WASP-family protein [13.6
	105200	AA193359	Hs.24641	ESTs	13.5
	106527	AA281245	Hs.73317	ESTs	13.5
	114986	AA251010	Hs.87807	ESTs	13.5
80	116336	H52844	Hs.189808	ESTs	13.5
	134472	N97749	Hs.87827	ESTs; Weakly similar to cDNA EST EMBL700542	13.5
	110915	N46252	Hs.29724	ESTs	13.3
	117984	N51919	Hs.47368	ESTs	13.3

	132550	AA029597	Hs.170195	bone morphogenetic protein 7 (osteogenic prot	13.3
	124315	H94892	Hs.6906	viral simian leukemia viral oncogene homolog	13.2
	102547	U57911	Hs.46638	chromosome 11 open reading frame 8	13.2
5	125134	W15228	Hs.100748	ESTs	13.2
	111806	R33468	Hs.24651	ESTs	13.1
	106983	AA521195	Hs.10887	similar to lysosome-associated membrane glyco	13.0
	106498	AA452141	Hs.7171	ESTs	13.0
	110787	NQ4716	Hs.12244	ESTs; Weakly similar to C4469.1 [C.elegans]	13.0
10	122850	AA644414	Hs.112159	ESTs	13.0
	131535	AA504642	Hs.28438	ESTs; Weakly similar to coded for by C. eleg	13.0
	116186	AA464728	Hs.184558	ESTs	13.0
	107243	D59496	Hs.34723	ESTs	12.9
	129300	C20976	Hs.110185	ESTs; Highly similar to ribosomal protein L26	12.8
	134487	R38185	Hs.83954	Homo sapiens unknown mRNA	12.8
15	102348	U37519	Hs.87535	aldehyde dehydrogenase 8	12.8
	131836	H69522	Hs.33010	KIAA3531 protein	12.8
	115620	W47620	Hs.56009	2'-5'-oligoadenylate synthetase 3	12.8
	120802	AA343533	Hs.128777	ESTs; Weakly similar to predicted using Genef	12.7
20	102250	U28014	Hs.74122	cathepsin 4; apoptosis-related cysteine proteas	12.7
	105538	AA358873	Hs.25242	ESTs	12.7
	114865	AA250737	Hs.72472	ESTs	12.7
	118001	N52151	Hs.47447	ESTs	12.7
	100448	D87489	Hs.57552	EGF-like domain; multiple 2	12.6
25	132020	D60975	Hs.75525	calreticulin	12.8
	131075	Y05757	Hs.2255	secretory granule; neuroendocrine protein 1 (12.8
	105496	AA255323	Hs.25264	DKFZP434N126 protein	12.5
	109225	AA193592	Hs.42300	ESTs; Weakly similar to III ALU SUBFAMILY SQ	12.5
	118215	N52195	Hs.27310	3-hydroxy-3-methylglutaryl-Coenzyme A synthas	12.5
	134388	M15941	Hs.82575	small nuclear ribonucleoprotein polypeptide B	12.5
30	106897	AA489790	Hs.167495	RAN binding protein 6	12.4
	133050	S67325	Hs.63786	propionyl Coenzyme A carboxylase; beta polype	12.4
	109683	F03308	Hs.27097	ESTs	12.3
	121463	AA411745	Hs.239581	ESTs; Weakly similar to KIAA0554 protein [Ha	12.3
	102876	X03563	Hs.174142	colony stimulating factor 1 receptor; format	12.2
35	101804	M06999	Hs.189940	TKT protein kinase	12.2
	123017	H13106	Hs.107962	ESTs	12.1
	105812	AA394126	Hs.20814	ESTs; Highly similar to CGI-27 protein [H.sap	12.0
	106459	AA487471	Hs.4029	glioma-amplified sequence-41	12.0
40	107059	AA508545	Hs.23044	RAD51 (S. cerevisiae) homolog (E coli RaxA ho	12.0
	107060	AA606210	Hs.15221	ESTs	12.0
	110799	N25101	Hs.7838	Human ring zinc-finger protein (ZNF127-Xp) ge	12.0
	112253	S51818	Hs.104222	Homo sapiens mRNA; cDNA DKFZp596B.034 (from d	12.0
	115760	H11034	Hs.155342	protein kinase C delta	12.0
	120314	AA194168	Hs.221040	KIAA1028 protein	12.0
45	123005	AA478726	Hs.105577	ESTs	12.0
	132572	AA484297	Hs.237825	signal recognition particle 7kD	12.0
	110551	H58617	Hs.5199	ESTs; Weakly similar to UBQUITIN-CONJUGATING	12.0
	101923	S75256	Hs.107962	HNL/neutrophil lipocalin (human, ovarian conc	11.9
50	134992	H05625	Hs.92414	ESTs	11.8
	105516	AA267971	Hs.21214	ESTs	11.7
	105248	AA228968	Hs.22826	ESTs	11.7
	109130	AA172040	Hs.20161	ESTs; Weakly similar to IgE receptor beta sub	11.7
	115955	AA446121	Hs.44198	Homo sapiens BAC clone RG054D04 from 7q31	11.7
55	116135	AA603114	Hs.94179	ESTs	11.7
	116284	AA487252	Hs.237809	ESTs; Weakly similar to hypothetical protein	11.7
	132384	AA479533	Hs.48567	Human DNA sequence from clone 167A19 on chrom	11.7
	134753	Y09216	Hs.173135	dual-specificity tyrosine-(Y)-phosphorylation	11.7
	125136	W31479	Hs.129051	ESTs	11.7
60	133328	N34096	Hs.7795	ubiquitin-conjugating enzyme E2E 1 (homologou	11.6
	117395	N03330	Hs.53701	ESTs	11.5
	127007	AA295360	Hs.10608	EST11867 U59 tumor 1 Homo sapiens cDNA 5'	11.5
	130557	L07493	Hs.1908	replication protein A3 (14kD)	11.5
	135073	AA452000	Hs.94039	Homo sapiens mRNA; cDNA DKFZp596B1.624 (from c	11.5
	115140	AA258030	Hs.55358	ESTs; Weakly similar to supported by GENSCAN	11.4
65	115535	AA347193	Hs.62180	ESTs	11.4
	133240	D31161	Hs.58613	ESTs	11.3
	106521	AA453431	Hs.147322	maltase enzyme 1; NADP(+)-dependent; cytosolic	11.3
	107674	AA011027	Hs.41143	KIAA0581 protein	11.3
	114149	Z38814	Hs.27195	ESTs	11.3
70	132478	H02036	Hs.49300	KIAA0746 protein	11.2
	104252	U302246	Hs.210653	cell adhesion molecule with homology to L1CAM	11.2
	102436	U46459	Hs.760	microsomal glutathione S-transferase 1	11.2
	106728	AA465339	Hs.7141	ESTs	11.2
	100116	D0854	Hs.77443	actin; gamma 2; smooth muscle; enteric	11.2
75	110970	H51374	Hs.58870	Homo sapiens mRNA full length insert cDNA do	11.2
	130417	N65622	Hs.155485	huntingtin-interacting protein 2	11.2
	132906	AA142857	Hs.234896	ESTs; Highly similar to geminin [H.sapiens]	11.2
	107853	AA024427	Hs.59451	DKFZP434C245 protein	11.2
	134647	Y00451	Hs.78712	aminolevulinic acid: delta ² -synthase 1	11.1
80	104338	D67448	Hs.91417	topoisomerase (DNA) II binding protein	11.1
	102654	U68494	Hs.24385	Human hbc47 mRNA sequence	11.1
	103172	X68742	Hs.116774	integrin; alpha 1	11.1
	108556	AA46183	Hs.13639	ESTs; Weakly similar to similar to oxysterol-	11.1
	108255	AA053157	Hs.172508	ESTs	11.1

124308	H53575	Hs.227146	Homo sapiens mRNA; cDNA DKFp564J142 (from d	11.1
129057	X52466	Hs.214742	COWS2 antigen (CAMPATH-1 antigen)	11.1
128845	AA455658	Hs.10649	basement membrane-induced gene	11.1
129025	AA209392	Hs.103441	EST; Weakly similar to testicular tectin B1-	11.0
107638	AA005281	Hs.42743	EST; Weakly similar to predicted using GeneF	11.0
134480	AA024654	Hs.83916	NADH dehydrogenase (ubiquinone) 1 alpha subuo	11.0
115262	AA279112	Hs.88594	ESTs	11.0
102580	U50808	Hs.152581	CDP-diacylglycerol synthase (phosphatidate cy	10.9
106614	AA458934	Hs.172912	ESTs	10.9
107115	AA610108	Hs.27683	ESTs; Highly similar to CG-124 protein (H-La	10.9
115764	AA421562	Hs.91011	anterior gradient 2 (Xenopus laevis) homolog	10.9
121770	AA421714	Hs.11469	KIAA0896 protein	10.9
132181	AA454331	Hs.136569	KIAA0741 gene product	10.9
133214	Y10559	Hs.250911	Interleukin 13 receptor; alpha 1	10.9
133914	N23811	Hs.77542	ESTs	10.8
101973	S52597	Hs.80120	UDP-N-acetyl-alpha-D-glucosaminase:polypeptid	10.8
102669	U71237	Hs.18349	eyes absent (Drosophila) homolog 2	10.8
104147	AA451892	Hs.225799	ESTs; Highly similar to HSPC039 protein (H-La	10.8
106474	AA450212	Hs.42484	Homo sapiens mRNA; cDNA DKFp564C053 (from d	10.8
115881	AA335577	Hs.164942	G protein-coupled receptor 64	10.8
129550	M31516	Hs.1339	decay accelerating factor for complement (CD5	10.8
132763	N74897	Hs.6583	DEADH (Asp-Glu-Ala-AspHis) box polypeptide	10.8
133784	AA214305	Hs.76173	ESTs	10.8
134248	AA292677	Hs.80524	ESTs	10.8
103565	AA273302	Hs.18349	ESTs; Weakly similar to partial CD5 (c.elegan	10.8
127099	AA837455	Hs.69851	ESTs; Weakly similar to Wiskott-Aldrich syndr	10.8
108040	AA041551	Hs.48544	ESTs	10.7
133037	Z38901	Hs.8768	ESTs; Weakly similar to IIII ALU SUBFAMILY SQ	10.7
108539	AA364677	Hs.54558	ESTs; Weakly similar to protein 6 (H.sapien)	10.7
111345	N98520	Hs.14559	ESTs	10.7
115583	AA388913	Hs.45231	LDOC1 protein	10.7
128955	T17440	Hs.107418	ESTs	10.7
101396	M15796	Hs.75995	proliferating cell nuclear antigen	10.6
132184	U84573	Hs.412710	procollagen-lysine, 2-oxoglutarate 5-dioxygen	10.6
101275	L37636	Hs.3273	Ts transition elongation factor; mitochondri	10.6
104660	AA007160	Hs.14848	Homo sapiens mRNA; cDNA DKFp564D016 (from d	10.6
108049	AA100594	Hs.63493	Human DNA sequence from BAC 15C1 on chromos	10.6
112441	RA3300	Hs.22929	ESTs	10.6
114208	Z39301	Hs.7859	ESTs	10.6
118537	N67974	Hs.75431	barbitogen; gamma polypeptide	10.6
106919	AA458855	Hs.17656	ESTs	10.6
115984	AA447687	Hs.91109	ESTs	10.6
105538	AA258860	Hs.32597	ring finger protein (CH2C3 type) 6	10.6
102200	U21551	Hs.157205	branched chain aminotransferase 1; cytosolic	10.5
116170	F10577	Hs.70312	ESTs	10.5
119780	W72567	Hs.191381	ESTs; Weakly similar to hypothetical protein	10.5
112996	T23539	Hs.7165	zinc finger protein 259	10.5
103029	X54489	Hs.789	GRD1 oncogene (melanoma growth stimulating ac	10.4
101255	L34600	Hs.149894	mitochondrial transitional initiation factor	10.4
107032	AA599472	Hs.247309	succinate-CoA ligase; GDP-forming; beta subun	10.4
125617	A0287461	Hs.164549	ESTs	10.4
131475	Z39063	Hs.27283	ESTs	10.4
132073	N67408	Hs.38516	ESTs	10.4
101459	N22877	Hs.165248	Human somatic cytochrome c (HCS) gene; comple	10.3
102437	U46569	Hs.221986	aquaporin 5	10.3
104301	D45332	Hs.8783	ESTs	10.3
127236	AA141818	Hs.98658	binding uninhibited by benzimidazoles 1 (yeas	10.3
101465	M22612	Hs.241395	protease; serine; 1 (trypsin 1)	10.3
113805	W42557	Hs.250617	ESTs	10.2
133536	Y00284	Hs.177496	amyloid beta (A4) precursor protein (protease	10.2
109799	F10770	Hs.180378	Homo sapiens clone G69 unknown mRNA; complete	10.2
113523	T90037	Hs.16688	ESTs	10.2
116195	AA465148	Hs.72402	ESTs	10.2
134542	X57025	Hs.85112	trastin-like growth factor 1 (somatomedin C)	10.2
125228	Z39255	Hs.233250	YOD19 protein	10.2
119387	T78324	Hs.80905	ESTs	10.2
134470	X54942	Hs.83758	CDC28 protein kinase 2	10.2
134288	AA430028	Hs.81117	ESTs	10.1
105127	AA152132	Hs.11817	ESTs; Weakly similar to coactin similarity 1	10.1
110627	T70465	Hs.35225	ESTs; Weakly similar to MEN1 protein (H.sapie	10.1
115188	AA261819	Hs.88367	ESTs	10.1
132632	N57874	Hs.5338	guanine-monomophosphate synthetase	10.1
124049	F10523	Hs.174519	primase; polypeptide 2A (Sbc)	10.1
100079	AB002365	Hs.23311	KIAA0367 protein	10.0
113987	W87494	Hs.9641	ESTs; Moderately similar to COMPLEMENT C1Q SU	10.0
117280	K22107	Hs.172241	ESTs	10.0

TABLE 9b:

Phy: Unique Eos probeset Identifier number

CAT number: Gene cluster number

Accession: Genbank accession numbers

Phy	CAT Number	Accession
100661	Z182_1	BE623001 L05096 AA383604 AW56416 NS3295 AA460213 AW571519 AA603655

	428227	AA321649	Hs.2248	INTERFERON-GAMMA INDUCED	18.3
	418854	AW664873	Hs.87838	Homo sapiens PAC clone RPS-1087M1 from 7q11.	18.3
	439706	AW872527	Hs.59761	ESTs	18.3
5	428579	NM_005756	Hs.164542	G protein-coupled receptor 64	17.4
	416247	AF161721	Hs.151345	RUG2	17.0
	428153	AW513143	Hs.98387	hypothetical protein FLJ22252 similar to SRY-	16.9
	415076	NM_000857	Hs.77850	guanylate cyclase 1, soluble, beta 3	16.6
	416209	AA235776	Hs.79078	MAO2 (mitotic arrest deficient, yeast, homolog)	16.6
10	424995	NM_002497	Hs.153704	NIMA (never in mitosis gene a-related kinase)	16.2
	423685	BE350494	Hs.49753	Homo sapiens mRNA for KIAA1561 protein, partial	15.9
	428187	AW687303	Hs.285529	ESTs	15.9
	438517	AA023799	Hs.163242	ESTs	15.9
	424996	AA565086	Hs.153716	Homo sapiens mRNA for hmo33 protein, 3' untranslated	15.9
	407721	112725	Hs.33018	dual-specificity tyrosine-(Y)-phosphorylation	15.7
15	412723	AA648459	Hs.179912	ESTs	15.3
	424717	H03754	Hs.152213	wingless-type MMTV Integration site family, m	15.2
	443646	AA051588	Hs.298999	ESTs	15.2
	424345	AA001380	Hs.145479	Homo sapiens cDNA FL110518 fs, clone NT2RP20	14.8
20	428976	AL037824	Hs.194695	ras homolog gene family, member 1	14.6
	418738	AW388633	Hs.6662	solute carrier family 7, member 11	14.3
	428479	Y00272	Hs.184572	cell division cycle 2, G1 to S and G2 to M	14.2
	435209	AW855417	Hs.254020	ESTs, Moderately similar to unnamed protein p	14.1
	427356	AW023482	Hs.97849	ESTs	13.9
25	418601	AA279490	Hs.86368	calmagin	13.8
	416681	AA834543	Hs.79440	TGF-1 mRNA-binding protein 3	13.7
	428532	AF157328	Hs.184785	TGF-1 interacting protein	13.6
	402408			0	13.6
	447350	AJ375572	Hs.172634	ESTs; HER4 (c-erb-B4)	13.4
30	451807	W62854	Hs.27089	DKFZP954J0563 protein	13.4
	423575	C18603	Hs.163443	ESTs	13.2
	443211	A1128388	Hs.143655	ESTs	13.2
	437872	AK002015	Hs.5887	RNA binding motif protein 7	13.0
	451659	BE379761	Hs.14248	ESTs, Weakly similar to ALUB_HUMAN ALU SUBFAM	12.7
35	452804	A1157481	Hs.20557	Homo sapiens mRNA, cDNA DKFZp434E0626 (from c	12.5
	442655	AW027457	Hs.30323	ESTs	12.5
	452096	BE394801	Hs.228785	ESTs	12.4
	414972	BE263782	Hs.71695	KIAA0008 gene product	12.3
	435039	AW043821	Hs.133535	ESTs	12.3
	447033	AJ357412	Hs.157601	EST - not in UniGene	12.3
40	437364	AW753676	Hs.39582	ESTs	12.2
	442611	BE077155	Hs.177537	ESTs	12.0
	408552	AJ493323	Hs.21141	Homo sapiens mRNA for KIAA1568 protein, partial	11.9
	427344	NM_000869	Hs.2142	5-hydroxytryptamine (serotonin) receptor 3A	11.8
	421478	AH83243	Hs.97258	ESTs	11.8
45	426633	BE391109	Hs.123327	ESTs	11.8
	415889	AJ057700	Hs.111128	ESTs	11.7
	433159	AB035858	Hs.150587	kinesin-like protein 2	11.5
	452249	BE394412	Hs.61252	ESTs	11.4
50	418505	AA084448	Hs.65339	G protein-coupled receptor 39	11.3
	442553	BE378594	Hs.49135	ESTs	11.3
	447700	AA020183	Hs.171077	ESTs, Weakly similar to similar to serine/thr	11.3
	450480	X82125	Hs.25040	zinc finger protein 239	11.2
	425176	AW015844	Hs.301439	ESTs, Moderately similar to TEFL_HUMAN TRANS	11.2
55	435496	AW040171	Hs.265388	ESTs, Weakly similar to transformation-related	11.2
	433133	AB027248	Hs.104741	PDZ-binding kinase; T-cell originated protein	11.1
	445258	AH359331	Hs.147613	ESTs	11.1
	432677	NM_004482	Hs.278611	UDP-N-acetyl-alpha-D-glucosamine pyrophosphat	11.0
	430782	NM_005754	Hs.220889	Ras-GTPase-activating protein SH3-domain-bind	10.9
	404567			0	10.8
60	423811	AW295598	Hs.50895	homeo box C4	10.7
	452891	N75852	Hs.212875	ESTs, Weakly similar to KIAA0357 [H.sapiens]	10.6
	441627	AA347582	Hs.50085	ESTs	10.3
	433555	N71710	Hs.21398	ESTs, Moderately similar to GNP_HUMAN GLUCOS	10.3
	412140	AA219591	Hs.73825	RAB6 Interacting, kinesin-like (rabkinesin6)	10.2
65	427469	AA403384	Hs.268247	ESTs	10.1
	415227	AW621113	Hs.72402	ESTs	10.1
	445413	AA151342	Hs.12577	CGI-147 protein	10.0
	425734	AF055209	Hs.159395	peptidylglycine alpha-amidating monooxygenase	10.0
	421451	AA291977	Hs.50261	ESTs	10.0
70	410044	BE565742	Hs.58169	highly expressed in cancer, rich in leucine h	9.8
	427878	C05756	Hs.181022	CGI-47 protein	9.7
	408480	AA054726	Hs.285574	ESTs	9.7
	422972	AH5319	Hs.145404	ESTs	9.7
	443715	AH53187	Hs.9700	cyclin E1	9.7
75	440901	AA509358	Hs.128612	ESTs	9.6
	453160	AJ283307	Hs.146228	ESTs	9.6
	415211	RA74737 camp	Hs.155685	ESTs; Highly similar to SPERM SURFACE PROTEIN	9.5
	425282	AW163516	Hs.155485	huntingtin interacting protein 2	9.5
	402750			0	9.5
80	410568	AW162948	Hs.64542	pro-mRNA cleavage factor III (68kD)	9.3
	449852	AF49862	Hs.43397	ESTs	9.3
	445922	AF053306	Hs.38708	budding uninhibited by benzimidazoles 1 (yeas	9.2
	434401	AH64131	Hs.71119	Pulvate prostate cancer tumor suppressor	9.2
	453628	AW243307	Hs.170187	ESTs	9.1

452056	A1377431	Hs.233772	ESTs	9.1
424086	A1351010	Hs.102267	lysyl oxidase	9.1
442875	BE623003	Hs.23625	Homo sapiens clone TCCCTA00142 mRNA sequence	9.1
416288	AA291108	Hs.41295	ESTs	9.0
407166	RM5175	Hs.117163	gbly740d.1 Soares Infant brain 1N18 Homo s	9.0
445537	AJ245671	Hs.12844	EGF-like domain; multifig 6	8.9
409269	AA576553	Hs.22972	Homo sapiens cDNA FLJ13352 fs, clone OVARC10	8.9
433527	AW236613	Hs.133020	ESTs	8.9
409228	A1137163	Hs.57549	hypothetical protein d147384	8.8
423020	AA383092	Hs.1908	replication protein A3 (14d)	8.7
425665	AK001050	Hs.159095	ESTs	8.6
443204	AW235878	Hs.29643	Homo sapiens cDNA FLJ13103 fs, clone NT2RP30	8.6
449433	AE72095	Hs.8912	ESTs	8.6
453978	AW94440	Hs.19025	ESTs	8.6
450505	NM_004572	Hs.25051	phallophilin 2	8.6
407001	UT2471	Hs.247954	Human fibronectin-binding protein-1 gene, partial cds	8.5
414315	Z24878		gb-HS650202 STRATAGENE Human skeletal muscle	8.5
425482	AL021918	Hs.158174	zinc finger protein 184 (Knuppel-like)	8.5
436181	AA669339	Hs.28838	KIAA1571 protein	8.5
435356	AB63467	Hs.299112	Homo sapiens cDNA FLJ11441 fs, clone HEMBA10	8.5
416384	AW146256	Hs.29130	ESTs	8.4
453370	AJ470523	Hs.182356	ESTs, Moderately similar to translation init	8.4
409041	AB033025	Hs.50081	KIAA1199 protein	8.4
447078	AW685727	Hs.301570	ESTs	8.4
446574	W01178	Hs.154140	ESTs	8.3
433353	AF028554	Hs.98074	atrophin-1 interacting protein 4	8.3
433496	AF064254	Hs.49765	VERY-LONG-CHAIN ACYL-COA SYNTHETASE	8.2
421155	H87879	Hs.102257	lysyl oxidase	8.2
438394	BE378623	Hs.27693	CD-124 protein	8.2
400258	AA032279	Hs.51635	STEAP1	8.1
409092	AJ735283	Hs.172608	ESTs	8.1
440250	AA576179	Hs.134650	ESTs	8.1
405143	AW026980	Hs.138965	ESTs	8.1
407771	AL136272	Hs.62713	ESTs	8.1
419088	AS36323	Hs.77496	ESTs	7.9
431725	W65724	Hs.2639	Horne disease (pseudoglyoma)	7.9
431750	AA514986	Hs.263705	ESTs	7.9
435635	AF220050	Hs.181385	uncharacterized hematopoietic stem/progenitor	7.9
441825	AW503803	Hs.129915	phospholipase related	7.8
417728	AW135437	Hs.24750	KIAA1573 protein	7.8
419845	AA852065	Hs.82322	chromobox homolog 5 (Drosophila HP1 alpha)	7.8
421039	NM_003478	Hs.101259	cullin 5	7.8
446999	AA151520	Hs.278525	hypothetical protein PR02605	7.7
426009	AF02246	Hs.210863	cell adhesion molecule with homology to L1CAM	7.8
415139	AW975942	Hs.46524	ESTs	7.7
450192	AA263143	Hs.24556	RAD51-interacting protein	7.7
423992	AW862922	Hs.137208	Homo sapiens mRNA; cDNA DKFZp564H1663 (from c	7.7
436211	AK001081	Hs.50961	polymyosin (DNA directed), gamma	7.7
450101	AW649989	Hs.24385	Human hbc547 mRNA sequence	7.5
426921	AA037145	Hs.172855	cleavage stimulation factor, 3' pre-RNA, subu	7.5
433330	AW207084	Hs.132816	ESTs	7.5
437579	AL320055	Hs.57709	Homo sapiens mRNA full length insert cDNA do	7.5
427660	AT741320	Hs.114121	Homo sapiens cDNA: FLJ23228 fs, clone CAE066	7.5
422095	AB68872	Hs.288956	ceruloplasmin (ferroxidase)	7.5
435476	AA326108	Hs.53631	ESTs	7.5
412170	D16532	Hs.37329	very low density lipoprotein receptor	7.4
428554	AF100781	Hs.194678	WNT1 Inducible signaling pathway protein 3	7.4
450221	AA328102	Hs.24641	cytoskeleton associated protein 2	7.4
439262	AA832333	Hs.124399	ESTs	7.4
435420	A928513	Hs.39202	ESTs	7.3
422892	AA598176	Hs.121553	hypothetical protein FLJ20641	7.3
457030	AA301740	Hs.173381	dihydropyrimidinase-like 2	7.2
411571	AA122383	Hs.70811	hypothetical protein FLJ23516	7.2
409916	BE313825	Hs.37435	soluble center family 11 (proton-coupled dha	7.2
418007	MI3509	Hs.83169	Matrix metalloproteinase 1 (interstitial collag	7.2
420900	AL045633	Hs.44269	ESTs	7.2
424001	W67883	Hs.137476	KIAA1051 protein	7.2
400301	X03635	Hs.1657	Estrogen receptor 1	7.1
400238			O	7.1
413573	AT733859	Hs.149089	ESTs	7.1
428071	AF212848	Hs.182339	transcription factor ESE-38	7.1
447164	AF026941	Hs.175198	Homo sapiens cigs mRNA, partial sequence	7.1
453062	AW207538	Hs.51603	ESTs	7.1
456965	AW131888	Hs.127292	ESTs, Weakly similar to hypothetical protein	7.1
442500	AB19908	Hs.209122	ESTs	7.1
446142	AT74683	Hs.145928	ESTs	7.0
417791	AW956339	Hs.111471	ESTs	7.0
418524	AA300576	Hs.85769	ack18 82 kDa protein mRNA	7.0
451797	AW638358	Hs.56120	ESTs	7.0
452809	NM_015368	Hs.30985	parminin 1	7.0
453516	NM_003462	Hs.33646	dysmelin, axonemal, light intermediate polypept	7.0
436281	AW411194	Hs.120051	ESTs	7.0
449897	AW819942	Hs.24135	transmembrane protein vezatin; hypothetical p	6.9
414142	AW358937	Hs.160942	ESTs	6.9

	448776	BE302464	Ha.30057	transporter similar to yeast MRS2	6.9
	419423	D26488	Ha.90315	KAA0007 protein	6.8
	425036	AL049974	Ha.100261	Homo sapiens mRNA; cDNA DKFZp5648222 (from d	6.8
5	452971	AB078078	Ha.91789	ESTs	6.8
	413597	AW302885	Ha.117183	ESTs	6.8
	415138	C18356	Ha.78045	tissue factor pathway inhibitor 2 TFP12	6.8
	437476	AL350172	Ha.118811	ESTs	6.7
	422592	NM_005624	Ha.155545	37 kDa leucine-rich repeat (LRR) protein	6.7
10	421184	NM_003616	Ha.102456	survival of motor neuron protein interacting	6.7
	410227	AB009284	Ha.61152	exostoses (multiple)-like 2	6.6
	446638	FM2717	Ha.257048	ESTs	6.6
	438167	R23893	Ha.24286	ESTs	6.6
	445459	AJ476029	Ha.158405	ESTs	6.6
15	452281	AF015592	Ha.28853	CDC7 (cell division cycle 7, S. cerevisiae), h	6.6
	410011	AB020641	Ha.97856	PETAIRE protein kinase 1	6.6
	410222	AJ443037	Ha.124194	ESTs	6.5
	415716	NS9294	Ha.301141	Homo sapiens cDNA FLJ11689 fs, clone HEMBA10	6.5
	424770	AA225562		gbcw4605.1 Soares, total_fetus_Nb2HF8_9w Ho	6.5
20	438122	AB020270	Ha.129837	ESTs	6.5
	439500	AL360204	Ha.283353	Homo sapiens mRNA full length insert cDNA do	6.5
	444743	AJ404548	Ha.11817	nudix (nucleoside diphosphate linked moiety X	6.5
	450638	AK001826	Ha.25245	hypothetical protein FLJ11269	6.5
	418203	U54942	Ha.83758	CDC28 protein kinase 2	6.5
	435991	U73836	Ha.124169	ESTs	6.5
25	428758	AA433988	Ha.98502	Homo sapiens cDNA FLJ14303 fs, clone PLACE20	6.4
	404552			0	6.4
	404599			0	6.4
	419503	AJ243642	Ha.137422	ESTs	6.4
	420149	AJ259920	Ha.88095	ESTs	6.4
30	440411	N30256	Ha.150971	ESTs, Weakly similar to Weak similarity with	6.4
	449108	AJ140683	Ha.98328	ESTs	6.4
	452007	AB002364	Ha.97916	ADAM-TS3 : a disintegrin-like and metallopro	6.4
	453619	U97648	Ha.33922	Hsapiens novel gene from PAC 117P20, chromos	6.4
	410273	BE326877	Ha.281523	ESTs	6.3
35	434486	AA678816	Ha.117142	ESTs	6.3
	454036	AJ374756	Ha.53560	ESTs, Weakly similar to unnamed protein produ	6.3
	403391			0	6.2
	412308	AA687322	Ha.192843	ESTs	6.2
40	419346	AB034117		gbcw46412.x1 NCL_CGAP_CL11 Homo sapiens cDNA	6.2
	446140	AJ356170	Ha.26750	Homo sapiens cDNA: FLJ21986 fs, clone HEP036	6.2
	453047	AW023798	Ha.269025	ESTs	6.2
	442573	H93366	Ha.7567	Branched chain aminotransferase 1, cytosolic,	6.1
	410102	AW248508	Ha.279727	ESTs	6.1
45	410004	U298027	Ha.239115	ESTs	6.1
	413335	AB13318	Ha.46442	ESTs	6.1
	424945	AZ21919	Ha.173438	hypothetical protein FLJ10582	6.1
	427610	Z47542	Ha.179312	small nuclear RNA activating complex, polypep	6.1
	451229	AW957707	Ha.48473	ESTs	6.1
50	452641	AW952893	Ha.237825	signal recognition particle 72kd	6.1
	433172	AB037841	Ha.102652	hypothetical protein ASH1	6.1
	425465	L18964	Ha.1904	protein kinase C, beta	6.1
	437117	ALJ49256	Ha.122393	ESTs	6.0
	423440	R25234	Ha.143434	contactin 1	6.0
	430510	AW182916	Ha.241576	hypothetical protein PRO2577	6.0
55	433252	AB040957	Ha.151343	KAA1524 protein	6.0
	434609	AJ443537	Ha.149425	Homo sapiens cDNA FLJ11980 fs, clone HEMBB10	6.0
	436954	AA740151	Ha.130425	ESTs	5.9
	438032	AA150797	Ha.109276	latexin protein	5.9
	424590	AA965399	Ha.46821	hypothetical protein FLJ20686	5.9
60	444078	BE246916	Ha.102930	US antiNP-specific 40 kDa protein (pHp8-bind)	5.9
	418379	AA218940	Ha.137516	ldgfatn-like 1	5.9
	438081	H49546	Ha.298964	ESTs	5.8
	443270	NM_004272	Ha.91919	Homer, neuronal immediate early gene, 1B	5.8
	459463	AB071853	Ha.238554	ESTs	5.8
65	433612	AF078164	Ha.61188	Homo sapiens Ku70-binding protein (KUB3) mRNA	5.8
	449048	Z45051	Ha.229200	similar to G68401 (calle) glucose induced ge	5.8
	417251	AW015242	Ha.99468	ESTs; Weakly similar to ORF YKR074w [S.cerev	5.7
	429181	AW979104	Ha.294609	ESTs	5.7
	454833	BE141714		gbc-QV0-HT0101-061109-032-c04 HT0101 Homo sap	5.7
70	455553	AA721325	Ha.189058	ESTs, Weakly similar to cAMP-regulated guanin	5.7
	450371	D87408	Ha.240112	KJA0076 protein	5.7
	452371	Q49441	Ha.155261	mesothelin	5.7
	424513	BE385864	Ha.149694	mitochondrial translational initiation factor	5.6
75	432015	AL157504	Ha.159115	ESTs	5.6
	438109	AJ076621	Ha.71367	ESTs, Moderately similar to ALU7_HUMAN ALU SU	5.6
	407137	T87207	Ha.189507	v-erbB-2/ret-1 murine erythroblastic leukemia viral	5.6
	407345	X69208	Ha.506	ATPase, Cu++-transporting, alpha polypeptid	5.6
	416565	AW000960	Ha.44570	ESTs	5.6
80	417830	AW504796	Ha.132808	epithelial cell transforming sequence 2 oncog	5.5
	419752	AJ248873	Ha.152616	ESTs	5.5
	422093	AF151852	Ha.111449	CGI-94 protein	5.5
	424583	AF017445	Ha.150926	fructose-1-phosphate guanylyltransferase	5.5
	430388	AJ356523	Ha.240770	nuclear cap binding protein subunit 2, 20kd	5.5
	425234	AW033022	Ha.149425	Homo sapiens cDNA FLJ11980 fs, clone	5.5

	453279	AW093940	Hs.59698	ESTs	5.5
	424188	AW954552	Hs.142634	zinc finger protein	6.5
	453884	AA355925	Hs.36232	KIAA0186 gene product	5.5
5	424641	AB001106	Hs.161413	gla maturation factor, beta	5.5
	444478	W07316	Hs.240	M-phase phosphoprotein 1	5.5
	427375	AK58065	Hs.122460	ESTs	5.5
	424520	AA101043	Hs.161254	kallikrein 7 (chymotrypsin; stratum corneum)	5.5
	442514	AW188551	Hs.99519	Homo sapiens cDNA FLJ14007 fls, clone Y79AA10	5.4
10	417995	AW974175	Hs.182781	ESTs	5.4
	418946	AT788941	Hs.132103	ESTs	5.4
	419963	AA742276	Hs.301052	ESTs	5.4
	420362	U79734	Hs.97206	huntingtin interacting protein 1	5.4
	422670	AA371612	Hs.115351	ESTs	5.4
15	423237	AA130633	Hs.276512	HSP-C72 protein	5.4
	447020	T27306	Hs.16386	hypothetical protein FLJ11046	5.4
	458027	L49054	Hs.85195	ESTs, Highly similar to K3-8(c25.1,p34) fus	5.4
	426217	AL070696	Hs.165174	CDC6 (cell division cycle 5, S. pombe, homologue)	5.4
	422533	NM_018109	Hs.1694	cestroneme protein A (TPO)	5.4
20	450434	AA166950	Hs.18545	ESTs, Weakly similar to partial CDS [C.elegans]	5.4
	438279	AA806156	Hs.165165	ESTs, Moderately similar to ALL8_HUMAN ALLU SU	5.4
	413384	NM_000401	Hs.75334	exonuclease (multipipe) 2	5.3
	423328	Y19062	Hs.96870	ctatufen (Drosophila, RNA-binding protein) hom	5.3
	435586	AI088662	Hs.167028	ESTs	5.3
25	435793	AB037734	Hs.4993	ESTs	5.3
	422306	BE044325	Hs.227290	Homo sapiens mRNA for Lam5 protein	5.3
	425164	NM_021851	Hs.154850	collagen, type IX, alpha 1	5.2
	453293	AA382267	Hs.106633	ESTs	5.2
	429944	R13549	Hs.226440	Homo sapiens clone 24881 mRNA sequence	5.2
30	434891	AA814309	Hs.123583	ESTs	5.2
	415263	AA948033	Hs.130853	ESTs	5.2
	409506	NM_006153	Hs.54589	NCK adaptor protein 1	5.2
	412848	AA121514	Hs.70832	ESTs	5.2
	421248	AW52962	Hs.300961	ESTs, Highly similar to AF151805 1 CGI-47 pm	5.2
35	431548	AK54273	Hs.9711	Homo sapiens cDNA FLJ13018 fls, clone NT2RP30	5.2
	412719	AW016610	Hs.129911	ESTs	5.2
	411945	AL033527	Hs.92137	v-myc avian myelocytomatous viral oncogene h	5.1
	424078	AB006625	Hs.139033	paternally expressed gene 3	5.1
	433558	AA833757	Hs.201769	ESTs	5.1
40	434265	AA846811	Hs.130554	Homo sapiens cDNA: FLJ23089 fls, clone LMG070	5.1
	453911	AW503857	Hs.4007	Sarcoplasmic-associated protein	5.1
	416539	AT733681	Hs.72472	BMPRIIb, bone morphogenetic protein receptor	5.1
	442717	R63652	Hs.186291	ESTs, Weakly similar to R6F5.5b [C.elegans]	5.1
	432358	AK053491	Hs.72630	ESTs	5.0
45	409731	AA125595	Hs.56145	thymosin, beta, identified in neuroblastoma c	5.0
	416639	AA248958	Hs.31246	ESTs	5.0
	420313	AB022320	Hs.89427	KIAA1013 protein	5.0
	422505	AL120862	Hs.124165	ESTs; (HSA)PAP protein (programmed cell death	5.0
	425733	F13287	Hs.159358	Homo sapiens clone 23578 mRNA sequence	5.0
50	434160	BE581196	Hs.114275	ESTs	5.0
	435094	AW501129	Hs.277523	EST	5.0
	435812	AW298067		gb:U1-H-BW0-sip-g-03-0-U1s1 NCL_CGAP_Sub6 Ho	5.0
	432415	T16971	Hs.289014	ESTs	4.9
	436117			0	4.9
55	438018	AK001160	Hs.6999	hypothetical protein FLJ10298	4.9
	447505	AL049266	Hs.18724	Homo sapiens mRNA; cDNA DKFZp564F093 (from cl	4.9
	448621	AA097144	Hs.5250	ESTs, Weakly similar to BACR37P7.g [D.melanog	4.9
	453001	AA511626	Hs.191260	ESTs	4.9
	410581	BE540255	Hs.6994	Homo sapiens cDNA: FLJ22044 fls, clone HEP091	4.9
60	418811	AK001407	Hs.88663	hypothetical protein FLJ10545	4.9
	433764	AK061288	Hs.133437	ESTs, Moderately similar to gonadotropin indu	4.8
	437212	AT656021	Hs.210775	ESTs	4.8
	447312	AA343435	Hs.36958	activating transcription factor 1	4.8
	409732	NM_016122	Hs.56148	NY-REN-58 antigen	4.8
65	434680	AB87679	Hs.148410	ESTs	4.8
	444172	BE147740	Hs.104558	ESTs	4.8
	424539	L02911	Hs.150402	activin A receptor, type I	4.8
	418677	S83308	Hs.87224	SRY (sex determining region Y)-box 5	4.8
	406076	AL390179	Hs.137011	Homo sapiens mRNA; cDNA DKFZp547P134 (from cl	4.8
70	420179	AT4530	Hs.21168	ESTs	4.7
	450376	AA009647	Hs.8850	a dielinoglin and metalloproteinase domain 12	4.7
	419247	S65791	Hs.89764	fragile X mental retardation 1	4.7
	420850	BE139590	Hs.122406	ESTs	4.7
	425420	BE536911	Hs.224545	ESTs	4.7
75	428564	AK001656	Hs.189095	similar to SALL1 (ps) (Drosophila)-like	4.7
	419131	AA406233	Hs.301622	ESTs	4.7
	422278	AF072873	Hs.114218	ESTs	4.7
	451884	AF216751	Hs.26813	CD44	4.6
80	400396	AA305527	Hs.139336	ATP-binding cassette, sub-family C (CFTR/MRP)	4.6
	408425	AW058674	Hs.44787	Homo sapiens mRNA; cDNA DKFZp434O0227 (from c	4.6
	417168	AL133117	Hs.81376	Homo sapiens mRNA; cDNA DKFZp586L1121 (from c	4.6
	429465	AF158827	Hs.203853	hypothetical protein FLJ10339	4.6
	442917	AA314597	Hs.86950	ESTs	4.6
	443268	AB002271	Hs.129445	hypothetical protein FLJ12496	4.6
	452795	AW392555	Hs.18878	hypothetical protein FLJ21620	4.6

457300	AW297436	Hs.158849	Homo sapiens cDNA: FLJ21663 fs, clone COL088	4.6
459551	AA72808	Hs.158849	gbt70007.31 Soares_NSF_F8_9W_OT_PA_P_S1 Hom	4.6
421977	WS4197	Hs.110165	ribosomal protein L26 homolog	4.6
429441	AJ224172	Hs.264066	lipophilin B (pteroglycin family member), pro	4.6
459722	BE280074	Hs.23969	cyclin B1	4.5
431689	AA305688	Hs.267695	UDP-Gal4betaGal4Nuc beta1 1,3-galactosyltransferase	4.5
425178	HL16097	Hs.161027	ESTs	4.5
423557	NM_003816	Hs.2442	a disintegrin and metalloproteinase domain 9	4.5
435556	AC564997	Hs.7572	ESTs	4.5
400534		0	0	4.5
417845	AL117461	Hs.82719	Homo sapiens mRNA: cDNA DKF2p586f1822 (from c	4.5
423123	NM_012247	Hs.124037	SELENENOPHOSPHATE SYNTHETASE; Human selenium d	4.5
434305	AA622007	Hs.494915	Homo sapiens cDNA FLJ12938 fs, clone NT2RP20	4.5
441006	AW605267	Hs.7627	CGI-60 protein	4.5
414569	AF109298	Hs.118298	Prostate cancer associated protein 1	4.5
447924	AB167226	Hs.170337	ESTs	4.4
423505	NM_003566	Hs.159205	basic leucine zipper nuclear factor 1 (JEM-1)	4.4
411630	U42349	Hs.71119	Putative prostate cancer tumor suppressor	4.4
432842	AW674093	Hs.279525	hypothetical protein PRO2605	4.4
413472	BE242870	Hs.75379	solute carrier family 1 (glut high affinity	4.4
414659	AB185233	Hs.70530	synuclein, alpha (non A4 component of amyloid	4.4
412733	AA984472	Hs.74554	KIAA0090 protein	4.4
419790	U79250	Hs.93201	glycerol-3-phosphate dehydrogenase 2 (mitochond	4.4
433377	AF152713	Hs.43845	ESTs	4.4
440535	W15267	Hs.23872	low density lipoprotein receptor-related prot	4.4
453900	AW003582	Hs.226414	ESTs, Weakly similar to ALU8_HUMAN ALU SUBFAM	4.4
443881	R64512	Hs.237146	Homo sapiens cDNA FLJ14234 fs, clone NT2RP40	4.4
423025	AA831267	Hs.12244	Homo sapiens cDNA: FLJ23561 fs, clone LNC6136	4.4
409621	AB706772	Hs.46038	chromosome 11 open reading frame 6; fetal br	4.4
418241	N52639	Hs.32683	ESTs	4.3
432005	AA524190	Hs.120777	ESTs, Weakly similar to ELL2_HUMAN RNA POLYME	4.3
435532	AW291488	Hs.117305	ESTs	4.3
451813	NM_016117	Hs.27182	phospholipase A2-activating protein	4.3
454193	BE141183	Hs.27182	gbtMRD-HT0071-191195-001-804 HT0071 Homo sapi	4.3
418478	U39345	Hs.11174	cyclin-dependent kinase inhibitor 2A (melanoma	4.3
406089		0	0	4.3
419465	AW500239	Hs.21187	Homo sapiens cDNA: FLJ23068 fs, clone LNC055	4.3
418413	R95735	Hs.117753	ESTs, Weakly similar to analog of the monod	4.3
452028	AK001859	Hs.27595	hypothetical protein FLJ10997	4.3
416693	AF193678	Hs.87409	thrombospondin 1	4.3
410361	BE391804	Hs.62651	guanylate binding protein 1, interferon-induc	4.2
409743	AL043212	Hs.816	gbtDKFZp434H0623_r1 434 (synonym: hles3) Homo	4.2
455601	AC356880	Hs.816	SRY (sex determining region Y)-box 2, partial	4.2
409908	BE256247	Hs.48915	serine/threonine kinase 15	4.2
413582	AW265677	Hs.71331	Homo sapiens cDNA: FLJ121971 fs, clone HEP057	4.2
423248	AA380177	Hs.125845	ribulose-5-phosphate-3-epimerase	4.2
425024	R39235	Hs.12407	ESTs	4.2
447153	AA065202	Hs.173912	eukaryotic translation initiation factor 4A,	4.2
447406	BE618050	Hs.226282	ESTs	4.2
440347	AV649748	Hs.295901	ESTs	4.2
414279	AW021691	Hs.3804	DKF2P564C1940 protein	4.2
428855	AA436735	Hs.183171	Homo sapiens cDNA: FLJ22002 fs, clone HEP066	4.2
407872	AB039703	Hs.40735	titfizzed (Drosophila) homolog 3	4.2
421502	AF111856	Hs.105039	solute carrier family 34 (sodium phosphates),	4.2
438406	AW105723	Hs.125346	ESTs	4.2
432609	AL120559	Hs.8111	KIAA0307 gene product	4.2
443553	AA137043	Hs.95693	programmed cell death 6-interacting protein	4.1
454556	AW807073	Hs.153408	gbtMR4-ST0062-Q31199-019-J05 ST0062 Homo sapi	4.1
424834	AK001432	Hs.153408	Homo sapiens cDNA FLJ10570 fs, clone NT2RP20	4.1
412593	Y07559	Hs.74708	early growth response 3	4.1
416566	NM_003914	Hs.79378	cyclin A1	4.1
426342	AF093419	Hs.169378	multiple PDZ domain protein	4.1
428417	AK001859	Hs.184227	F-box only protein 21	4.1
428317	AA831552	Hs.163046	solute carrier family 5 (proteol transporter	4.1
446880	AB11807	Hs.108546	Homo sapiens cDNA FLJ12534 fs, clone NT2RM40	4.1
422888	AW673847	Hs.97321	ESTs	4.0
434657	AA641876	Hs.191840	ESTs	4.0
412494	AL133900	Hs.7192	ADP-ribosylation factor domain protein 1, 64k	4.0
443271	BE568568	Hs.195704	ESTs	4.0
421437	AW821252	Hs.104336	ESTs	4.0
401644		0	0	4.0
405995		0	0	4.0
418417	R77182	Hs.153408	gbtY55602r1 Soares placenta Nb2HP Homo sapi	4.0
420807	AA280627	Hs.57846	ESTs	4.0
429529	AA454190	Hs.193811	ESTs, Moderately similar to reduced expresso	4.0
457726	A2174177	Hs.194091	ESTs	4.0
431130	NM_006103	Hs.2719	epididymis-specific; whey-acidic protein type	4.0
453403	BE466639	Hs.81779	Homo sapiens cDNA FLJ13591 fs, clone PLACE10	4.0
442768	AL048334	Hs.49458	ESTs, Weakly similar to ALU8_HUMAN ALU SUBFAM	4.0
413430	U22479	Hs.24680	Homo sapiens cDNA FLJ13047 fs, clone NT2RP30	4.0
424081	NM_005413	Hs.139120	ribonuclease P (30kD)	4.0
425692	D90041	Hs.155956	NAT1; n-lysine N-acetyltransferase	4.0
407792	A077715	Hs.39394	putative secreted ligand homologous to fpl1	4.0
406353	BE439638	Hs.44290	hypothetical protein	4.0

	421175	A1879099	Hs.102397	GOT-3 for gonadotropin inducible transcript	3.9
	426324	AF163474	Hs.96744	OKFZP5860823 protein, Prostate androgen-regu	3.9
	417531	NM_003157	Hs.1087	serine/threonine kinase 2	3.9
5	458524	BE242138	Hs.24427	OKFZP56501646 protein	3.9
	401195		0		3.9
	401480		0		3.9
	410360	AW663690		gbj3121g03.1 NC1_CGAP_L18 Homo sapiens cDNA	3.9
	410908	AA121685	Hs.10592	ESTs	3.9
10	420150	AS27440	Hs.95785	ESTs	3.9
	422805	AA436989	Hs.121017	H2A histone family; member A	3.9
	424639	A1917494	Hs.131329	ESTs	3.9
	428555	NM_002214	Hs.18498	Integrin, beta 8	3.9
	431659	NM_001173	Hs.28781	Homo sapiens cDNA FLJ12952 fs, clone NT2RP20	3.9
15	433703	AA210853	Hs.3532	nemo-like kinase	3.9
	437144	AL049466	Hs.7859	ESTs	3.9
	452728	AB15676	Hs.239708	ESTs	3.9
	430417	W17054	Hs.741451	SWI/SNF related, matrix associated, actin dep	3.9
20	440594	AW445167	Hs.126036	ESTs	3.9
	408938	AA059013	Hs.22607	ESTs	3.9
	427051	BE178110	Hs.173374	ESTs	3.9
	447568	AF155655	Hs.18885	CCA-116 protein	3.9
	457211	AW972565	Hs.32399	ESTs; Weakly similar to Similar to Ena-VASP1	3.9
	443475	AO66470	Hs.134482	ESTs	3.9
25	433447	U29195	Hs.3281	neuronal plectradin II	3.9
	425093	AW594506	Hs.104630	ESTs	3.9
	437938	AB500097		ESTs; Weakly similar to Gag-Pol polyprotein [3.8
	408829	NM_006042	Hs.46384	heparan sulfate (glucosamine) 3-O-sulfotransf	3.8
	429250	H56585	Hs.198308	tryptophan rich basic protein	3.8
30	411655	AW194364	Hs.128022	ESTs; Weakly similar to FIG1 MOUSE FIG-1 PROT	3.8
	437700	AA766960	Hs.122848	ESTs	3.8
	430560	BE555647	Hs.74899	hypothetical protein FLJ12820	3.8
	409364	AA043857	Hs.54943	fracture callus 1 (rat) homolog	3.8
	429474	AA452441	Hs.31511	ESTs	3.8
35	431965	BE175190		gln:QV2-HT0577-010500-165-g04 HT0577 Homo sap	3.8
	454018	AW016892	Hs.241652	ESTs	3.8
	426320	W47595	Hs.169300	transforming growth factor, beta 2	3.8
	429535	AA477288	Hs.94691	Homo sapiens cDNA: FLJ22728 fs, clone HSI156	3.8
	417517	AF001176	Hs.82238	POP4 (processing of precursor, S. cerevisiae	3.8
40	446402	AB681145	Hs.160724	ESTs	3.8
	450236	AW162998	Hs.24484	KIAA1376 protein	3.8
	410804	U54820	Hs.66521	Hashado-Joseph disease (spinocerebellar ataxi	3.8
	400268		0		3.8
	418217	A1910647	Hs.13442	ESTs	3.8
	421928	AF013768	Hs.169543	poly(adenylate) binding protein-interacting pro	3.8
45	417300	AF766227	Hs.55610	soluble carrier family 30 (zinc transporter),	3.8
	414136	AB812434	Hs.178227	ESTs	3.8
	453945	NM_005171	Hs.36908	activating transcription factor 1	3.7
	402420		0		3.7
50	407877	AW010811	Hs.234478	Homo sapiens cDNA: FLJ22648 fs, clone HSI073	3.7
	450581	AF081513	Hs.25195	endometrial bleeding associated factor (left-	3.7
	418223	NM_014733	Hs.83790	KIAA0305 gene product	3.7
	411704	AA058228	Hs.71573	hypothetical protein FLJ10974	3.7
	432112	AB016247	Hs.203031	stard-C5-desaturase (lung) ERG3, delta-5-de	3.7
55	422809	AK001379	Hs.121028	hypothetical protein FLJ10549	3.7
	402820		0		3.7
	406090	BE173621	Hs.252470	ESTs	3.7
	415421	AA134006	Hs.73306	eukaryotic translation initiation factor 4E	3.7
	418282	AA215535	Hs.98133	ESTs	3.7
60	418454	AA135308		gln:EST 187095 Colon carcinoma (HCC) cell line	3.7
	418658	AW407987	Hs.87150	Human clone AS42BR11 (CAC)n(GTG)n repeat-con	3.7
	422290	AA463854	Hs.48827	hypothetical protein FLJ12005	3.7
	432824	AK001783	Hs.279012	hypothetical protein FLJ10921	3.7
	435907	AA853978	Hs.124577	ESTs	3.7
65	447479	AB037634	Hs.18655	Homo sapiens mRNA for KIAA1413 protein, parti	3.7
	451073	A758955	Hs.205063	ESTs	3.7
	450377	AB033091	Hs.24936	ESTs	3.7
	414343	AL036166	Hs.75914	coated vesicle membrane protein	3.7
	446807	AS71940	Hs.7548	ESTs	3.7
70	442821	BE381828	Hs.81752	Pulsative type II membrane protein	3.7
	426300	U15979	Hs.169228	delta-like homolog (Drosophila)	3.7
	418098	AW971155	Hs.253002	ESTs; Weakly similar to prolyl 4-hydroxylase	3.7
	411263	BE297602	Hs.83660	kinesin-like 6 (mitotic centrosome-associated	3.7
	443054	A745165	Hs.8539	yes-associated protein 65 kDa	3.7
75	421154	AA264333	Hs.287631	Homo sapiens cDNA FLJ14269 fs, clone PLACE10	3.7
	411402	BE297855	Hs.69555	NRAS-related gene	3.7
	450447	AF212223	Hs.25010	hypothetical protein P15-2	3.6
	414705	AW040125	Hs.76869	KIAA0057 gene product	3.6
	434228	Z4247	Hs.283978	ESTs; KIAA0738 gene product	3.6
80	434164	AW207019	Hs.148135	ESTs	3.6
	403933	AW959543	Hs.21291	mitogen-activated protein kinase kinase kinase	3.6
	402222		0		3.6
	404915		0		3.6
	404996		0		3.6
	411560	AW851186		gbl:3L-CT0220-150200-071-H05 CT0220 Homo sap	3.6

	419750	AL079741	Hs.183114	Homo sapiens cDNA FLJ14236 fs, clone NT2RP40	3.6
	426010	AA135653	Hs.1975	Homo sapiens cDNA: FLJ21007 fs, clone CAE038	3.6
	427038	NM_014633	Hs.173288	KAA0155 gene product	3.6
5	439255	BE164500	Hs.28465	gbrC4-H10469-23030-014-e10 H10469 Homo sapi	3.6
	458242	BE265988	Hs.127751	Homo sapiens cDNA: FLJ21869 fs, clone HEP024	3.6
	415115	AA214228	Hs.127751	hypothetical protein	3.6
	453468	W00712	Hs.32990	DKFZP566F054 protein	3.6
	441205	AW137827	Hs.176504	ESTs	3.6
10	452633	T9153	Hs.40589	zinc finger protein 228	3.6
	417389	BE260964	Hs.82045	Midkine (neurtin growth-promoting factor 2)	3.6
	448105	AW591433	Hs.170675	ESTs, Weakly similar to TMS2_HUMAN TRANSMEMBR	3.6
	451522	BE356817	Hs.26498	hypothetical protein FLJ21557	3.6
	440048	AA527451	Hs.158469	ESTs, Weakly similar to envelope protein [Hs	3.5
15	419359	AL043202	Hs.59073	chromosome segregation 1 (yeast homolog)-like	3.5
	452030	AL137578	Hs.27607	Homo sapiens mRNA; cDNA DKFZP564N2464 (from c	3.5
	400666	H87863	Hs.151389	ESTs	3.5
	422846	AA425002	Hs.40403	Ctbp3/300-Interacting transactivator, with G	3.5
20	407846	AV660717	Hs.47144	DKFZP568N0819 protein	3.5
	401517	AW462934	Hs.75538	nucleolar GTPase	3.5
	413775	NM_004458	Hs.81452	fatty-acyl-Coenzyme A ligase, long-chain 4	3.5
	427943	AW959075	Hs.163887	gbrEST371145 MAGE sequences, MAGE Homo sapi	3.5
25	439107	AL046134	Hs.27895	ESTs	3.5
	447268	AJ370413	Hs.35553	Homo sapiens cDNA: FLJ22418 fs, clone HRC085	3.5
	412504	AW976324	Hs.47144	DKFZP568N0819 protein	3.5
	427134	AA398409	Hs.173561	EST	3.5
	430273	AJ311127	Hs.125522	ESTs	3.5
30	433571	AW137159	Hs.146151	ESTs	3.5
	433057	NM_014158	Hs.279338	HSPC067 protein	3.5
	453745	AA552989	Hs.63908	Homo sapiens HSPC216 mRNA, partial cds	3.5
	400531	AF151064	Hs.36069	hypothetical protein	3.5
	433345	AJ081545	Hs.152862	EST cluster (not in UniGene)	3.4
35	406400	AA343529	Hs.104570	kallistatin 8 (neuropilin/vasilin)	3.4
	407596	R66913	Hs.43388	gbrny3005.r1 Soares fetal liver spleen 1NFLS	3.4
	453779	N35167	Hs.43388	ESTs	3.4
	444658	A1199738	Hs.208275	ESTs, Weakly similar to unnamed protein produ	3.4
	447688	N87079	Hs.19236	NAIDH dehydrogenase (ubiquinone) 1 beta subcom	3.4
40	424855	AA347746	Hs.9521	ESTs, Weakly similar to KAA1015 protein [Hs	3.4
	407854	AF069291	Hs.40539	chromosome 8 open reading frame 1	3.4
	404108			0	3.4
	403729			0	3.4
	404232			0	3.4
45	423687	AA329533	Hs.133011	ESTs, Highly similar to Z117, HUMAN ZINC FINGER	3.4
	428372	AQ000884	Hs.163887	hypothetical protein FLJ22104	3.4
	439741	BE379546	Hs.5904	Homo sapiens mRNA full length insert cDNA clo	3.4
	441447	AA934077	Hs.126590	ESTs	3.4
	448358	R44433	Hs.105614	Human DNA sequence from clone RP4-534K7 on ch	3.4
50	450226	AT414361	Hs.205391	ESTs, Weakly similar to zinc finger protein P	3.4
	458477	NM_000314	Hs.10712	phosphatase and tensin homolog (mutated in mu	3.4
	421379	Y15221	Hs.103582	small inducible cytokine subfamily 8 (Cys-X-C	3.4
	452822	X95589	Hs.268617	Homo sapiens cDNA: FLJ22621 fs, clone HS1056	3.4
	441111	AJ060867	Hs.126594	ESTs	3.4
55	447519	U46258	Hs.23446	ESTs	3.4
	446913	AA430650	Hs.16529	transmembrane 4 superfamily member (tetraspan	3.4
	449581	AJ989317	Hs.181605	ESTs	3.4
	450132	BE219171	Hs.227146	Homo sapiens cDNA FLJ14234 fs, clone NT2RP40	3.4
	448196	AA262105	Hs.4094	Homo sapiens cDNA FLJ14208 fs, clone NT2RP30	3.4
60	422611	AA158177	Hs.118722	lucosyltransferase 8 (alpha (1,5) fucosyltran	3.4
	441433	AA333009	Hs.42746	ESTs	3.4
	417637	AL079505	Hs.1163	transforming growth factor, beta 1	3.4
	450516	AA902656	Hs.21943	NIF3 (Ngi1 Interacting factor 3, S.pombe homo	3.4
	407796	AA195509	Hs.272239	lymphocyte activation-associated protein	3.3
65	419200	AW596405	Hs.26855	prokinin 5	3.3
	423161	AL045227	Hs.124776	Homo sapiens mRNA; cDNA DKFZP564N1116 (from c	3.3
	454579	AJ343858	Hs.58800	Homo sapiens cDNA FLJ12488 fs, clone NT2RM20	3.3
	435014	BE560898	Hs.10026	ribosomal protein L17 Isolog	3.3
	446819	AJ076543	Hs.313	saccharyl phosphatase 1 (osteopontin, bone	3.3
70	435170	AA332626	Hs.165339	ESTs	3.3
	429830	AJ537278	Hs.225841	DKFZP434D193 protein	3.3
	428943	AW086180	Hs.37636	ESTs, Weakly similar to KAA1352 protein [Hs	3.3
	445817	NM_005842	Hs.13340	histone acetyltransferase 1	3.3
	428005	H62912	Hs.48269	vacuolin related kinase 1	3.3
	441134	W25092	Hs.7678	cellular retinoic acid-binding protein 1	3.3
75	408532	AJ453137	Hs.63176	ESTs	3.3
	402517	XJ07780	Hs.54658	inopinon 1, cardiac	3.3
	414304	AJ621276	Hs.165998	DKFZP564N2423 protein	3.3
	436427	AJ344378	Hs.143399	ESTs	3.3
	436652	AJ582393	Hs.126695	ESTs	3.3
80	440304	BE169584	Hs.125395	ESTs	3.3
	447355	F12683	Hs.19375	gbrHSC3FE081 normalized infant brain cDNA Hom	3.3
	451177	AJ969716	Hs.13034	ESTs	3.3
	428949	AA442153	Hs.104744	ESTs, Weakly similar to AF208555 1 BM-013 [H	3.3
	451743	AW074266	Hs.23071	ESTs	3.3

	421515	Y11339	Hs.105352	GaiNAc alpha-2, 6-sialyltransferase I, long f	3.3
	446351	AW444551	Hs.258532	ESTs	3.3
	435102	AW839053	Hs.78917	F-box only protein 8	3.3
	418216	AA662240	Hs.283099	AF15q14 protein	3.3
5	401508			0	3.3
	437108	AA434054	Hs.80624	Homo sapiens cDNA: FLJ23442 fs, clone HS1009	3.3
	416530	U62601	Hs.79351	kallikrein 6 (neurosin, zyme)	3.3
	443171	BE281128	Hs.90303	TGN40	3.3
10	435627	AW080642	Hs.97894	ESTs; Weakly similar to WASP-family protein 1	3.3
	412078	X59599	Hs.73149	paired box gene 8	3.2
	414080	AA135257	Hs.47783	ESTs, Weakly similar to T12540 hypothetical p	3.3
	401197			0	3.3
	422134	AW179019	Hs.112110	ESTs	3.3
15	409044	AI129585	Hs.33033	ESTs	3.3
	416198	H27332	Hs.99598	ESTs	3.2
	434841	AA379597	Hs.5199	HSPC150 protein similar to ubiquitin-conjugat	3.2
	435525	AA721428	Hs.26145	Homo sapiens cDNA FLJ14127 fs, clone MAMMA10	3.2
	409142	AL136877	Hs.50758	chromosome-associated polypeptide C	3.2
	428819	AL135523	Hs.183914	KIAA0575 gene product	3.2
20	428728	NM_016625	Hs.191381	ESTs; Weakly similar to hypothetical protein	3.2
	41261	AA509053	Hs.98133	ESTs	3.2
	445219	AI287344	Hs.149827	ESTs	3.2
	457574	H88717	Hs.27774	ESTs, Highly similar to AF161349 1 HSPC066 [H	3.2
	409172	Z99399	Hs.118145	ESTs	3.2
25	413888	T67012	Hs.75323	proteobin	3.2
	434167	AA527098	Hs.99103	ESTs, Weakly similar to U38428 T-complex prot	3.2
	445060	AA830811	Hs.88808	ESTs	3.2
	448254	AA828900	Hs.22929	ESTs	3.2
	452943	BE247448	Hs.31082	Hypothetical protein FLJ10525	3.2
30	411393	AW787437	Hs.63771	B-factor, propeptin	3.2
	453775	NM_002916	Hs.35120	replication factor C (activator 1) 4 (37KD)	3.2
	408418	AW953887	Hs.44743	KIAA1435 protein	3.2
	442025	AW887434	Hs.11810	ESTs, Weakly similar to CD4-2 [C.elegans]	3.2
	417006	AW673565	Hs.80758	aspartyl-tRNA synthetase	3.2
35	407881	AW072003	Hs.40958	heparan sulfate (glucosamine) 3-O-sulfotransf	3.2
	444755	AA431791	Hs.183001	ESTs	3.2
	402829			0	3.2
	451553	AF151879	Hs.26706	CSG-121 protein	3.2
	419926	AW900992	Hs.93795	DKFZP580D2223 protein	3.2
40	434551	BE387162	Hs.280858	ESTs, Highly similar to XPB_HUMAN DNA-REPAIR	3.2
	445929	AA505690	Hs.76338	matkaka, dog faggar protein, 1	3.2
	406365	AA702376	Hs.226440	Homo sapiens clone 24881 mRNA sequence	3.2
	418836	AI655499	Hs.161712	ESTs	3.2
	444020	W79283	Hs.35962	ESTs	3.1
45	422363	T55079	Hs.115474	replication factor C (activator 1) 3 (38KD)	3.1
	413010	AA393273	Hs.75133	transcription factor 6-like 1 (mitochondrial	3.1
	452092	BE245374	Hs.27842	hypothetical protein FLJ11210	3.1
	410486	AW253994	Hs.183424	ESTs, Weakly similar to KIAA1064 protein [Hs	3.1
	434540	NM_016043	Hs.5184	TH1 drosophila homolog	3.1
50	409178	BE393948	Hs.50915	kallikrein 5	3.1
	439480	AL038511	Hs.125316	ESTs	3.1
	417848	AA205681	Hs.28457	ESTs	3.1
	446253	AA402213	Hs.149722	ESTs	3.1
	408108	AI580492	Hs.42743	hypothetical protein	3.1
55	415947	U04045	Hs.78934	mutS (E. coli) homolog 2 (colon cancer, nonpo	3.1
	410519	AW612264	Hs.131705	ESTs	3.1
	421987	AI133161	Hs.286131	CSG-101 protein	3.1
	440046	AW402306	Hs.6877	hypothetical protein FLJ10483	3.1
	453931	AL121278	Hs.25144	ESTs	3.1
60	454423	AW603985	Hs.179562	nucleosome assembly protein 1-like 1	3.1
	459089	F13036	Hs.27373	Homo sapiens mRNA, cDNA DKFZp564O1783 (from c	3.1
	418735	N48769	Hs.44609	ESTs	3.1
	414245	BE146072	Hs.75850	WAS protein family, member 1	3.1
	410909	AW889161	Hs.53112	ESTs, Weakly similar to ALUS_HUMAN ALU SUBFAM	3.1
65	434526	BE543269	Hs.80282	Homo sapiens HSPC283 mRNA, partial cds	3.1
	409239	AA740875	Hs.44307	ESTs	3.1
	428017	AA463605	Hs.238995	ESTs	3.1
	444702	D61894	Hs.17229	pregnancy specific beta-1-glycoprotein 9	3.1
	425514	BE516833	Hs.201122	SEC22, vesicle trafficking protein (S. cerevis	3.1
70	448133	AA723157	Hs.73769	SRB2 (suppressor of RNA polymerase B; yeast)	3.1
	418792	AB037805	Hs.88442	KIAA1384 protein	3.1
	427528	AJ077143	Hs.179565	minichromosome maintenance deficient (S. cere	3.1
	403077			0	3.1
	440671	AW257920	Hs.130054	ESTs	3.1
75	419690	X17360	Hs.278255	homeo box D4	3.1
	406687	M31126	Hs.272620	pregnancy specific beta-1-glycoprotein 9	3.1
	409151	AA336105	Hs.50795	SEC22, vesicle trafficking protein (S. cerevis	3.1
	431221	AA449015	Hs.286145	SRB2 (suppressor of RNA polymerase B; yeast)	3.1
	443584	AI807036	Hs.101619	ESTs	3.1
80	443525	BE149566	Hs.14831	ESTs	3.1
	410441	BE265610		gb-R01118016F1 NIH_MGC_17 Homo sapiens cDNA c	3.1
	422634	NM_016010	Hs.118821	CGA-62 protein	3.0
	420022	AA256253	Hs.120317	ESTs	3.0
	453912	AL121031	Hs.32556	KIAA0379 protein	3.0

5	45684	A264155	Hs.162981	COP-diacylglycerol synthase (phospholipase cy	3.0
	414941	C14865	Hs.182199	ESTs	3.0
	407807	AL031427	Hs.40094	Human DNA sequence from clone 167A19 on chrom	3.0
	414725	AA769791	Hs.120355	Homo sapiens cDNA FLJ13148 fls, clone NT29P30	3.0
	444420	AI48157	Hs.145766	EST	3.0
10	431742	NM_016652	Hs.258231	CGI-201 protein	3.0
	412519	AA196241	Hs.73980	troponin T1, skeletal, slow	3.0
	418348	AI537167	Hs.96322	Homo sapiens cDNA: FLJ23550 fls, clone LUNG098	3.0
	444261	AA298958	Hs.10724	HD0322 protein	3.0
	457465	AW301344	Hs.196599	ESTs	3.0
15	443933	AI091531	Hs.135501	Homo sapiens two pore potassium channel K13.3	3.0
	442150	AI358158	Hs.128864	ESTs	3.0
	414853	AA326580	Hs.76750	CC23 protein kinase 1	3.0
	442879	AF332322	Hs.8113	synaptin binding protein 3	3.0
	437949	U78519	Hs.41654	ESTs	3.0
20	403515		0	0	3.0
	403954		0	0	3.0
	407785	AW207285	Hs.98279	ESTs	3.0
	426199	AA371865	Hs.97050	ESTs	3.0
	426324	AW281787	Hs.200933	ESTs	3.0
25	427738	NM_000318	Hs.160812	peroxisomal membrane protein 3 (39kD, Zellweg	3.0
	427837	U87309	Hs.160941	vesicular protein sorting 4 (yeast homolog)	3.0
	439430	AF124250	Hs.6554	breast cancer anti-estrogen resistance 3	3.0
	442038	AW275240	Hs.128352	ESTs, Weakly similar to p80 (Puruvigous)	3.0
	446978	NM_001938	Hs.16697	down-regulator of transcription 1, TBP-binding	3.0
30	452431	U68078	Hs.25459	cell-surface receptor 3	3.0
	452841	U71431	Hs.65412	DEAD(H) (Glu-Ala-Ala-Asp) box polypeptide	3.0
	432114	AL036021	Hs.225597	ESTs	3.0
	445840	AW969326	Hs.31704	ESTs, Weakly similar to KIA04227 [H.sapiens]	3.0
	442607	AA507576	Hs.293361	KIA0471 gene product	3.0
35	453920	AI133148	Hs.36502	C factor (complement)	3.0
	430000	AW205931	Hs.95598	ESTs	3.0
	428164	AW68663	Hs.116586	ESTs	3.0
	453331	AA240585	Hs.9885	ESTs	3.0
	448663	BE814599	Hs.106823	H.sapiens gene from PAC 42616, similar to syn	3.0
40	425776	U25128	Hs.159499	parathyroid hormone receptor 2	3.0
	407174		0	0	3.0
	407893		0	0	3.0
	428428	AL037544	Hs.184298	cyclin-dependent kinase 7 (homolog of Xenopus	3.0
	443761	AA523743	Hs.160903	ESTs	3.0
45	451640	AA195501	Hs.26771	Human DNA sequence from clone 747H23 on chrom	3.0
	442580	AT33682	Hs.130239	ESTs	3.0

TABLE 10B:

Play: Unique ex probe/ Identifier number
CAT number: Gene cluster number
Accession: Genbank accession numbers

Play	CAT Number	Accession
50	407596	R06913 RB6901 H25352 R01370 H43764 AW044451 W21298
	409363	AL043212 AA077575 AA077655 R19502 BE545457 AIC8421 R14093
	410760	AW663690
	410441	BE20210 A1672315 AW086489 BE298417 AA455921 AA902537 BE327124 R14563 AA085210 AW274273 A333594 A369742 A036558
		A1885095 AA76740 A128755 A1885299 A865381 A18592624 AW340136 A2269556 A456390 A310815 AA484951
55	411560	1249443_1
	414315	143512_1
	418417	176916_1
	418454	175999_1
	419346	184129_1
60	424770	243504_1
	427943	264802_1
	431965	33559_2
	436812	427233_1
	437938	44573_2
65		BE175190 A0731645 AAB10101 AW194180 A1850673 A978773
		A950087 N10208 R97040 N38089 A308119 AW967677 N53320 A251473 H53397 AW971573 R57278 W01059 AW967671 AA308598
		AA251475 A1820501 A1820532 W01801 T85004 U71456 T82381 BE328571 T78192 K34725 AA894922 BE328517 A217978 AA488444
		N92578 T13453 AA527754 A5180251 AW874068 AL130403 AW235363 A6653345 AW002882 AA488964 AA283144 A593587 A1030344
		AT714346 A1898062 AA282915 AW102896 A872193 A7163273 AW173586 AW150329 A1853932 A1762688 AA988777 AA488892 A1856394
70		AW103813 A1853642 AA642785 AA856975 A9505512 A1861530 AW829570 BE12891 AW276997 AHW513601 AHW512643 AA044269
		A18865338 A1810008 A337459 AW061101 AA251653 AW151874 AW195225 AW205962 A1853338 A1855629 AW277605 A1853306 AA072584
		AA908741 AW072629 AHW513996 AA293373 AA069759 N75628 N22388 H84728 H20052 T32487 A1020208 AA780419 AAS51005 W08701
		AW1813456 A473032 A1564269 F00531 H83458 W37811 W78802 R56056 A1002839 R67840 AW959801 BE141592 AW45801 BE141592 AW178155 BE141592
		BE164500 AA832158 BE164502
75		T71812_1
		BE141183 AW178167 AW178162 AW178166 AW178172 AW178164 AW178159 AW178157 AW178222 AW178213 AW178215 AW178090 AW178091
		AW178161 AW178207 AW178210 AW178214 AW178212 BE140918 BE140917 AW178135 AW178205 AW178209 AW178223 AW178220
		AW178206 AW178203 AW178165 AW178168 AW178176 AW178136 AW1845878 AW178131 AW178138 AW178105 AW1845894 AW178129
		AW1845810 AW1845808 AW178161 AW178162 AW178163 AW178164 AW178165 AW178166 AW178167 AW178168 AW178169 AW178170 AW178171
80		AW178133 AW178164 AW178218 AW178171 AW178157 AW178158 AW178103 BE141189 AW178170 AW1845816 BE141596 AW178156
		AW178104 AW178163 AW178093 AW178208 AW178137 AW178140 AW178219 BE141592 AW45801 BE141592 AW178155 BE141592
		BE140957
		AW8077073 AW807655 AW807667 AW807276 AW807030 AW807353 AW845892 AW807091 AW807275 AW807284 AW807287 AW845891
		AW807195 AW807271
	454933	1245515_1
		BE141714 AW845993 AW845999

TABLE 10C

Play: Unique number corresponding to an Eos probe set

Ref: Sequence source. The 1-687 numbers in this column are Genbank Identifier (GI) numbers. "Dunham I. et al." refers to the publication entitled "The DNA sequence of human chromosome 22" Dunham, et al. (1999) *Nature* 402:483-495

Strand: Indicates DNA strand from which exons were predicted

NL_position: Indicates nucleotide positions of predicted exons

Play	Ref	Strand	NL_position
400534	6981826	Minus	27937-279292
400666	8118456	Plus	17992-18115,20297-20456
400903	2911732	Plus	59113-59228
401197	8719305	Plus	176341-176452
401480	7321503	Plus	166120-166347,166451-166557,169651-169832
401508	7534110	Minus	110779-110933
401517	7677912	Plus	25278-26170
401644	8576138	Plus	82655-83559
401714	8715702	Plus	96484-96681
402077	8117414	Plus	65014-65155
402222	9598105	Plus	3261-3634,3639-4269
402408	9795229	Minus	110326-110491
402820	6459853	Minus	82274-82443
402829	8918414	Plus	101532-101852,102006-102263
403381	9438267	Minus	25009-26178
403515	7655757	Minus	173358-176553
403729	7543752	Minus	37682-37909
403864	7709019	Minus	51753-51850,72290-79445
404108	8247074	Minus	63603-64942
404232	8218845	Minus	71800-71955
404552	7243881	Plus	19854-20010
404557	7249169	Minus	101320-101501
404599	8705107	Plus	110443-110733
404915	73411766	Minus	100915-110187
404996	6007830	Plus	37999-38145,38852-38998,39727-39872,40557-40674,42351-42450
405095	8072599	Plus	138877-139056
405089	9117732	Plus	68880-69374
406117	9142932	Plus	54304-54594

Table 11A lists about 222 genes up-regulated in ovarian cancer compared to normal adult tissues that are likely to encode extracellular or cell-surface proteins. These were selected as for Table 10A, except that the ratio was greater than or equal to 2.0, and the predicted protein contained a structural domain that is indicative of extracellular localization (e.g., Ig, IgG, IgM, IgA, IgD, IgE, IgG, IgM domains, signal sequences, transmembrane domains). Predicted protein domains are noted.

TABLE 11A: ABOUT 222 UP-REGULATED GENES ENCODING EXTRACELLULAR/CELL SURFACE PROTEINS, OVARIAN CANCER VERSUS NORMAL ADULT TISSUES

Play: Primkey

Ex. Acc: Exon/Accession

UG ID: UniGene ID

Title: UniGene title

PFAM domain: predicted protein structural domains

ratio: ratio tumor vs normal tissue

Play	Ex. Acc	UG ID	Title	PFAM domain	ratio
400292	AA250737	Hs.72472	BM-PR-4; bone morphogenetic pro	plateau,Activin_rcp	30.0
400289	X07820	Hs.2258	Matrix metalloproteinase 10 (Strom	SS,heparin,Peptidase	25.2
427858	C11152	Hs.179723	collagen, type X, alpha 1 (Schmidt m	C1q,Collagen	22.0
435952	AB016305	Hs.5378	spondin 1, (I-spondin) extracellular m	bsp_1	19.7
428579	NM_005756	Hs.184942	G protein-coupled receptor 64	TM	17.4
443646	AA085198	Hs.296899	ESTs	TSNP,vcw,bsp_1,EGF	15.1
436209	AA050417	Hs.254020	ESTs, Moderately similar to unname	TM	14.1
418501	AA279490	Hs.86368	cathepsin	SS,cathepsin	13.8
428532	AF157328	Hs.184706	TSP-interacting protein	TM	13.6
427344	NM_000689	Hs.2142	5-hydroxytryptamine (serotonin) rec	TM,neur_chan	11.8
432677	NM_004482	Hs.278811	UDP-N-acetyl-alpha-D-galactosamin	TM,Glycos_transf_2,R	11.0
464587	NM_015902	Hs.278428	progenin induced protein (CDS)	TM,HECT,af-UBR1	10.8
445537	U24567	Hs.12944	EGF-like domain, multiple 6	SS,MAM,EGF	8.9
409928	AL137163	Hs.57549	hypothetical protein dJ47384	TM,MSP_domain	8.8
407001	U12471	Hs.247954	Human thrombospondin-1 gene, par	TSNP,vcw,bsp_1,EGF	8.5
453370	AA076523	Hs.182556	ESTs, Moderately similar to transit	ABC_tran,ABC_member	8.4
400298	AA032279	Hs.51555	ESTs	STE4P	7.9
431725	X65724	Hs.2839	Norrie disease (pseudoglioma)	SS,Cys_invol	7.4
429509	AF002246	Hs.210863	cell adhesion molecule with homolo	TM,fn3	7.4
412170	D16532	Hs.37329	very low density lipoprotein recepto	TM,LDL_recept_LDL_rec	7.0
428554	AF100781	Hs.194678	WNT1 Inducible signaling pathway	SS,ICPBP,Cys_invol,bsp	7.4
418007	M13509	Hs.83169	Matrix metalloproteinase 1 (interStia	SS,heparin,Peptidase	7.2
424001	M57883	Hs.137476	KIAA1051 protein	Pept_M12B_propep,Rep	7.2
455985	AW131688	Hs.172792	ESTs, Weakly similar to hypothetical	TM	7.1
461412	A75485	Hs.145968	ESTs	Cu,hepato_C_term,cach	6.8
415138	C18356	Hs.78045	tissue factor pathway inhibitor 2 TFP	Kunitz,BPTL,G-gamma	6.1
438167	R28363	Hs.24286	ESTs	7tm_1	6.1
452097	AB022354	Hs.27916	ADAM-TS3 : a disintegrin-like and	Pept_M12B_propep,Rep	6.4
449048	Z15051	Hs.52202	similar to S66401 (cathe) glucose in	SS	6.4
425271	D49441	Hs.155881	mesothelin	SS	5.7
407945	X93208	Hs.606	ATPase, Cu++-transporting, alpha p	TME1-E2,ATPase,H	5.6
424620	AA101043	Hs.151254	kallitinin 7 (chymotryptic) stratum c	SS,lysin	5.5
423562	U79734	Hs.37286	huntingtin interacting protein 1	TM,HTL,LMWQ	5.4

413384	NM_000401	Ha.75334	exostoses (multiple) 2	TM	5.3
425154	NM_001851	Ha.154950	collagen, type DC, alpha 1	Collagen,TSPN	5.2
411945	AL033527	Ha.92137	v-myc avian myelocytomatous viral	TGF-beta,TGFb_propep	5.1
415538	A173381	Ha.72472	BMPR-1b, bone morphogenetic pro	pkinnase,Activin_rec	5.1
430018	AK001180	Ha.5999	hypothetical protein FLJ10298	TM	4.8
424539	U02911	Ha.150402	activin A receptor, type I	Activin_recep,pkinnase	4.8
450375	AA009647	Ha.8850	a disintegrin and metalloproteinase d	disintegrin,Reprolysin,P	4.7
451684	AF16751	Ha.26813	CD414	TM	4.6
400236	AA355627	Ha.139336	ATP-binding cassette, sub-family C	TM,ABC_tran,ABC_m	4.6
429597	NM_003816	Ha.2442	a disintegrin and metalloproteinase d	TM	4.5
400534	AP00541		predicted exons	TM,KRAB,zf-C2H2	4.5
425506	NM_003656	Ha.158205	basic leucine zipper nuclear factor 1	TM,ZIPper_carrier	4.5
453472	BC242870	Ha.75379	soluble carrier family 1 (gel high aff	TM,SDF	4.4
440535	W10287	Ha.25872	low density lipoprotein receptor-like	SS,LDL_recep,L_kid_recep	4.4
450228	AK001859	Ha.27555	hypothetical protein FLJ10957	Zn_carcOep,Propep_M	4.4
418693	A1705878	Ha.87409	thrombospondin 1	EGF,TSPN,sp_1,sp_3	4.3
410361	BC391804	Ha.52661	guanylate binding protein 1, interfer	TM,GSP	4.2
407872	AB033923	Ha.40735	fizzled (Drosophila) homolog 3	Fizzled,Fz,Tm_2	4.2
421502	AF111656	Ha.105039	soluble carrier family 34 (sodium pho	TM,Na_PL_cotrans	4.2
412494	AL133900	Ha.792	ADP-ribosylation factor domain pro	arfz4-B_box,zf-C3HC4	4.2
465095	NM_014179	Ha.145256	disintegrin protease	Reprolysin,disintegrin	4.0
431130	NM_009103	Ha.2719	epididymis-specific, whey-acidic pro	SS_wcp	4.0
407792	AJ077115	Ha.35384	putative secreted ligand homologous	SS	4.0
408829	NM_003042	Ha.48384	heparan sulfate (glucosamine) 3-O-s	TM	3.8
450981	AF081513	Ha.25195	endometrial bleeding associated fact	SS,TGF-beta,TGFb_pro	3.7
432712	AB015247	Ha.280301	cloned-C5-desaturase (Rungel ERK3)	TM,Sterol_desat	3.6
450447	AF212223	Ha.25010	hypothetical protein P15-2	TM,ANF_receptor,guan	3.6
414706	AW340125	Ha.76589	KIAA097 gene product	TM	3.6
417389	BE260564	Ha.82045	Midline (neurile growth-promoting	TM,PTH_MK	3.4
400656	W07620	Ha.2298	Mutic Metalloproteinase 10 (Strom	SS,hemopexin,Peptidase	3.5
406400	AA343625	Ha.104570	kallikrein 8 (neuropilin-1)	SS,hyalua	3.5
407864	AF063231	Ha.40539	chromosome 8 open reading frame 1	TM,FHA,BRCT	3.4
427222	X05659	Ha.289517	Homo sapiens cDNA: FLJ2621 fls,	EGF,kinase	3.4
445913	AA430650	Ha.16529	Transmembrane 4 superfamily memb	SS,transmembrane4	3.4
422611	AA156177	Ha.118722	lucosyltransferase 8 (alpha 1,6) fuc	SS	3.4
423161	AL049227	Ha.124776	Homo sapiens mRNA: cDNA DKF2	Cadherin,Cadherin_C_to	3.3
435102	AW69503	Ha.76917	F-box only protein 6	TM,Suez7	3.3
416530	U52601	Ha.79361	kallikrein 6 (lysosomal, zyme)	SS,TM,tyrosin	3.3
401197			predicted exons	arf,Elts	3.3
435625	AA721428	Ha.26145	Homo sapiens cDNA FLJ14127 fs,	TM	3.2
452443	BE247449	Ha.21082	hypothetical protein FLJ10525	TM	3.2
411393	AW074137	Ha.80771	B-factor, propeptide	SS,austh,tyrosin,mem,fb	3.2
407881	AW072003	Ha.40968	heparan sulfate (glucosamine) 3-O-s	SS	3.2
418835	AA555499	Ha.161712	ESTs	pkinnase,Activin_rec	3.2
409178	BE383046	Ha.50915	kallikrein 5	SS,tyrosin	3.1
421987	AL131511	Ha.286131	COG-101 protein	TM	3.1
447072	D61994	Ha.17279	tyrosylprotein sulfotransferase 1	SS	3.1
426514	BE016533	Ha.301122	bone morphogenetic protein 7 (osteo	SS,TGFb_propeptide,T	3.1
448133	AA723157	Ha.73769	folate receptor 1 (adult)	TM	3.1
456687	K51128	Ha.272620	pregnancy specific beta-1-glycoprot	SS,Peptidase_M10,hem	3.1
456844	AA261555	Ha.152581	ODP-diacylglycerol synthase (phosph	TM,CytochromeP450	3.0
414725	AA769791	Ha.120355	Homo sapiens cDNA FLJ13148 fls,	SPRY,Tm_1	3.0
407785	AW027265	Ha.38279	ESTs	Sema3	3.0
427738	NM_000318	Ha.180612	peroxisomal membrane protein 3 (35	TM,zf-C3HC4	3.0
452431	U88878	Ha.29499	toll-like receptor 3	TM,TIR,LRRC7	3.0
453920	AL133148	Ha.35952	CD4 (complement)	toll_recep,L,tyrosin,SRC	3.0
453331	AA246655	Ha.8955	ESTs	disintegrin,Reprolysin,P	3.0
425776	U25128	Ha.159499	parathyroid hormone receptor 2	TM,Tm_2	3.0
428428	AL037544	Ha.184298	cyclin-dependent kinase 7 (homolog	TM,kinase	3.0
407910	AA550274	Ha.41266	fibronectin leucine rich transmembr	TM,LRRC7,LRRCNT,LR	2.9
400550	AF123650	Ha.44532	disintegrin	TM,ubiquitin,Tm_3,AN	2.9
407763	AW595872	Ha.172028	a disintegrin and metalloproteinase d	disintegrin,Reprolysin	2.9
420757	X78592	Ha.99915	androgen receptor (dihydrotestoster	TM,Androgen_recep,ho	2.9
424405	D54120	Ha.146409	wingless-type MMTV integrin sil	cadherin,Cadherin_C_to	2.9
428549	AA350564	Ha.220929	ESTs, Moderately similar to ADF-4	arf	2.9
419452	U33335	Ha.90572	PTK7 protein tyrosine kinase 7	TM,phkinase,Jb	2.9
452281	T33500	Ha.28792	ESTs	TGFb_propeptide,TGF-	2.9
420440	NM_002407	Ha.97644	mannaglobin 2	SS,Ubiquitin	2.9
418848	AJ520961	Ha.13465	ESTs	pkinnase,Activin_rec	2.9
421991	NM_014918	Ha.110488	KIAA0990 protein	SS	2.9
433190	ME2691	Ha.3210	renin	SS,asp	2.9
424538	NM_005095	Ha.150390	zinc finger protein 262	TM	2.8
433002	AF048720	Ha.279506	cyclin T1	SS	2.8
444542	NM_014398	Ha.10887	similar to lysosome-associated mem	TM,Lamp	2.8
430598	AK001764	Ha.247112	hypothetical protein FLJ10902	TM	2.8
428450	NM_014791	Ha.164339	KIAA0175 gene product	TM,kinase,KAI	2.8
450711	AL133661	Ha.24563	hypothetical protein DKFZp434C03	TM	2.8
423554	MS0516	Ha.1574	glutamine-fructose-6-phosphate tran	TM,GATase_2,SIS	2.8
430016	NM_004738	Ha.227555	xenotropic and polytropic retrovirs	TM	2.8
417865	AW067903	Ha.82772	collagen, type XI, alpha 1	Collagen,COLFI,TSPN	2.8
424854	BS5528	Ha.153638	nonproteolitic B	SS,UBX	2.8
430551	AA361894	Ha.105167	kinasin protein 9 gene	SS	2.7
414853	U31116	Ha.77501	sarcophagan, beta (43kD dystrophin-	TM	2.7
448595	AB014544	Ha.21572	KIAA0544 gene product	TM,LRRC7,LRRC	2.7

	452835	AK001269	He.30738	ESTs	TM	2.7
	4603019	AA834626	He.66718	RAD54 (S.cerevisiae)-like	SS,Anf1_proliferat	2.7
	420281	AB23893	He.191533	ESTs	Cafoxn_8lux	2.7
	434815	AF155582	He.46744	core 1 UDP-galactose 4-epimerase	SS	2.6
5	432201	AF1558613	He.136567	TMPRSS3 mRNA for serine protease	trefol1brypin	2.6
	430450	BZ3553	He.241489	hypothetical protein	SS	2.6
	448402	BE244226	He.21054	RAS1, member RAS oncogene fam	nc-araf	2.6
	421802	BE251458	He.105408	CG-76 protein	TM	2.6
	452355	NS4926	He.25202	G protein-coupled receptor 34	TM,7m_1	2.6
10	417742	R64719	He.26312	gbc.ETSD2111 WATM1 Homo sapie	ank,death,RHD,TIG	2.6
	451346	NM_005338	He.26312	glutamate aminopeptidase on chromosome 1	TM,lg,LRAL,PRNT,LR	2.6
	431447	AF081454	He.94856	platelet derived growth factor C	TM,PDGF_CUB	2.6
	420079	NM_014051	He.94856	PDGF1 protein	SS,TM	2.6
	419918	X80700	He.93728	pre-B-cell leukemia transcription fac	homocobox,lg,Acyltransf	2.5
15	423250	NM_005865	He.214740	protease, serine, 16 (thymus)	SS	2.5
	406871	A1126547	He.263754	mit proto-oncogene (protophyte) gro	phnase,Sema,Plasid,re	2.5
	417412	X16896	He.82112	Interleukin 1 receptor, type 1	SS,TIR,lg	2.5
	422530	AW972300	He.118110	bone marrow stromal cell antigen 2	TM	2.5
	433929	AU75459	He.27379	ESTs	EGF,ML_recep,Lalid,re	2.5
20	433552	AF118838	He.9599	soluble carrier family 25, member 13	TM,mlto_scar	2.5
	414386	X00442	He.75990	haptoalbumin	sush1,lypsin	2.5
	417576	AA339449	He.82285	phosphoribosylglycinamide formyltr	AIRS,formyl_transf,GA	2.5
	449207	AL044222	He.23255	nucleoside 1550D	SS	2.5
	415107	AA173846	He.73015	antigen identified by monoclonal ant	TM,lg	2.4
25	421750	X000768	He.107872	hypothetical protein FLJ20761	TM,PH	2.4
	414812	XZ7255	He.77367	monokine induced by gamma Interfe	SS,IL8	2.4
	406137	R42764	He.3248	MS (E. coli) homolog 6	TM,MSIS_C,MS_N,P	2.4
	450710	AW653081	He.18627	ESTs, Weakly similar to G01447 GP	TM	2.4
	430291	AW660345	He.238125	OCI-43 protein	TM	2.4
30	425184	BE278288	He.155048	Lutheran blood group (Aubergier b a	lg	2.4
	451418	BE387190	He.26369	ESTs	TM	2.4
	412277	BE778288	He.73799	guanine nucleotide binding protein (c	TM,lg-alpha	2.4
	413719	BE435580	He.75498	small inducible cytokine subfamily A	SS,IL8	2.4
35	451806	NM_003729	He.27076	RNA 3-terminal phosphatase	TM,RCCT	2.4
	416224	NM_002902	He.79098	reticulocalbin 2, EF-hand calcium bi	SS,ehand	2.3
	452268	NM_003512	He.26789	RZA histone family, member L	histone,CGRP,J44	2.3
	451668	Z43498	He.26789	ASPC (acidic secreted protein) in ca	SS,TM	2.3
	400880	M84349	He.119653	CD59 antigen	SS,UPAR,LY6	2.3
40	421340	F07783	He.1369	decay accelerating factor for comple	SS,sash1	2.3
	433966	AUS11750	He.283437	HTGCS protein	SS	2.3
	430337	AW500305	He.8906	synaptotagmin 7	TM,Synaptin	2.3
	440516	S42303	He.161	cadherin 2, type 1, N-cadherin (neur	RHN,Cadherin,Cadherin	2.3
	404877	A334145	He.18048	melanoma antigen MAGE-10	TM,MAGE	2.3
45	440704	A63241	He.162	insulin-like growth factor binding pr	SS,hyroglycolin_1,IGF	2.3
	437552	D63209	He.5944	soluble carrier family 11 (proton-cou	TM	2.3
	418624	AT734080	He.104211	ESTs	Sema,lg	2.2
	410434	AF051152	He.63668	tol-like receptor 2	SS,TIR,LRCT,LR	2.2
	424687	J05070	He.151738	matrix metalloproteinase 9 (matelina	SS,M2,homoprotin,Pepl	2.2
50	431457	NM_012211	He.255297	integrin, alpha 11	TM,FG-GAP,wa	2.2
	407907	AT752235	He.41270	procollagen-lysine, 2-oxoglutarate 5	SS,Lysyl_hydro	2.2
	400889	AF200303	He.125300	Homo sapiens tripartite motif protein	SPRY7,7m_1	2.2
	403003	AA242768	He.79136	Human breast cancer, estrogen regul	SS,TA	2.2
	411789	AF245505	He.72157	Homo sapiens mRNA; cDNA DKFZ	lg,LRCT	2.2
55	414809	AI434699	He.77356	transferrin receptor (p80, CD71)	TM,PA,Ribosomal_S2	2.2
	401131	NM_001651	He.258023	Homo sapiens aquaporin 5 (AQP5)	TM,MP	2.2
	402077	Y03261	He.2290	Human mRNA for ribophorin 1	TM	2.1
	409317	U20165	He.53250	bone morphogenetic protein recepto	TM,kinase	2.1
	409956	AW103354	He.727	H.sapiens actin beta-A subunit (ex	TGF-beta,TGFb_prop	2.1
	451253	H48209	He.26126	claudin 10	TM,MP22_Claudin	2.1
60	428638	AF116882	He.211577	Kinesin 1 (kinesin receptor)	TM	2.1
	409267	NM_012453	He.52515	transducin (beta)-like 2	TM,WD40	2.1
	418414	J04977	He.84981	X-ray repair complementing defectiv	SS	2.1
	449857	AB037784	He.22541	ESTs	TM	2.1
	417666	AA348091	He.82380	menage a trois 1 (CAK assembly fac	zf-C3HC4	2.1
65	428485	NM_002950	He.2280	ribophorin 1	TM	2.1
	445798	NM_012421	He.13321	rearranged L-myc fusion sequence	TM,zf-C2H2	2.1
	430057	AWAS1503	He.2534	bone morphogenetic protein recepto	TM,Activin_recep,kinase	2.1
	425189	H1652	He.22541	glycylglycyl-2607.1 Source: infant brain	Res,GEP,PH,ubiquitogen	2.1
70	413063	AL035737	He.75184	chitinase 3-like 1 (cartilage glycopro	SS,Glyco_hydro_18	2.1
	421343	BE284444	He.283685	hypothetical protein FLJ20396	TM	2.1
	426527	AF116512	He.267007	ESTs	TM	2.1
	426261	AW922245	He.116870	peroxisomal fatty-acylated protein	E1-E2_ATPase,Cation	2.1
	431636	NM_000916	He.2820	oxylodan receptor	TM,7m_1	2.1
75	455546	AF080321	He.203845	ESTs, Weakly similar to TWK-rela	TM	2.1
	421685	AF169723	He.186718	calcium transport ATPase ATP2C1	TM,E1-E2_ATPase,ly	2.1
	424029	AF071202	He.135335	ATP-binding cassette sub-family C	TM,ABC_tran,ABC_m	2.1
	424800	AL035598	He.153203	MyoD family inhibitor	TM	2.1
	410007	AW950887	He.57813	zinc ribbon domain containing 1	TRIS	2.1
80	436135	D53530	He.5057	carboxypeptidase D	SS,Zn_carboxypept	2.1
	420533	NM_014581	He.95526	oncogene-binding protein 28	TM,pocabin	2.1
	420162	BE378432	He.95577	cyclin-dependent kinase 4	phnase,ank,ArtGap,PH	2.1
	426156	BE244537	He.167382	natriuretic peptide receptor Aiguany	TM,ANF_receptor,guan	2.1
	441271	AF151073	He.8645	hypothetical protein	TM	2.0
	411872	AW327356	He.90918	chromosome 11 open reading frame	TM	2.0

427601	AW979155	Hs.234433	hypothetical protein PRO1068	TMaa_trans	2.0
430268	AK006737	Hs.237480	hypothetical protein FLJ20730	TM	2.0
431183	NM_006555	Hs.255096	KDEL (Lys-Asp-Glu-Leu) endoplasmic reticulum protein 18	TM,ER_lumen_recept	2.0
431846	BE019924	Hs.271580	Unoplain 18	TM,transmembrane4	2.0
440410	U02478	Hs.100459	Human AF-6 mRNA	TAFRA,CDL,PDZ,FHA	2.0
435840	AF220053	Hs.54560	uncharacterized hematopoietic stem/	TM,SET,zf,C10C,PHD	2.0
447906	AL050062	Hs.19599	DKFZP566K023 protein	SS	2.0
412666	AL080116	Hs.74420	origin recognition complex, subunit	TM	2.0
417181	L10123	Hs.1071	surfactant protein A binding protein	TM	2.0
423945	AA410843	Hs.72472	BMPRII; bone morphogenetic pro	TM,pkinase,Activin_re	2.0
411773	NM_005799	Hs.72026	protease, sorfin, 21 (testis)	SS,hyprin	2.0
448350	L14561	Hs.78545	Homo sapiens clone 24411 mRNA s	TM,EF-E2_ATPase,Hy	2.0
401093	AF955244	Hs.121520	HYPOTHETICAL 16.4 kDa PROTE	TM,LR,CT	2.0
415664	NM_024939	Hs.78550	DEAD (Asp-Glu-His-Asp) box	DEAD,decase,C,SPRY	2.0
448165	NM_005591	Hs.203279	melotic recombination (S. cerevisiae	DNA_repair,Glyco,tran	2.0
416391	AB78927	Hs.79284	mesoderm specific transcript (mouse	TM,abhydrolase	2.0
422926	NM_016102	Hs.121748	ring finger protein 16	SPRY,zf-C5HC,zf-B_	2.0
440849	AJ070617	Hs.16251	cleavage and polyadenylation specifi	TM	2.0
427617	DA2053	Hs.179825	RAN binding protein 2-like 1	TM,Ran_BP1,zf-RanBP	2.0
411678	AB071114	Hs.71465	squalene epoxidase	TM,Monooxygenase	2.0
432554	AF479813	Hs.278411	NCK-associated protein 1	TM	2.0

TABLE 11B:

Pkey: Unique Eos probe/Identifier number

CAT number: Gene cluster number

Accession: Genbank accession numbers

Pkey	CAT Number	Accession
417742	1696282_1	R84719 244680 R12451
425189	247825_1	H16822 R17321 A331959

TABLE 11C:

Pkey: Unique number corresponding to an Eos probe/Identifier

Ref: Sequence source. The 7 columns are Genbank Identifier (G) numbers. "Dunham I. et al." refers to the publication entitled "The DNA sequence of human chromosome 22" Dunham, et al. (1999) Nature 402:489-495

Strand: Indicates DNA strand from which exons were predicted

NL_position: Indicates nucleotide positions of predicted exons

Pkey	Ref	Strand	NL_position
400534	6981826	Minus	278637-278292
401197	9719705	Plus	176341-176452

Table 12A lists about 57 genes up-regulated in ovarian cancer compared to normal adult tissues that are likely to encode either enzymes or proteins amenable to modulation by small molecules. Those were selected as for Table 10A, except that the ratio was greater than or equal to 2.0, and the predicted protein contained a structural domain that is indicative of enzymatic function or of being modulated by small molecules (e.g., kinase, phosphatase, isomerase, transporter). Predicted protein domains are noted.

TABLE 12A: ABOUT 57 UP-REGULATED GENES ENCODING EXTRACELLULAR/CELL SURFACE PROTEINS, OVARIAN CANCER VERSUS NORMAL ADULT TISSUES

Pkey: Pkeykey

Ex. Accn: Exon/Alternative Accession

UG ID: UniGene ID

Title: UniGene title

PFAM domains: predicted structural domains

ratio: ratio tumor vs. normal

Pkey	Ex. Accn	UG ID	Title	PFAM domains	ratio
402092	AA20737	Hs.72472	BMPRII; bone morphogenetic pro	pkinase,Activin_recp	30.0
402098	X07620	Hs.2258	Matrix Metalloproteinase 10 (Strom	SS_Peptidease_M10	25.2
426427	M66569	Hs.169840	TTK protein kinase	pkinase	18.7
424905	NM_002497	Hs.153704	NIMA (never in mitosis gene a)-rela	pkinase	16.2
433159	AB035638	Hs.150567	kinase-like protein 2	kinase	11.5
463370	AB076237	Hs.182566	ESTs, Moderately similar to translat	ABC_tran	8.4
418007	M13309	Hs.83159	Matrix metalloproteinase 1 (Intersia	SS_Peptidease_M10	7.2
425465	L18594	Hs.1904	protein kinase C, beta	SH_Sn_pkinase_C	6.1
409305	NM_005153	Hs.54569	NCK adaptor protein 1	SH2,SH3	5.2
415529	AF230681	Hs.72472	BMPRII; bone morphogenetic pro	pkinase,Activin_recp	6.1
424539	L02911	Hs.150402	activin A receptor, type I	Activin_recp,pkinase	4.8
400296	AA305627	Hs.135336	ATP-binding cassette; sub-family C	TM,ABC_tran	4.6
431869	NM_001173	Hs.267631	Homo sapiens cDNA FLJ12552 fa,	RhoGAP,PPase	3.9
435660	BE056447	Hs.74490	hypothetical protein FLJ12820	C2,PL-PLC-V,PI-PLC-X	3.8
450447	AF212223	Hs.25010	hypothetical protein P15-2	ANF_receptor,pkinase	3.6
400666	X07620	Hs.2258	Matrix Metalloproteinase 10 (Strom	SS_Peptidease_M10	3.5
452822	X85689	Hs.268617	Homo sapiens cDNA: FLJ22621 fa,	EGF,fn3,pkinase	3.4
416330	U52801	Hs.73581	kinase; 6 (neurokinin, zyma)	SS,TM,hyprin	3.3
411393	AW797437	Hs.69771	B-factor, propeptin	SS,sushi,hyprin,wva,fn3,	3.2
444755	AA431791	Hs.183001	ESTs	AAA	3.2
418836	AB55498	Hs.161712	ESTs	pkinase,Activin_recp	3.2
420178	BE303548	Hs.52915	kalirin 5	SS,hyprin	3.1
406887	M31126	Hs.272620	pregnancy specific beta-1-glycoprot	SS,Pepidase_M10, jg	3.1
453920	AI133148	Hs.36902	I factor (complement)	tdl_recept_a,hyprin,SRCR	3.0
404553	AA923729	Hs.26222	0	pkinase	2.9
419462	U33535	Hs.60572	PTK7 protein tyrosine kinase 7	pkinase,tyr	2.9
418848	AB02961	Hs.193465	ESTs	pkinase,Activin_recp	2.9
428450	NM_014791	Hs.184339	KIA0175 gene product	TM,pkinase,KAT1	2.8

401323	AL158037		predicted exon	lactamase_B	2.7
444798	BE242144	Hs.12013	ATP-binding cassette, sub-family E	SH3,phkinase,ABC_tran	2.7
432201	AJ388613	Hs.135857	TMPRSS3a mRNA for serine protease	trifol, trypsin	2.8
448402	BE244228	Hs.21094	RAB18, member RAS oncogene fam	rac, raf	2.6
405671	AA128447	Hs.285764	met proto-oncogene (hepatocytic pro	phkinase, sema	2.5
453448	AL033710	Hs.209527	EST6	CNH,phkinase	2.5
414388	X00442	Hs.75990	haptoprotein	sush, trypsin	2.5
421270	H98337	Hs.108146	ESTs	RhoGAP	2.4
414695	BE439915	Hs.78913	proteasome (prosome, macropain) su	prosome	2.4
431341	AA307211	Hs.261631	proteasome (prosome, macropain) su	prosome	2.4
424085	NM_002914	Hs.138226	replication factor C (activator 1) 2 (4	AAA,Viral_helicase1	2.2
424687	J05070	Hs.151738	matrix metalloproteinase 9 (gelatin	SS,ln2, Peptidase_M10	2.2
416517	AA175387	Hs.108859	proteasome (prosome, macropain) 28	AAA	2.1
417801	NM_014735	Hs.82292	KIAA0215 gene product	PHD	2.1
400509	M57639	Hs.155585	receptor tyrosine kinase-like orphan	pro_isomerase	2.1
430507	AW453003	Hs.2534	bone morphogenetic protein recepto	Activ,uncsp,phkinase	2.1
421841	AA091197	Hs.108859	KIAA0238 protein	TPR,phkinase	2.1
453078	AF053551	Hs.31584	metaxin 2	pro_isomerase	2.1
424099	AF071202	Hs.139336	ATP-binding cassette, sub-family C,	TM,ABC_tran	2.1
411190	AA303542	Hs.89171	protein kinase C- η 2	phkinase,phkinase_C,HR1	2.1
407740	AA235547	Hs.82665	ESTs	PAF1	2.1
420162	BE378432	Hs.95577	cyclin-dependent kinase 4	phkinase,ank,ArfGap_ras	2.1
420490	H65894	Hs.183041	ESTs	PI3Ka,PI3_P14_kinase	2.1
428156	BE244537	Hs.167382	neurotrophin peptide receptor A/guan	TM,ANF_receptor,phkinase	2.0
425945	AA104043	Hs.72472	BMPK- β , bone morphogenetic pro	TM,phkinase,Activ,resp	2.0
411773	NM_006799	Hs.72028	protease, serine, 21 (testisin)	SS,trypsin	2.0
472588	BE617527	Hs.180450	ribosomal protein S24	PI3Ka, P14_kinase	2.0
427617	AD20263	Hs.178825	RAN binding protein 2-like 1	TPR,pro_isomerase	2.0
453546	AF042385	Hs.33251	peptidylprolyl isomerase E (cycloph	pro_isomerase,rm	2.0

TABLE 12C:

Play: Unique number corresponding to an Eos probe set

Ref: Sequence source. The 7 digit column are Genbank Identifier (GI) numbers. "Dunham L et al." refers to the publication entitled "The DNA sequence of human chromosome 22" Dunham, et al. (1999) M02:489-495

Strand: Indicates DNA strand from which exons were predicted

NL_position: Indicates nucleotide positions of predicted exons

Play	Ref	Strand	NL_position
401323	9212516	Plus	213509-214450

Table 13A lists about 1066 genes up-regulated in ovarian cancer compared to normal ovaries. These were selected as for Table 10A, except that the ratio was greater than or equal to 10, and the denominator was the median value for various non-malignant ovary specimens.

TABLE 13A: About 1066 UP-REGULATED GENES, OVARIAN CANCER VERSUS NORMAL OVARY

Play: Primerkey

Ex_Accn: Exonplay Accession

UG ID: UniGene ID

Title: UniGene title

ratio: ration tumor vs. normal ovary

Play	Ex_Accn	UG ID	Title	ratio
437006	AW072527	Hs.69761	ESTs	109.2
446619	AJ076543	Hs.313	secreted phosphoprotein 1 (osteopontin, bone	107.8
422095	AJ688872	Hs.288986	ceruloplasmin (ferroxidase)	104.4
447111	AJ017574	Hs.17409	cysteine-rich protein 1 (fibrinectin)	88.3
431132	NM_005103	Hs.2719	epididymis-specific, whey-acidic protein type	82.8
431369	BE184465	Hs.251754	secretory leukocyte protease inhibitor (anti	81.9
413859	AW982356	Hs.8394	ESTs	73.9
446281	BE387753	Hs.14823	interleukin, gamma-inducible protein 30	72.7
426050	AF017337	Hs.165508	ET-4-like factor 3 (ets domain transcription f	68.1
411469	T09997	Hs.70327	cysteine-rich protein 2	66.6
429504	X99133	Hs.204238	lipocalin 2 (oncogene 24p3)	65.7
416971	R34657	Hs.80658	uncoupling protein 2 (mitochondrial, proton c	62.5
453273	AE026454	Hs.24743	hypothetical protein FLJ20171	62.5
446441	AK001782	Hs.15053	hypothetical protein	60.7
428758	AA433938	Hs.95502	Homo sapiens cDNA FLJ14303 fs, clone PLACE20	59.7
441408	Z45957	Hs.783	Homo sapiens cDNA FLJ10467 fs, clone NT2P18	57.8
441859	AW194364	Hs.128022	ESTs, Weakly similar to FIC1 MOUSE FIC1-PROT	56.1
448406	AW772298	Hs.21103	Homo sapiens mRNA; cDNA DKFZp564B076	55.7
414602	AW630088	Hs.76550	Homo sapiens mRNA; cDNA DKFZp564B1264	55.2
418058	AW671155	Hs.293502	ESTs, Weakly similar to prolyl 4-hydroxylase	54.8
438330	L22524	Hs.2285	myofibrin protein 7 (myofibrin, ucler)	53.4
412636	NM_004415	Hs.74316	desmoplakin (DPL, DPL1)	51.4
430634	AJ850551	Hs.26685	ESTs	50.7
439318	AW637046	Hs.6527	G protein-coupled receptor 56	50.7
417259	AW503836	Hs.81600	chondroitin sulfate proteoglycan 2 (versican)	50.6
407786	AA687536	Hs.39872	tetraspan 1	50.4
428636	N41720	Hs.172884	vesicle-associated membrane protein 8 (endob	49.7
417308	H69720	Hs.81892	KIAA0701 gene product	48.5
439876	AA124766	Hs.5337	locustaine dehydrogenase 2 (NAD(P)-), mitochond	48.4
439180	AJ33742	Hs.199567	v-crb- δ 2 avian erythroblastic leukemia viral	47.1
428289	M26301	Hs.2253	complement component 2	46.3
405484			0	46.1

	425371	D49441	Hs.155981	mesothelin	45.7
	403912			0	45.0
	443021	AA368546	Hs.8904	lg superfamily protein	44.6
	427697	T18997	Hs.180372	BCL2-bio 1	44.3
5	425227	AA321649	Hs.2248	INTERFERON-GAMMA INDUCED PROTEIN 0	44.0
	404678			0	43.9
	400289	X07820	Hs.2258	Matrix Metalloproteinase 10 (Stromelysin 2)	43.8
	451035	AJ076785	Hs.430	pistin 1 (I isoform)	43.8
10	440848	BE314680	Hs.7476	ATPase, H ⁺ -transporting, lysosomal (vacuolar)	42.8
	438278	BE336290	Hs.5097	synaptophysin 2	42.4
	413936	AF113576	Hs.75521	serine (or cysteine) proteinase inhibitor, cl	42.1
	420859	AW463397	Hs.100000	S100 calcium-binding protein A8 (calgranulin)	42.1
	429411	AW291464	Hs.10339	S100 calcium-binding protein A8 (calgranulin)	41.8
	422166	W72424	Hs.112405	S100 calcium-binding protein A9 (calgranulin)	41.5
15	412477	AA150864	Hs.790	microosomal glutathione S-transferase 1	40.7
	417130	AW275658	Hs.81258	S100 calcium-binding protein A4 (calcium prot	40.1
	424673	AA345051	Hs.294092	ESTs	39.7
	416530	U62801	Hs.79381	kallikrein 6 (neurokinin, zyme)	39.8
20	443182	T49951	Hs.9029	ESTs; Highly similar to KERATIN; TYPE I CYTO	39.5
	413719	BE435950	Hs.78498	small inducible cytokine subfamily A (Cys-Cys	39.3
	424687	JE5070	Hs.151738	matrix metalloproteinase 9 (matrilysin B, 95k	38.9
	413063	AL035737	Hs.75194	chitinase 3-like 1 (cartilage glycoprotein-39)	38.5
	429441	AJ224172	Hs.204096	lipophilin B (vitroglubulin family member), pro	38.1
	418526	BE019020	Hs.85838	solute carrier family 16 (monocarboxylic acid	37.9
25	415511	AJ732017	Hs.162362	ESTs	37.7
	409453	AB855116	Hs.95612	ESTs	37.7
	445537	AJ245071	Hs.12844	EGF-like domain; multiple 6	37.3
	442432	BE053989	Hs.38178	Homo sapiens cDNA: FLJ23456 fls, clone HS1116	37.3
	406243	Y00787	Hs.524	histidinef 16	37.3
30	419902	J05591	Hs.88803	mucin 1, transmembrane	36.7
	444172	BE147740	Hs.104558	ESTs	36.0
	412115	AK001763	Hs.73239	hypothetical protein FLJ10901	35.8
	426440	NM_002407	Hs.97644	mammaglobin 2	35.7
	414388	X00442	Hs.75990	haptoglobin 2	35.3
35	423225	AA852604	Hs.125359	Thy-1 cell surface antigen	35.1
	440596	H13032	Hs.103378	ESTs; Weakly similar to DRR1 (IL13 receptors)	35.0
	413278	BE053085	Hs.823	interferon-stimulated protein, 15 kDa	34.9
	418506	AA084248	Hs.85339	G protein-coupled receptor 39	34.8
	445919	T53519	Hs.290357	ESTs	34.7
40	416854	H40164	Hs.80296	Purkinje cell protein 4	34.4
	414186	U33446	Hs.75799	protease, serine 8 (procathepsin)	34.2
	443471	AA631382		gbrp85d01.s1 NC_CGAP_Thy1 Homo sapiens cDNA	33.9
	421937	AJ878857	Hs.109706	HN1 protein	33.9
45	449722	BE280074	Hs.23950	cydin b1	33.8
	420955			0	33.7
	452203	X57522	Hs.158164	ATP-binding cassette, sub-family B (MDR/TAP),	33.5
	411945	AL033527	Hs.92137	v-myc avian myelocytomatosis viral oncogene h	33.5
	425811	AL039104	Hs.153557	karyopherin alpha 2 (RAG cohort 1, importin a	33.4
50	428901	AK001330	Hs.48855	hypothetical protein FLJ10498	33.3
	438461	AW075485	Hs.286049	phosphoserine aminotransferase	33.3
	422963	M79141	Hs.13234	ESTs	33.3
	426158	NM_001982	Hs.199067	v-erb-b2 avian erythroblast leukemia viral	33.2
55	421826	AF118832	Hs.271411	beta-actin ATP-ase/ATPase enzyme 2	32.8
	421502	AF111856	Hs.105039	solute carrier family 34 (sodium phosphate),	32.5
	431211	M68849	Hs.5566	Homo sapiens connexin 26 (Cx26) mRNA, complete	32.5
	436552	NM_014038	Hs.5216	HSPC028 protein	32.5
	442533	AA151224	Hs.8372	ubiquitin-cytochrome c reductase (L-4K3) subu	32.5
	406460	AA343629	Hs.104670	kallikrein 8 (neuropilin-associated)	32.4
	450353	AJ244651	Hs.103296	ESTs	32.4
60	422158	L10343	Hs.112341	protease inhibitor 3, skin-derived (SKALP)	32.4
	434112	AV653729	Hs.1188	C23-44 protein; acidic dehydrogenase like ty	31.7
	441020	W79283	Hs.35962	ESTs	32.2
	432201	AS38613	Hs.135657	TMPPR353 mRNA for serine protease (ECHOS1) (T	32.0
	442425	M01669	Hs.1735	inhibin, beta B (activin AB beta polypeptide)	31.9
65	453309	AF111809	Hs.32940	defensin, beta 1	31.8
	408380	AF123050	Hs.44532	disubiquitin	31.7
	419329	AY007220	Hs.288598	S100-type calcium binding protein A14	31.6
	409231	AA446544	Hs.692	GAT33-2, epithelial glycoprotein (EGP) (KSA)	31.6
70	422861	D13566	Hs.136348	Homo sapiens mRNA for osteocalcin specific iso	31.2
	413840	AJ301558	Hs.298081	ESTs	30.8
	440943	AW082298	Hs.146161	ESTs; Weakly similar to KIAA0859 protein (Hs	30.8
	419329	AA468163	Hs.184598	Homo sapiens cDNA: FLJ23241 fls, clone COL013	30.4
	410132	NM_003480	Hs.56862	Microfilament-associated glycoprotein-2	30.1
	418203	X54942	Hs.83758	CDC28 protein kinase 2	30.1
75	417219	AW016510	Hs.129911	ESTs	30.0
	407862	BE548257	Hs.50724	Homo sapiens cDNA FLJ10934 fls, clone OVARC10	30.0
	431563	AJ027643	Hs.120912	ESTs	29.9
	431743	AW972642	Hs.293055	ESTs	29.8
	443295	AJ049783	Hs.241284	ESTs	29.7
80	413745	AW247252	Hs.75514	nucleoside phosphorylase	29.7
	441028	AJ333660	Hs.17558	ESTs	29.6
	442315	AA173992	Hs.7956	ESTs	29.6
	452838	U63011	Hs.30743	Preferentially expressed antigen in melanoma	29.5
	428479	Y00272	Hs.184572	cell division cycle 2, G1 to S and G2 to M	29.5

	432280	BE440142	Has.2943	signal recognition particle 19kD	29.4
	420158	AI791505	Has.95549	hypothetical protein	29.3
	445033	AV852462	Has.155145	ESTs	29.2
5	452367	U71207	Has.25279	eyes absent (Drosophila) homolog 2	29.1
	432706	NM_013230	Has.286124	CD24	29.0
	422163	AF027208	Has.297332	prominin (mouse)-like 1	28.7
	447035	NM_004753	Has.17144	short-chain dehydrogenase/reductase 1	28.6
	443968	BE241880	Has.10025	calnexin C	28.2
	422356	BE545072	Has.122579	ESTs	28.1
10	450377	AB033091	Has.24936	ESTs	28.0
	447471	AF039443	Has.18676	apertury (Drosophila) homolog 2	27.8
	444725	AV852092	Has.224174	Homo sapiens cDNA: FLJ13819 ts, clone THYRO10	27.7
	430250	NM_015929	Has.283021	chloride intracellular channel 5	27.7
15	416305	AU078628	Has.79187	coxsackie virus and adenovirus receptor	27.6
	418174	L20888	Has.83556	Rho GDP dissociation inhibitor (GDI) beta	27.5
	417233	W02205	Has.24356	small inducible cytokine subfamily 6 (Cys-X-C	27.4
	417866	AW067903	Has.82772	collagen, type XI, alpha 1	27.3
	427344	NM_000859	Has.2142	5-hydroxytryptamine (serotonin) receptor 3A	27.2
20	442993	BE018692	Has.44343	ESTs	27.0
	407137	T97307	Has.159057	v-erb-b2 avian erythroblastic leukemia viral	27.0
	418356	AJ561166	Has.7331	ESTs	27.0
	433662	W07162	Has.150826	CATX-8 protein	26.7
	422576	BE548955	Has.118554	CGI-83 protein	26.4
25	423271	W47225	Has.126256	interleukin 1, beta	26.3
	443715	AI563187	Has.9700	cyclin E1	26.1
	420186	NM_015925	Has.95997	liver-specific bHLH-Zip transcription factor	26.0
	419551	AW522256	Has.91011	anterior gradient 2 (Xenopus laevis) homolog	25.9
	443672	AA323362	Has.9567	hydroxylation (gamma), 2-oxoglutarate dehydroge	25.8
	415889	AW250318	Has.80395	mat, T-cell differentiation protein	25.3
30	408474	AA188823	Has.83196	Homo sapiens cDNA: FLJ23597 ts, clone LNG152	25.3
	411825	AK000334	Has.72289	hypothetical protein FLJ20327	25.3
	403081			0	25.2
	440594	AW445167	Has.126036	ESTs	25.1
	414586	AA308160	Has.76506	lymphocyte cytosolic protein 1 (L-plastin)	25.1
35	411925	AW014598	Has.73225	chromosome 11 open reading frame 13	25.1
	417869	AF076254	Has.82763	proteasome (prosome, macropain) subunit, beta	25.0
	433447	U29195	Has.3281	neuronal pentraxin II	25.0
	450858	C18458	Has.25597	elongation of very long chain fatty acids (FE	24.8
40	410819	BE312730	Has.65114	Keratin 18	24.8
	434094	AA305569	Has.238255	hypothetical protein PR02013	24.6
	421924	BE314514	Has.109606	coronin, actin-binding protein, 1A	24.6
	446859	AA94299	Has.18297	COX17 (yeast) homolog, cytochrome c oxidase a	24.6
	421451	AA291377	Has.50831	ESTs	24.3
45	433929	AF374499	Has.73739	ESTs	24.3
	438930	AW843633	Has.81256	S100 calcium-binding protein A4 (calcium prot	24.2
	444212	AW503976	Has.10649	basement membrane-induced gene	24.2
	441633	AW555544	Has.112242	ESTs	24.2
	441134	W22932	Has.7676	cellular retinoic acid-binding protein 1	24.2
50	417715	AW365987	Has.86366	ESTs	24.1
	405361	NM_005982	Has.54416	snrle oculis homeobox (Drosophila) homolog 1	24.1
	416934	U38765	Has.80705	dephosphore (NADH:ADP) (cytochrome b-5 reduc	24.1
	439125	U48418	Has.233950	serine protease inhibitor, Kunitz type 1	23.9
	434078	AW980709	Has.283683	EST	23.8
55	408669	AA93591	Has.78146	platelet/endothelial cell adhesion molecule (23.8
	439413	AI352522	Has.37810	ESTs	23.7
	448934	AI824046	Has.277523	glt3t4u29.x1 NC1_CGAP_U11 Homo sapiens cDNA	23.6
	420344	BE463721	Has.97101	Putative G protein-coupled receptor GPCR150	23.6
	431243	U46455	Has.252189	syndecan 4 (amphiglycan, ryudocan)	23.6
	417615	L24203	Has.82237	ataxia-telangiectasia group D-associated prot	23.5
60	451267	AU033994	Has.117865	soluble carrier family 17 (solotransp transpo	23.4
	450101	AW649969	Has.24385	Human hbc67 mRNA sequence	23.4
	419893	AA1133749	Has.92323	FKBP domain-containing ion transport regula	23.4
	431103	K57209	Has.44	phallophylin (heparin binding growth factor 8	23.4
	451110	AW55040	Has.301584	ESTs	23.3
65	428295	AW367283	Has.75839	zinc finger protein 6 (CMFX1)	23.2
	448517	AA082750	Has.42194	hypothetical protein FLJ25649 similar to sign	23.1
	424670	W61215	Has.116551	epithelial V-beta antigen 1	23.1
	417847	AS271588	Has.288512	Homo sapiens cDNA: FLJ22316 ts, clone HRC052	23.1
70	449027	AJ271216	Has.22380	dispeptidylpeptidase III	23.1
	424969	AW509228	Has.153598	creatine kinase, mitochondrial 1 (ubiquitous)	23.1
	433159	AW535659	Has.155687	kininins-tha protein 2	23.1
	411393	AW797437	Has.69771	B-factor, proferdin	23.0
	434815	AF155582	Has.46744	core1 UDP-galactose-4-epi/galactosamine-4-ep	22.8
75	427585	D31152	Has.179729	collagen, type X, alpha 1 (Schmid metaphysa	22.7
	445721	H82138	Has.13144	HSPC160 protein	22.6
	448268	BE386883	Has.85015	ESTs, Wntless similar to A4P, HUMAN INTESTINAL	22.6
	456844	AI264155	Has.152981	CDP-diacylglycerol synthase (phospholipidate cy	22.6
	456298	NM_001285	Has.301921	ESTs	22.5
80	418863	AI750878	Has.87460	isovalerylglycine 1	22.4
	414880	AW247395	Has.119140	eukaryotic translation initiation factor 5A	22.4
	401519			0	22.3
	402496			0	22.3
	420324	AF163474	Has.96744	DKFZP6850823 protein, Prostate androgen-regu	22.3
	403022			0	22.2

5	434042	AU89941	Ha.8254	hypothetical protein PRO0899	22.1
	419080	AW150835	Ha.18878	hypothetical protein FLJ21620	22.1
	406545	AB018249	Ha.10458	small inducible cytokine subfamily A (Cys-Cys	22.1
	447382	AW178120	Ha.9081	ESTs	22.0
	42547	AK039186	Ha.98376	ESTs	22.0
10	427954	JO3060	Ha.247551	metadax 1	22.0
	423161	AL049227	Ha.124776	Homo sapiens mRNA; cDNA DKFpZp564N1116 (from c	22.0
	423392	HI10233	Ha.2265	secretory granule, neuroendocrine protein 1	21.9
	444107	T46829	Ha.10319	UDP-glucosyltransferase 2 family, polypeptide	21.7
	144421	AS21130	Ha.65567	ESTs, Weakly similar to LAK-4p [H.sapiens]	21.5
15	412589	R28660	Ha.24305	ESTs	21.5
	446525	AW957069	Ha.211556	Homo sapiens cDNA: FLJ23378 fs, clone HEP162	21.5
	416847	LC3621	Ha.80261	enhancer of filamentation 1 (cas-like docking	21.5
	436972	AA284679	Ha.25640	claudin 3	21.5
	428698	AA852773	Ha.297939	ESTs; Weakly similar to neonogen (H.sapiens)	21.5
20	421340	F07763	Ha.1369	decay accelerating factor for complement (CD5	21.4
	413996	AA133935	Ha.173704	ESTs	21.4
	448243	AW369771	Ha.77496	ESTs	21.2
	421928	AF013758	Ha.105643	polyadenylate binding protein-interacting pro	21.3
	403399			0	21.3
25	435733	AB037734	Ha.4993	ESTs	21.3
	432629	AW960548	Ha.280659	ESTs	21.2
	449057	AB037784	Ha.22941	ESTs	21.2
	437675	AW954355	Ha.36529	ESTs	21.2
	401131			0	21.0
30	407207	T03651	Ha.179561	tubulin, beta polypeptide	20.8
	444783	AK021468	Ha.62180	ESTs	20.8
	428220	AA367019	Ha.241395	protease, serine, 1 (trypsin 1)	20.8
	447343	AA256941	Ha.238834	ESTs; Highly similar to LOW-DENSITY LIPOPROTE	20.7
	409041	AB033025	Ha.50081	KIAA1199 protein	20.6
35	421305	BE397354	Ha.289721	diphtheria toxin resistance protein required f	20.6
	411704	AI492220	Ha.71573	hypothetical protein FLJ10074	20.5
	417018	AI6528	Ha.80387	v-type 1 Yamanashi sarcoma viral related oncop	20.5
	432827	Z98128	Ha.3109	Rho GTPase activating protein 4	20.4
	401074	AA306007	Ha.59461	DKFZP434C245 protein	20.4
40	425184	BE278288	Ha.155048	Lutheran blood group (Aubenger b antigen incl	20.4
	432322	BE556143	Ha.26988	glutaredoxin (thioltransferase)	20.3
	447526	AL048753	Ha.340	small inducible cytokine A2 (monocyte chemo	20.2
	447335	BE617695	Ha.286192	protein phosphatase 1, regulatory (inhibitor)	20.2
	424887	A024880	Ha.135391	Nos6 (D, melanogaster)-like protein	20.1
45	410275	AE5658	Ha.51796	transcription factor AP-2 gamma (activating a	20.1
	429083	Y05397	Ha.227817	BCL2-related protein A1	20.0
	401073	AA706017	Ha.119944	ESTs	19.8
	433047	M08135	Ha.27946	methyltransferase	19.8
	419088	AS38323	Ha.77496	ESTs	19.7
50	403381			0	19.6
	409162	H25530	Ha.50868	solute carrier family 22 (organic cation tran	19.5
	426150	NM_003658	Ha.167219	Ber14-like homeobox 2	19.4
	449292	AJ990222	Ha.225457	ESTs	19.4
	425207	AB014551	Ha.155120	rhox4; guanine nucleotide exchange factor (G	19.4
55	419950	AK001645	Ha.93871	hypothetical protein FLJ10783	19.3
	436481	AA379597	Ha.5159	HSP150 protein similar to ubiquitin-conjugat	19.3
	449320	AF055009	Ha.13436	Homo sapiens clone 24747 mRNA sequence	19.2
	446608	N75217	Ha.257846	ESTs	19.1
	425222	M85430	Ha.155191	villin 2 (zeatin)	19.1
60	428309	M97815	Ha.183630	cellular retinoic acid-binding protein 2	19.1
	420005	AW271106	Ha.133294	ESTs	19.1
	435982	AB016305	Ha.5378	spondin 1, (I)-spondin extracellular matrix p	19.0
	407142	AA412535	Ha.55235	sphingomyelin phosphodiesterase 2, neutral ma	19.0
	430122	NM_013342	Ha.233765	TCF3 (E2A) fusion partner (in childhood Leuk	19.1
65	446293	AA020113	Ha.148722	ESTs	18.9
	444825	AW167613	Ha.248	mitogen-activated protein kinase kinase kinase	18.9
	407634	AW016569	Ha.301280	UOP-GlcNAc-betaGal beta-1,3-N-acetylglucosami	18.9
	445200	AA084460	Ha.12409	sonatinin	18.9
	418917	X02594	Ha.1217	adenosine deaminase	18.8
70	435777	AW419202	Ha.286192	protein phosphatase 1, regulatory (inhibitor)	18.8
	431049	AA846576	Ha.103267	hypothetical protein FLJ22548 similar to gene	18.7
	426427	M0669	Ha.108840	TKK protein kinase	18.7
	436281	AW411194	Ha.120951	ESTs	18.6
	429507	AA365752	Ha.155985	ESTs	18.6
75	459720			ESTs	18.6
	421242	AW161386	Ha.13661	ESTs, Weakly similar to DJ37E16.5 [H.sapiens]	18.5
	457115	AA642402	Ha.59142	ESTs	18.5
	451698	Z43948	Ha.26789	ASPC (acidic secreted protein in cartilage)A	18.4
	437142	AT91617	Ha.145068	ESTs	18.4
80	418588	BE367040	Ha.182476	ESTs, Weakly similar to similar to alpha/beta	18.3
	433058	NM_005466	Ha.268215	shalytransferase	18.3
	419854	AW654673	Ha.87838	Homo sapiens PAC clone RP6-1087M19 from Tq11	18.3
	444726	NM_006147	Ha.11801	interferon regulatory factor 6	18.3
	423011	NM_003083	Ha.298447	ESTs, Highly similar to ACAD_HUMAN ALPHA-2C-2	18.2
	451428	AW685384	Ha.111067	ESTs, Weakly similar to K02E10.2 [C.elegans]	18.2
	424895	AF011333	Ha.153563	lymphocyte antigen 75	18.2
	418742	AW451197	Ha.113418	ESTs	18.1
	446627	A973016	Ha.15725	ESTs; hypothetical protein SBB48	18.1

	424885	A1333771	Hs.82204	ESTs	18.1
	402926			0	18.0
	405452			0	18.0
5	42641	AA431367	Hs.234546	GNP2 for guanosine monophosphate reductase I	18.0
	454390	AB020713	Hs.56996	KIA0508 protein	18.0
	441784	AS22132	Hs.28700	ESTs	18.0
	418756	AW959311	Hs.87019	ESTs	17.9
	405621	AB70672	Hs.46638	chromosome 11 open reading frame 8, fetal br	17.9
10	425301	AW102614	Hs.12849	ESTs	17.8
	410442	X73424	Hs.63788	propionyl Coenzyme A carboxylase, beta polype	17.8
	456423	AW748920		glt:CM2-BT0306-17119-034-gt02-BT0306 Homo sapi	17.8
	422857	L32137	Hs.1564	cartilage oligomeric matrix protein	17.7
	448110	AA520537	Hs.181551	hypothetical protein FLJ20761	17.7
15	421750	AK003768	Hs.107872	0	17.7
	405224			0	17.7
	447630	AG60148	Hs.44855	lymphoid enhancer-binding factor 1	17.7
	407663	NM_015429	Hs.37482	CCP2 for nonhistidin coat protein zeta-COP	17.7
	427490	ZS5152	Hs.178625	mitogen-activated protein kinase 13	17.6
	414812	X72755	Hs.77367	monokine induced by gamma interferon	17.6
20	427651	AW194426	Hs.20726	ESTs	17.5
	420650	AA455705	Hs.41581	heat shock protein hsp70-related protein	17.5
	439841	AF038961	Hs.6710	mannose-6-phosphate utilization defect 1	17.5
	425810	AJ923627	Hs.31903	ESTs	17.5
	425387	J04088	Hs.156346	topoisomerase (DNA) II alpha (170kD)	17.5
25	456988	AW747800	Hs.55016	hypothetical protein FLJ21035	17.4
	428579	NM_005755	Hs.164542	G protein-coupled receptor 64	17.4
	410381	BE391804	Hs.62661	guanylate binding protein 1, interferon-induc	17.4
	442402	NM_000954	Hs.8272	prostaglandin D2 synthase (21kD, brain)	17.4
	411734	AW374954	Hs.71779	Homo sapiens DNA from chromosome 15, cosmid F	17.3
30	405295			0	17.3
	408340	AB037762	Hs.44288	myelin gene expression factor 2	17.3
	450586	AB77897	Hs.76940	RGC32 protein	17.3
	446571	AA456794	Hs.66915	ESTs, Weakly similar to 15.7kd protein [H.sap	17.2
	411829	AL117482	Hs.7978	KIF2P/43C131 protein	17.2
35	418004	U37519	Hs.87539	aldehyde dehydrogenase 8	17.2
	412078	XG9899	Hs.73149	paired box gene 8	17.2
	414658	XG5828	Hs.76781	ATP-binding cassette, sub-family D (ALD), mem	17.2
	418478	U38945	Hs.1174	cyclin-dependent kinase inhibitor 2A (retinoblo	17.0
	426805	AB032945	Hs.172506	myosin VB	17.0
40	410247	AF181721	Hs.61345	RU25	17.0
	434516	AB078114	Hs.70582	ESTs, Moderately similar to AF144056 1 apop	16.9
	426153	AW513143	Hs.98367	hypothetical protein FLJ22522 similar to SRY-	16.9
	417793	AW405434	Hs.82575	small nuclear ribonucleoprotein polypeptide B	16.9
	454163	AW773957		glt:CV0-BT0078-190859-005-E02 BT0078 Homo sapi	16.9
45	415402	AA154697	Hs.297889	ESTs	16.9
	420309	AW043637	Hs.21766	ESTs	16.9
	419201	M22324	Hs.1238	alanyl (membrane) aminopeptidase (aminopeptid	16.9
	444381	AL137597	Hs.11114	hypothetical protein dJ1181N3.1	16.9
50	457705	AW074668		glt:ST366757 IMAGE sequences, MAGM Homo sapi	16.8
	412723	AA648459	Hs.179912	ESTs	16.8
	435774	R88065	Hs.4992	tumor suppressing subtransferable candidate 1	16.8
	408753	A337162	Hs.47438	SH3 domain binding glutamate acid-rich protein	16.8
	447783	AF054178	Hs.19591	NADH dehydrogenase (ubiquinone) 1 alpha subco	16.8
55	418085	R40328	Hs.258822	ESTs	16.7
	452472	AW957300	Hs.294142	ESTs, Weakly similar to SP45_HUMAN SPLICEOSOM	16.7
	459112	BE243971	Hs.50649	quinone oxidoreductase homolog	16.7
	410250	AJ923777	Hs.51384	KIAA1445 protein	16.7
	446219	AJ287344	Hs.149827	ESTs	16.6
	429928	BE409838	Hs.194657	cathepsin 1, type 1, E-cadherin (epithelial)	16.6
60	425812	AA354128	Hs.245633	ESTs	16.6
	411742	AW047933	Hs.71819	eukaryotic translation initiation factor 4E b	16.6
	415076	NM_000857	Hs.77890	guanylate cyclase 1, soluble, beta 3	16.6
	416209	AA236776	Hs.79078	MAC2 (mitotic arrest deficient, yeast, homolog	16.6
	440657	BE176589	Hs.7337	hypothetical protein FLJ19336	16.6
65	430375	AW371048	Hs.53758	H4 histone family, member H	16.6
	419507	FS2557	Hs.51579	Homo sapiens clone 23783 mRNA sequence	16.6
	410328	BE080190	Hs.62275	CO-141 protein	16.5
	405426			0	16.5
	426336	AA340864	Hs.275562	claudin 7	16.5
70	434725	AK000795	Hs.4104	hypothetical protein	16.5
	414683	S78296	Hs.76888	intermedial neuronal intermediate filament pro	16.5
	425500	X78565	Hs.289114	hematuration (Bosaurus C. cytostatin)	16.5
	449444	AF290512	Hs.58251	Homo sapiens fibronin mRNA, partial cds	16.4
	400666			0	16.4
75	421536	BE250630	Hs.105509	CTL2 gene	16.4
	430632	AA150797	Hs.105278	ESTs	16.4
	418196	AT145649	Hs.26549	ESTs, Weakly similar to T00066 hypothetical p	16.4
	452323	W44355	Hs.292812	ESTs, Weakly similar to C43H8.1 [C.elegans]	16.4
	407699	AA825974	Hs.32646	Homo sapiens cDNA: FLJ21901 ts, clone HEP034	16.4
80	414617	AJ339520	Hs.20524	ESTs, Moderately similar to hexokinase 1 [H.s	16.3
	438024	AA454591	Hs.43566	protein tyrosine phosphatase type IVA, member	16.3
	452650	AW270150	Hs.254516	ESTs	16.3
	432906	BE265489	Hs.3123	lethal giant larvae (Drosophila) homolog 2	16.3
	424048			0	16.3

	408805	H69912	Ha. 48269	vaccinia related kinase 1	16.3
	447155	AA106065	Ha. 121557	ESTs, Weakly similar to AF251041 1 SGC32445 p 0	16.3
	405699			gblHuman intrastinal mucin mRNA, partial cds.	16.2
5	405853	M22408		growth factor receptor-bound protein 7 (GRB7)	16.2
	418629	HE247550	Ha. 86689	NIMA (never in mitosis gene a)-related kinase	16.2
	424905	NM_002497	Ha. 153704	ESTs, Highly similar to cdc Golgi-localized c	16.2
	424243	A949359	Ha. 301837	integrin, beta 4	16.1
	118462	BE001596	Ha. 85286	NADH dehydrogenase (ubiquinone) 1 beta subcom	16.1
10	457205	A025780	Ha. 198272	transglutaminase 1 (K) polypeptide epidermal t	16.1
	428188	M58447	Ha. 22	ESTs	16.1
	449845	AW971183	Ha. 60054	0	16.0
	408429			gbl00815.5eq.F Human fetal heart, Lambda ZAP	16.1
	447375	AJ091354		ESTs	16.1
15	448377	AM94514	Ha. 171380	inositol 1,4,5-bisphosphate 3-kinase A	16.0
	431156	NM_002220	Ha. 2722	CGI-25 protein	16.0
	450043	AA885699	Ha. 24332	0	16.0
	403121			0	15.9
	400214			ESTs	15.9
20	453262	R02436	Ha. 215725	neurogranin (protein kinase C substrate, RC2)	15.9
	451734	NM_005176	Ha. 26944	calcyon, D1 dopamine receptor-interacting pro	15.9
	416855	AA180763	Ha. 36733	Homo sapiens mRNA for KIAA1581 protein, parti	15.9
	424474	AA308883	Ha. 146800	ESTs	15.9
	423685	BE350494	Ha. 49753	ESTs	15.9
	428187	A087303	Ha. 285529	NAT1; nylamine N-acetyltransferase	15.9
25	456817	A023799	Ha. 153242	neuronal PAS domain protein 2	15.9
	425652	D50041	Ha. 153655	ras homolog gene family, member E	15.9
	421674	T10707	Ha. 295355	peroxisomal acyl-CoA biosynthase	15.9
	439999	AA115811	Ha. 6838	RAP1, GTPase activating protein 1	15.9
30	411351	M02819	Ha. 263476	KIAA0166 gene product	15.8
	413027	NM_002885	Ha. 75151	phosphoinositide-specific phospholipase C-beta	15.8
	453884	AA355925	Ha. 36232	ESTs	15.8
	407894	AJ278133	Ha. 41143	ESTs	15.8
	423168	AA316286	Ha. 125949	ESTs	15.8
35	414691	A088460	Ha. 55902	mitochondrial ribosomal protein L12	15.8
	421877	AW250380	Ha. 109059	0	15.8
	404780			0	15.8
	401192			ESTs	15.8
	447519	U48258	Ha. 23448	sorting nexin 8	15.7
40	434262	AF121858	Ha. 12169	claudin 10	15.7
	451253	H48239	Ha. 26126	ESTs	15.7
	439499	R08344	Ha. 14148	prostate differentiation factor; placental bo	15.7
	422424	A1185431	Ha. 116577	Homo sapiens cDNA FLJ10570 fs, clone NT2RP20	15.7
45	424834	AK001432	Ha. 153408	basic transcription element binding protein 1	15.7
	424562	A1202659	Ha. 150557	ESTs	15.7
	432427	BE114387	Ha. 47378	ESTs	15.6
	430696	AA531276	Ha. 59509	ESTs, highly similar to differentially expres	15.6
	437044	AL035864	Ha. 69517	killer cell lectin-like receptor F1	15.6
50	428237	AF175205	Ha. 183125	ESTs, Weakly similar to envelope protein p15	15.6
	440048	A4087461	Ha. 150469	glycine cleavage system protein H (aminomethy	15.6
	414922	D08723	Ha. 77631	estrogen-related receptor alpha	15.6
	422030	X51416	Ha. 110849	ESTs	15.5
	408716	A567809	Ha. 151714	6-phosphofructo-2-kinase/fructose-2,6-bisphos	15.5
55	410258	X52538	Ha. 738	ESTs, Highly similar to VAB1_HUMAN VACUOLAR A	15.5
	410630	M25609	Ha. 64173	tyrosine protein sulfotransferase 1	15.5
	447072	D61594	Ha. 17279	NADH dehydrogenase (ubiquinone) Fo-S protein	15.5
	409015	BE393387	Ha. 49767	ESTs	15.5
	447549	A0711108	Ha. 231265	ESTs	15.5
	449704	AK000733	Ha. 23500	GTPase activating protein	15.4
60	427337	Z46223	Ha. 176553	Fc fragment of IgG, low affinity IIb, recept	15.4
	421630	NM_001956	Ha. 1467	endothelin 2	15.4
	433018	A056970	Ha. 189881	ESTs	15.4
	422938	NM_001809	Ha. 1594	centromere protein A (17kD)	15.3
	407014	U38268		gblHuman cytochrome b pseudogene, partial cds	15.2
65	420311	AF090157	Ha. 199958	conserved helix-loop-helix ubiquitinase kinase	15.2
	431042	NM_003764	Ha. 271473	epithelial protein up-regulated in carcinoma,	15.2
	406907	Z25427		gblH.sapiens protein-serine/threonine kinase	15.2
	458495	A1202029	Ha. 148593	ESTs	15.2
	428551	AL137692	Ha. 38796	Homo sapiens mRNA; cDNA DKFZP434P182 (from cl	15.1
70	448443	AW167128	Ha. 231934	ESTs	15.1
	434646	A0851598	Ha. 268699	ESTs	15.1
	431538	AL137547	Ha. 292619	Homo sapiens mRNA; cDNA DKFZP434B1120 (from c	15.1
	435887	AA686433	Ha. 129461	ESTs	15.0
	420917	AW135745	Ha. 117330	ESTs	15.0
75	428575	M19584	Ha. 184929	serine (or cysteine) proteinase inhibitor, cl	15.0
	403482			0	15.0
	421499	AJ271438	Ha. 105022	Homo sapiens PAC clone RP4-701016 from Tq33-q	15.0
	401047			0	14.9
	417749	U09196	Ha. 82520	polymerase (DNA-directed), delta 4	14.9
80	416693	A1373204	Ha. 79531	Homo sapiens TTF-1 interacting peptide 20 mRN	14.9
	428474	BE023182	Ha. 184623	KIAA0965 protein	14.9
	428552	NM_002046	Ha. 23116	SRY (sex-determining region Y)-box 9 (campom	14.9
	430271	T06199	Ha. 237506	heat shock cognate 40	14.9
	414328	Z11666	Ha. 75900	acolinase 2, mitochondrial	14.9
	415314	N88802	Ha. 5422	glycoprotein M68	14.8

	453735	A066629	Hs.125073	ESTs	14.8
	424345	A0001380	Hs.145479	Homo sapiens cDNA FLJ10518 fs, clone NT2RP20	14.8
	423575	C18653	Hs.163443	ESTs	14.8
	435081	H49548	Hs.298984	ESTs	14.8
5	403485			0	14.8
	452114	N22687	Hs.8236	ESTs	14.8
	426559	A8001914	Hs.170414	paired basic amino acid cleaving system 4	14.8
	412859	AA250712	Hs.82407	Homo sapiens HSPC256 mRNA, partial cds	14.8
10	452101	T82298		ghy50712.1 <i>Stratiotes litor</i> [307224] Homo	14.7
	429505	AW967984	Hs.291612	ESTs	14.7
	426125	X87241	Hs.165994	FAT tumor suppressor (<i>Drosophila</i>) homolog	14.7
	433336	AF017986	Hs.31386	ESTs; Highly similar to FRUZZLED PROTEIN PRE	14.7
	428577	A0001484	Hs.194508	cyclin D2	14.7
15	429785	H82114	Hs.301769	ESTs	14.7
	402424			0	14.7
	424971	AA479005	Hs.154036	tumor suppressing subtransferrable candidate 3	14.7
	433637	NM_014158	Hs.279936	BRCA1 associated protein-1 (ubiquitin carboxy	14.6
	421670	BE207318	Hs.105674	HSPC1 associated protein-1 (ubiquitin carboxy	14.6
20	438598	A0805943	Hs.5723	Homo sapiens cDNA: FLJ23438 fs, clone HSI001	14.6
	453370	AA70523	Hs.182356	ESTs, Moderately similar to translation Init	14.6
	410561	BE540255	Hs.6594	Homo sapiens cDNA: FLJ22044 fs, clone HEP091	14.6
	402287			0	14.6
	419741	NM_007019	Hs.93002	ubiquitin carrier protein E2-C	14.6
	442047	AA974598	Hs.150324	ESTs	14.5
25	425582	C333659	Hs.185055	DIENE proteog	14.5
	440006	AK000517	Hs.6844	hypothetical protein FLJ20510	14.5
	406851	AA509784	Hs.180255	major histocompatibility complex, class II, D	14.5
	457316	AI223657	Hs.127254	ESTs	14.5
	429453	AL157530	Hs.97840	Homo sapiens mRNA; cDNA DKFZP434G015 (from cd	14.5
30	436406	AW105723	Hs.125346	ESTs	14.5
	420736	AI263022	Hs.82204	ESTs	14.5
	419743	AA408762	Hs.127478	ESTs	14.5
	429113	D23275	Hs.198384	Prostaglandin-endoperoxide synthase 2 (COX-2)	14.5
	450256	AA286887	Hs.241724	MFI-amplified sequences with leucine-rich tan	14.5
35	424906	AI566086	Hs.153716	Homo sapiens mRNA for Hmo33 protein, 3' untr	14.5
	427414	F11150	Hs.6547	Homo sapiens cDNA FLJ13088 fs, clone NT2RP30	14.4
	419839	U24577	Hs.33304	phospholipase A2, group VII (platelet-activat	14.4
	418738	AW388833	Hs.6582	solute carrier family 7, member 11	14.3
	429414	AI783656	Hs.202095	empty spiracles (<i>Drosophila</i>) homolog 2	14.3
40	424668	AA417181	Hs.120858	Homo sapiens cDNA FLJ13945 fs, clone Y79AA10	14.3
	408989	AA351668	Hs.49550	KAR4745 protein	14.3
	406788	AA911841	Hs.5184	TH1 <i>drosophila</i> homolog	14.3
	417861	AA334551	Hs.82767	sperm specific antigen 2	14.3
45	402104			0	14.3
	416358	R88849		ghy5m6s06.r1 Soames adult brain N2b4HBSS5 Hs	14.2
	405802			0	14.2
	448357	N20169	Hs.108923	ESTs	14.2
	444261	AA258958	Hs.10724	MDX023 protein	14.2
50	407846	AA425522	Hs.40483	Ctbp3/300-interacting transactivator, with Glu	14.2
	425163	D10040	Hs.154890	fatty-acid-Coenzyme A ligase, long-chain 2	14.1
	402520			0	14.1
	429537	NM_003618	Hs.2442	a disintegrin and metalloproteinase domain 9	14.1
	430044	AA454510	Hs.132812	EST cluster (not in UniGene)	14.1
55	429683	M68874	Hs.211587	Human phosphatidylcholine 2-acylhydrolase (cP	14.1
	427036	AA397625	Hs.163913	ESTs	14.1
	444391	BE387335	Hs.283713	ESTs	14.1
	432030	AW972655	Hs.292933	ESTs	14.0
	406778	H05273	Hs.101651	Homo sapiens mRNA; cDNA DKFZP434C107 (from d	14.0
60	404961	AW972195	Hs.284236	aldo-keto reductase family 7, member A3 (alfa	14.0
	452313	Y00486	Hs.28914	adenine phosphoribosyltransferase	14.0
	423355	H54726	Hs.29202	G protein-coupled receptor 34	14.0
	429942	AA336993	Hs.134335	ESTs	14.0
	403185			0	13.9
	442150	A3368158	Hs.128854	ESTs	13.9
65	439709	AA401433	Hs.6649	hypothetical protein FLJ20128	13.9
	455799	AC004923	Hs.135187	Homo sapiens clone CDABP0025 mRNA sequence	13.9
	427356	AW023482	Hs.97849	ESTs	13.9
	446582	A036164	Hs.225520	ESTs	13.9
	432025	BE407132	Hs.111288	hypothetical protein FLJ22512	13.8
70	427505	AA361562	Hs.118761	26S proteasome-associated pad1 homolog	13.8
	402965			0	13.8
	418601	AA279490	Hs.86368	calmagin	13.8
	438654	AA740151	Hs.130425	ESTs	13.8
	405024			0	13.8
75	453976	BE463830	Hs.163714	ESTs	13.8
	431921	N46465	Hs.58879	ESTs	13.8
	401725			0	13.8
	445496	AB007860	Hs.12802	development and differentiation enhancing fac	13.8
80	425007	AA456483	Hs.172061	phosphodiesterase 4D, cAMP-specific (dunce (D	13.7
	409463	AA50165	Hs.17296	ESTs	13.7
	430193	A026653	Hs.102928	Homo sapiens cDNA FLJ13479 fs, clone PLACE10	13.7
	458689	A037934	Hs.224978	ESTs	13.7
	426769	AA075596	Hs.172153	glutathione peroxidase 3 (plasma)	13.7
	416661	AA634543	Hs.79440	IGF-II mRNA-binding protein 3	13.7

	439901	N73885	Hs.124169	ESTs	13.7
	431374	BE258532	Hs.261871	CTP synthase	13.7
	432861	AJ339526	Hs.279593	HSPC171 protein	13.7
5	441172	A279652	Hs.132879	ESTs	13.7
	410001	AS041036	Hs.257771	kallikrein 11; serine protease (TLSP)	13.7
	430315	NM_004293	Hs.239147	guanine deaminase	13.6
	422769	AA535905	Hs.289112	CGI-43 protein	13.6
	402389			0	13.6
10	446977	X91809	Hs.22698	regulator of G-protein signalling 19	13.6
	459646			glut3L3-CT0220-150205-079-B02 CT0220 Homo sapi	13.6
	452972	M31732	Hs.31210	B-cell CLL/lymphoma 3	13.6
	431441	U81951	Hs.2794	sodium channel, nonvoltage-gated 1 alpha	13.6
	446555	AB020676	Hs.215493	KIA0269 protein	13.6
15	435365	AF111213	Hs.164062	putative Ras-interacting protein	13.6
	434699	AB463687	Hs.149425	Homo sapiens cDNA FLJ11980 fs, clone HEMDB10	13.6
	447238	AW451876	Hs.158564	ESTs	13.6
	437108	AA434054	Hs.80622	Homo sapiens cDNA: FLJ23442 fs, clone HSI009	13.6
	425749	AW026587	Hs.159448	surfeit 2	13.5
20	425154	NM_001851	Hs.154650	collagen, type IX, alpha 1	13.5
	413763	U17760	Hs.301103	Laminin, beta 3 (nicotin 125kD), kalinin (140	13.5
	419034	NM_002110	Hs.85955	hemopoietic cell kinase	13.5
	446391	H82028	Hs.230707	Homo sapiens cDNA: FLJ22457 fs, clone HRC099	13.5
	412754	AW160375	Hs.74565	amyloid beta (A4) precursor-like protein 1	13.5
25	407732	AW158839	Hs.87191	ESTs	13.5
	423329	AF054910	Hs.127111	Estin 2 (testicular)	13.5
	422627	BC336857	Hs.118787	transforming growth factor, beta-induced, 68k	13.4
	439536	AF088467	Hs.82224	glt-Homo sapiens full length insert cDNA clone	13.4
30	417605	AF006699	Hs.11929	regulator of G-protein signalling 3	13.4
	445861	BE253423	Hs.11929	single 11u-related molecule	13.4
	447350	AJ375572	Hs.172634	ESTs; HER4 (c-erb-B4)	13.4
	451807	W52654	Hs.27099	DKFZP564J0663 protein	13.4
	421615	Y11339	Hs.105352	GNAc alpha-2, 6-sialyltransferase 1, long f	13.4
35	422443	NM_014707	Hs.119753	Nistone deacetylase 7b	13.4
	412504	Z44496	Hs.26039	Homo sapiens cDNA FLJ11937 fs, clone Y79AA10	13.4
	453344	BE349075	Hs.44571	ESTs	13.4
	428885			0	13.4
	439712	AW978161	Hs.169877	ESTs	13.4
40	421774	AL050374	Hs.108169	DKFZP586C1619 protein	13.3
	423538	NM_012337	Hs.158450	nasopharyngeal epithelium specific protein 1	13.3
	481897			0	13.3
	425601	AW823485	Hs.293352	ESTs	13.3
	405779	AW204145	Hs.156044	ESTs	13.3
45	444858	A159738	Hs.208275	ESTs, Weakly similar to unnamed protein produ	13.3
	442619	AA447492	Hs.20163	ESTs, Weakly similar to AF164793 1 protein x	13.3
	434263	K44865	Hs.44646	ESTs	13.3
	426059	BE292842	Hs.166120	Interferon regulatory factor 7	13.3
50	407467	D55638		glt-Human B-cell PABL (neuroblastoma) boundar	13.3
	412560	P24601	Hs.108300	CCNA-NOT transcription complex, subunit 3	13.2
	442896	A026980	Hs.285520	ESTs	13.2
	420317	AB006628	Hs.96485	KIAA0290 protein	13.2
	443211	A128388	Hs.143655	ESTs	13.2
	434261	AF129755	Hs.117772	ESTs	13.2
55	423493	AB15965	Hs.129693	ubiquitin-conjugating enzyme E2D 1 (homologous	13.2
	414183	AW957446	Hs.301711	ESTs	13.2
	447778	BE420592	Hs.71190	ESTs	13.2
	435106	AA100847	Hs.193390	ESTs, Highly similar to AF174600 1 f-box prot	13.1
	439490	AW049197	Hs.100043	ESTs, Weakly similar to PSF_HUMAN PT45S0CIA	13.1
	409606	AA444594	Hs.2387	transglutaminase 4 (prostate)	13.1
60	421308	AA687322	Hs.162843	ESTs	13.1
	414850	C15402		glt-C16407 Clontech human aorta polyA+ mRNA (6	13.1
	418763	AA205186	Hs.79889	monocyte to macrophage differentiation-associ	13.1
	415927	AL120168	Hs.78919	Kell blood group precursor (McLeod phenotype)	13.1
65	422605	H16546	Hs.118665	Human clone Z3759 mRNA, partial cds	13.0
	430427	AJ390701	Hs.241413	opicalin	13.0
	424620	AA101043	Hs.151254	kallikrein 7 (chymotryptic; stratum corneum)	13.0
	421693	X71450	Hs.106876	ATPase, H+ transporting, lysosomal (vacuolar	13.0
	407727	AW411148	Hs.38044	DKFZP564M082 protein	13.0
	427706	AW971871	Hs.263980	ESTs, Weakly similar to ALU_HUMAN ALU SUBFAM	13.0
70	406709	AJ355761	Hs.242463	keratin 6	13.0
	405353			0	13.0
	435690	AW294092	Hs.21594	ESTs	13.0
	452919	BE094291	Hs.155655	hepatocyte nuclear factor 3, beta	13.0
75	447843	AW337185	Hs.224891	ESTs	13.0
	446576	AJ659477	Hs.51620	ESTs, Moderately similar to ALU7_HUMAN ALU SU	13.0
	449700	L02667	Hs.76358	ESTs	13.0
	436476	AA326108	Hs.538331	ESTs	13.0
	432532	AW158459	Hs.162246	ESTs	13.0
80	408405	AK001332	Hs.44672	hypothetical protein FLJ10470	13.0
	432673	AB028859	Hs.276655	ER-associated DNAI; ER-associated Hsp40 co-ch	12.9
	414684	AW630629	Hs.76893	3-hydroxybutyrate dehydrogenase (heart, mito	12.9
	447210	AF035269	Hs.17752	phosphatidylserine-specific phospholipase A1e	12.9
	427923	AW274357	Hs.268384	Fer1 protein	12.9
	437395	AL365408	Hs.10632	hypothetical protein DKFZP762M436	12.9

441627	AA947552	Hs.58066	ESTs	12.9
419084	AA96539	Hs.179902	transporter-like protein	12.9
423087	AA321355	Hs.285401	ESTs	12.9
423070	BS5877	Hs.155565	ESTs	12.8
441344	BE250144	Hs.41514	ESTs	12.8
423527	AI026965	Hs.105861	Homo sapiens cDNA FLJ13824 fs, clone THYRO10	12.8
417005	AW673506	Hs.80758	aspartyl-4RNA synthetase	12.8
453582	AL041941	Hs.154725	3-phosphoinositide dependent protein kinase-1	12.8
453657	WY2327	Hs.296162	ESTs	12.7
434414	AI798376	Hs.76239	gbr34607.x1 NC1_CGAP_Ov23 Homo sapiens cDNA	12.8
456051	T55626	Hs.76239	hypothetical protein FLJ20608	12.7
451659	BE371971	Hs.142416	ESTs, Weakly similar to ALU8_HUMAN ALU SUBFAM	12.7
418216	AA652240	Hs.283099	AF15q14 protein	12.7
423281	AJ271684	Hs.126355	C-type (calcium dependent, carbohydrate-recog	12.7
424275	AW673173	Hs.144505	DKFZP566F0546 protein	12.7
443082	AS36518	Hs.126692	ESTs	12.7
444371	BE540274	Hs.239	Forhead box M1	12.7
412520	AA442324	Hs.795	H2A histone family, member O	12.7
413349	BE086592	Hs.795	gbcQV1-810678-130400-155-g07 BT0678 Homo sapi	12.6
414580	WZ4037	Hs.76285	DKFZP564B167 protein	12.7
429261	AW176254	Hs.143475	ESTs	12.6
402238			0	12.6
402080			0	12.6
421246	AW582862	Hs.300961	ESTs, Highly similar to AF151905 1 CGI-47 pro	12.6
442029	AW566598	Hs.14455	neuronal precursor cell expressed, development	12.6
435502	L13266	Hs.105	glutamate receptor, ionotropic, N-methyl D-as	12.6
409954	AW368226	Hs.67928	ESTs	12.6
418753	AW562887	Hs.84914	prostaglandin-endoperoxide synthase 1 (soluble)	12.5
432117	AJ017610	Hs.77870	Homo sapiens cDNA FLJ12750 fs, clone NT2RP20	12.5
448074	BE521355	Hs.27160	ESTs	12.5
442655	AW027457	Hs.30323	ESTs	12.5
409928	AL137163	Hs.67549	hypothetical protein dJ47394	12.5
409240			0	12.5
413048	M93221	Hs.75182	mannose receptor, C type 1	12.5
428215	AW563419	Hs.155223	ESTs	12.5
430024	AS869780	Hs.277730	integrin, alpha 6	12.4
449655	AJ873530	Hs.167746	B cell linker protein	12.5
419941	X56654	Hs.93357	phosphatidylinositol transfer protein, membra	12.5
425280	U01519	Hs.1872	phosphoenolpyruvate carboxykinase 1 (soluble)	12.5
427767	AB75283	Hs.180714	cytochrome c oxidase subunit IV polypeptide	12.4
450243	AW119C84	Hs.201037	ESTs	12.4
408930	AA146721	Hs.49005	hypothetical protein	12.4
418763	T41568	Hs.49005	ghp1Id1_191TV Outward Alu-primed hncDNA lib	12.4
452096	BE384901	Hs.226786	ESTs	12.4
424513	BE385864	Hs.148984	mitochondrial translational initiation factor	12.4
422306	BE044325	Hs.227280	Homo sapiens mRNA for Lem5 protein	12.4
409031	AA376836	Hs.76728	ESTs	12.4
453515	N40230	Hs.6879	DC13 protein	12.4
429583	NM_005412	Hs.209119	1-acylglycerol-3-phosphate O-acyltransferase	12.3
449543	R05989	Hs.19503	ESTs	12.3
440313	AL050060	Hs.17198	DKFZP568J073 protein	12.3
425583	AJ278921	Hs.1908	proteoglycan 1, secretory granule	12.3
447357	AJ375922	Hs.159367	ESTs	12.3
405089			0	12.3
414972	BE263782	Hs.77685	KIAA0008 gene product	12.3
433029	AW043921	Hs.130528	ESTs	12.3
447033	A037412	Hs.157601	EST - not in UniGene	12.3
427521	AW973352	Hs.299056	ESTs	12.3
409377	AA300274	Hs.115659	Homo sapiens cDNA: FLJ23461 fs, clone HS1077	12.3
400116			0	12.3
445806	AL137516	Hs.13323	hypothetical protein FLJ22059	12.2
457817	AA247751	Hs.79572	calthosin D (lysosomal aspartyl protease)	12.2
442410	AW996903	Hs.197680	ESTs	12.2
445404	AJ251887	Hs.145541	ESTs, Weakly similar to JCA974 sodium iodide	12.2
403372	AW249152	Hs.44017	SIR2 (silent mating type information regulati	12.2
427082	AB037858	Hs.173484	hypothetical protein FLJ10337	12.2
433764	AW753676	Hs.39582	ESTs	12.2
402588			0	12.2
433190	M26901	Hs.3210	renin	12.2
444863	AW084082	Hs.301323	ESTs	12.2
434779	AF153815	Hs.50151	potassium inwardly-rectifying channel, subuni	12.2
451346	NM_005338	Hs.26312	glioma amplified on chromosome 1 protein (Gu	12.2
432062	AA218780	Hs.237323	N-acetylglucosamine-phosphate mutase	12.2
421071	AJ312238	Hs.104476	ESTs	12.2
426773	NM_015556	Hs.172180	KIAA0440 protein	12.1
429178	BE33948	Hs.50915	callicrein 5	12.1
400250			0	12.1
428450	NM_014791	Hs.184339	KIAA0175 gene product	12.1
414531	T03587	Hs.76364	allograft inflammatory factor 1	12.1
448210	AW247775	Hs.7353	hypothetical protein from EUROMAGE 1987170	12.1
440081	AA863389	Hs.135643	ESTs	12.1
413179	N99592	Hs.75227	NADH dehydrogenase (ubiquinone) 1 alpha subuo	12.1
447551	BE066634	Hs.925	myosin, heavy polypeptide 7, cardiac muscle, la	12.1
400517	AF242398	Hs.149585	lengsin	12.1

	401610			0	12.0
	454381	A9352063	Hs.193428	ESTs	12.0
	443997	AW081465	Hs.299844	ESTs	12.0
5	402944			0	12.0
	430637	BE160081	Hs.256290	S100 calcium-binding protein A11 (calgizarin	12.0
	415099	AW62170	Hs.77917	ubiquitin carboxyl-terminal esterase L3 (ubiq	12.0
	445422	AV653731	Hs.282829	ESTs	12.0
	416667	AK000526	Hs.79457	hypothetical protein FLJ20519	12.0
10	442611	BE071155	Hs.177837	ESTs	12.0
	443271	BE368568	Hs.195704	ESTs	12.0
	415120	NS4464	Hs.34950	ESTs	12.0
	439574	AA469788	Hs.165190	ESTs	12.0
	405694			0	12.0
15	412519	AA196241	Hs.73380	troponin T1, skeletal, slow	12.0
	414135	NM_004419	Hs.2128	dual specificity phosphatase 5	12.0
	447075	AV662037	Hs.126740	ESTs	12.0
	416841	K13978	Hs.249495	heterogeneous nuclear ribonucleoprotein A1	12.0
	402943			0	11.9
20	416933	BE561850	Hs.80505	small nuclear ribonucleoprotein polypeptide A	11.9
	438744	AL339994	Hs.301272	ESTs, Weakly similar to homologue of Drosophila	11.9
	405762			0	11.9
	489683	NM_000492	Hs.653	cystic fibrosis transmembrane conductance reg	11.9
	455102	BE005496		gbc:CM1-BN0117-110400-183-b09 BN0117 Homo sapi	11.9
	402840			0	11.9
25	449163	AW445922	Hs.196895	Homo sapiens cDNA: FLJ21135 fls, clone CAS072	11.9
	432773	AW133069	Hs.269701	ESTs	11.9
	450464	BE220675		ghbH9B11.x.1 NCL_CGAP_Lu24 Homo sapiens cDNA	11.9
	445431	AF137365	Hs.12701	plasmiclipin	11.9
	401888			0	11.9
30	426037	AW160780	Hs.166071	cyclin-dependent kinase 5	11.9
	416742	R33644	Hs.248420	ESTs	11.9
	418324	AW246273	Hs.84131	thymidyl-URNA synthetase	11.8
	412870	K22788	Hs.62467	Homo sapiens HSPC290 mRNA, partial cds	11.8
35	435889	T47384	Hs.278813	Interferon, alpha-inducible protein 27	11.8
	421478	AI683243	Hs.97258	ESTs	11.8
	426635	BE395109	Hs.129327	ESTs	11.8
	426523	AA262999	Hs.42768	ESTs	11.8
	426227	U01658	Hs.168102	Human proteinase activated receptor-2 mRNA; 3	11.8
40	416658	U03272	Hs.76432	fibritin 2 (congenital contractual arachnoid	11.8
	441816	AA01807	Hs.149997	ESTs	11.8
	424596	AB020639	Hs.151017	estrogen-related receptor gamma	11.8
	409640			0	11.8
	448133	AA723157	Hs.73759	folate receptor 1 (adult)	11.8
	401532			0	11.8
45	400161			0	11.8
	442536	AL137761	Hs.8379	Homo sapiens mRNA; cDNA DKFZ596L2424 (from c	11.7
	451002	AA013299	Hs.8018	ESTs, Weakly similar to ALUS_HUMAN ALU SUBFAM	11.7
	401879			0	11.7
50	415889	AZ67700	Hs.111128	ESTs	11.7
	416434	AW163045	Hs.78334	nuclear factor, interleukin 3 regulated	11.7
	410816	AW873401	Hs.273599	ESTs	11.7
	449239	T24653	Hs.23360	likely ortholog of yeast ARV1	11.7
	447859	AL494985	Hs.19180	Homo sapiens mRNA; cDNA DKFZ554E122 (from d	11.7
55	416877	AA931484	Hs.121255	ESTs, Weakly similar to cDNA EST EMBL067419	11.7
	434660	R13052	Hs.3984	Homo sapiens clone 24877 mRNA sequence	11.7
	448105	AW591433	Hs.170675	ESTs, Weakly similar to TM62_HUMAN TRANSMEMBR	11.7
	400279			0	11.6
	440497	AA887265	Hs.144579	ESTs	11.6
60	451260	AW750773		gbc:CM0-CN0044-260100-164-h03 CN0044 Homo sapi	11.6
	429175	AB53040	Hs.127714	ESTs, Moderately similar to SOX30 protein (H	11.6
	408209	NM_004454	Hs.43657	ets variant gene 5 (ets-related molecule)	11.6
	428958	AA438735	Hs.183171	Homo sapiens cDNA: FLJ22002 fls, clone HEP065	11.6
	420153	NZ2120	Hs.75277	hypothetical protein FLJ13910	11.6
65	428760	AJ351459	Hs.193298	ESTs	11.6
	421461	AW410478	Hs.104019	transforming, acidic coiled-coil containing p	11.6
	404692			0	11.6
	430423	AI190548	Hs.143479	ESTs, Weakly similar to hypothetical protein	11.6
	405192			0	11.6
70	435922	AA830149		gbc:CM04498.8.1 NCL_CGAP_GC81 Homo sapiens cDNA	11.6
	401714			0	11.5
	438335	AA742697	Hs.62492	ESTs, Weakly similar to S59856 collagen alpha	11.5
	405082	S47833	Hs.82527	adenosine monophosphate deaminase 2 (isoform	11.5
	401610			0	11.5
75	412140	AA219991	Hs.73625	RAB6 Interacting, kinesin-like (rabkinesin6)	11.5
	409394	AB020586	Hs.54037	ectonucleotide pyrophosphatase/phosphodiester	11.5
	451051	BE254303	Hs.125262	ghba98a03.x1 Schiller meningioma Homo sapien	11.5
	415323	BE263352	Hs.949	neutrophil cytosolic factor 2 (65kD, chronic	11.5
	412153	R87634		ghcyo47b10.1 Soares adult brain N2b-HBSSY Ho	11.5
80	427256	AL042436	Hs.97723	ESTs	11.5
	408705	AJ282759	Hs.242463	keratin 8	11.4
	457644	AA770080	Hs.144962	ESTs, Moderately similar to I59365 ubiquitin	11.4
	422848	Z25884	Hs.121483	chloride channel 1, skeletal muscle (Thomson	11.4
	424134	AF070637	Hs.140950	hypothetical protein	11.4

451931	AK000208	Hs.27267	Homo sapiens cDNA FLJ20201 fls, clone COLF121	11.4
400438	AF185611	Hs.115352	growth hormone 1	11.4
412994	D32257	Hs.75113	general transcription factor IIA	11.4
408124	U93337	Hs.42853	cAMP responsive element binding protein-like	11.4
452249	BE304412	Hs.61252	ESTs	11.4
424627	AA344555		gh:EST50715 Gall bladder I Homo sapiens cDNA	11.4
405626			0	11.4
436590	AA373970	Hs.183096	ESTs	11.4
415892	RS1034	Hs.144513	ESTs	11.4
406755	N80129	Hs.94360	metallothionein 1L	11.4
433657	AJ244358	Hs.8124	PH domain containing protein in retina 1	11.4
425612	AF062849	Hs.252587	phillyary tumor-transforming 1	11.4
423534	AK000905	Hs.127273	hypothetical protein FLJ10044	11.4
433053	BE301909	Hs.279552	glutathione S-transferase subunit 13 homolog	11.4
428423	AJ076517	Hs.184276	solute carrier family 9 (sodium/hydrogen exch	11.3
442353	BE379594	Hs.49136	ESTs	11.3
447700	AA20193	Hs.171077	ESTs, Weakly similar to similar to sarin/thr	11.3
402077			0	11.3
409203	AA780473	Hs.687	cytochrome P450, subfamily IVB, polypeptide 1	11.3
405145			0	11.3
420348	AJ126772	Hs.40479	ESTs	11.3
425508	AA991551	Hs.97013	ESTs	11.3
428340	AF281088	Hs.154721	aconitase 1, soluble	11.3
431452	AJ073641	Hs.152372	ESTs	11.3
446651	AA383307	Hs.97179	ESTs	11.3
443755	C18397	Hs.9730	tachykinin 3 (neuromedin K, neurokinin beta)	11.3
436209	AW850417	Hs.254020	ESTs, Moderately similar to unnamed protein p	11.3
401020			0	11.3
456724	AW247388	Hs.301423	calcium binding protein 1 (calretin)	11.2
407227	H94949	Hs.171955	traphinin associated protein (taslin)	11.2
402066			0	11.2
442721	AJ015892	Hs.101282	Homo sapiens mRNA; cDNA DKFZp434B102 (from d	11.2
401025			0	11.2
452423	AA591724	Hs.180535	Homo sapiens cDNA: FLJ22711 fls, clone HSI133	11.2
431885	AW226135	Hs.267659	vav 3 oncogene	11.2
425176	AW015844	Hs.301430	ESTs, Moderately similar to TEF1_HUMAN TRANSC	11.2
435406	AW040171	Hs.265398	ESTs, Weakly similar to transformation-related	11.2
409079	W87707	Hs.82065	interleukin 6 signal transducer (gp130; oncos	11.2
456995	T85832	Hs.170278	ESTs	11.2
419223	X00111	Hs.1244	C29 antigen (p24)	11.2
407788	BE514982	Hs.38391	S100 calcium-binding protein A2	11.2
407604	AW191962	Hs.288051	actin, beta	11.2
437929	T09353	Hs.106542	ESTs, Weakly similar to hypothetical protein	11.1
416789	H16581		gby300R.1 Sources placenta Nb2HP Homo sap	11.1
424447	AL137376	Hs.147368	Homo sapiens mRNA; cDNA DKFZp434J0228 (from c	11.1
436034	AF282693	Hs.159185	Inflammation-related G protein-coupled recept	11.1
404931			0	11.1
445979	AJ695047	Hs.202395	ESTs	11.1
446733	AA663350	Hs.26040	ESTs; Highly similar to CYTOCHROME P450 N42	11.1
433133	AB027249	Hs.104741	PDZ-binding kinase; T-cell originated protein	11.1
445258	AK635931	Hs.147813	ESTs	11.1
417251	AKW15242	Hs.39458	ESTs; Weakly similar to ORF YK074w [S.cerev	11.1
421041	N36914	Hs.14691	ESTs	11.1
425537	AB007913	Hs.158291	KIAA0444 protein	11.1
435763	AJ243929	Hs.190419	ESTs	11.1
444790	AB030506	Hs.11955	S9 protein	11.1
453857	AL080255	Hs.33581	DKFZp586E1621 protein	11.1
433882	U90441	Hs.3622	procollagen-proline, 2-oxoglutarate 4-dioxyge	11.1
403558			0	11.1
435814	AW615179	Hs.152870	ESTs	11.0
422809	AK001379	Hs.121028	hypothetical protein FLJ10549	11.0
446772	AW294404	Hs.144515	Homo sapiens cDNA FLJ11672 fls, clone HEMBA10	11.0
456694	AW016382	Hs.105542	Homo sapiens cDNA: FLJ23271 fls, clone HEP001	11.0
441128	AA570256	Hs.54628	ESTs	11.0
432677	NM_004482	Hs.278611	UDP-N-acetyl-alpha-D-galactosamine:polypeptid	11.0
412576	AA447718	Hs.107057	ESTs	11.0
411122	F00809	Hs.143658	coactivator-associated arginine methyltransfer	11.0
427225	AA432391	Hs.255020	Homo sapiens mRNA for KIAA1640 protein, parti	11.0
426590	NM_002541	Hs.168659	oxoglutarate dehydrogenase (fipomide)	11.0
444652	BE513613	Hs.115338	actin related protein 2/3 complex, subunit 1A	11.0
431947	AL159613	Hs.49933	hypothetical protein UWFZp75221011	11.0
414432	BE378174	Hs.265326	Homo sapiens clone CDABP0055 mRNA HEPC90	11.0
458627	AW088642	Hs.97984	ESTs; Weakly similar to WASP-family protein [10.9
409142	AL136877	Hs.50758	chromosome-associated polypeptide C	10.9
447627	AF090922	Hs.285902	CG-113 protein	10.9
447658	NM_003726	Hs.19176	src kinase-associated phosphoprotein of 55 kD	10.9
454527	AW963897	Hs.44743	KIAA1435 protein	10.9
402927			0	10.9
422380	AA309881	Hs.135246	ESTs	10.9
455985	BE177728		gh:RC1-HT0598-14C300-021-gD6 HT0598 Homo sap	10.9
410862	BE273749	Hs.752	FK506-binding protein FLJ11240 (12kD)	10.9
450061	BE327108	Hs.202512	ESTs	10.9
457484	H57645		gby21e01.L1 Sources fetal liver spleen INFLS	10.9
407903	AJ267341	Hs.154029	bHLH factor Hox4	10.9

	403398		0	10.9
	401405		0	10.9
	405570		0	10.9
5	421240	R72730	Hs.29283	ESTs, Weakly similar to PLK_HUMAN PROTEOLYCA
	403649		0	10.9
	447824	BE620500		gib501483379T1 NIH_MGC_69 Homo sapiens cDNA c
	457935	BE514743	Hs.25564	tumor suppressor deleted in oral cancer-relat
	439553	AL119566	Hs.6721	lysophospholipase-like
	451852	RS1928		gby71c05.r1 Soares breast 2NblEst Homo sapi
10	431218	NM_002145	Hs.2753	homeo box B2
	457794	AA569262	Hs.246860	ESTs
	444374	AA028641	Hs.11039	Homo sapiens cDNA FLJ12756 Es, clone NT2RP20
	455566	AW235317	Hs.259214	ESTs
	405552		0	10.8
15	439436	BE140845	Hs.57868	ESTs
	435310	AA705075	Hs.169536	Rhesus blood group-associated glycoprotein
	411125	AA151947	Hs.68877	cytochrome b-245, alpha polypeptide
	415807	H03139	Hs.24683	ESTs
	409430	R21945	Hs.163975	splicing factor, arginine/serine-rich 5
20	417033	H83784	Hs.40532	ESTs, Weakly similar to PEBP_MOUSE PHOSPHATID
	418464	R87590		gby89h07.r1 Soares adult brain N2b4HBSSY Ho
	404567		0	10.8
	416384	AW149266	Hs.25130	ESTs
	421971	UE3127	Hs.110121	SEC7 homolog
25	428769	AW207175	Hs.106771	ESTs
	459104	R19238	Hs.282057	ESTs
	410396	AW859537		gibMRA-ST0124-261099-015-b07 ST0124 Homo sapi
	416989	AB15443	Hs.283404	organic cation transporter
	408796	AA688292	Hs.118533	ESTs
30	426298	AW955058	Hs.111583	ESTs
	421595	AB014520	Hs.109558	Homo sapiens cDNA: FLJ22735 fs, clone HUV001
	404007	AW133955	Hs.246783	ESTs
	400167		0	10.7
	445243	AJ217439	Hs.109854	ESTs, Weakly similar to ALU1_HUMAN ALU SUBFAM
35	421733	AL119671	Hs.1420	fibroblast growth factor receptor 3 (chondro
	411244	AA438343		gibRCs-MT0015-120400-031-c01 MT0015 Homo sapi
	425827	W28316		gib456 Human retina cDNA randomly primed sub
	420255	NM_007289	Hs.1298	membrane metallo-endopeptidase (neutral endop
40	432081	U22492	Hs.248118	G protein-coupled receptor 8
	407883		0	10.7
	423811	AW295938	Hs.50895	homeo box C4
	447078	AW885727	Hs.301570	ESTs
	414343	AL036166	Hs.75914	coated vesicle membrane protein
45	445913	AA430950	Hs.16529	transmembrane 4 superfamily member (tetraspan
	452279	AA286844	Hs.61260	hypothetical protein FLJ13164
	401220		0	10.7
	459259	AJ032394		gibAJ003294 Selected chromosome 21 cDNA libra
	414171	AA390328	Hs.865	RAPA1, member of RAS oncogene family
50	448449	BE314557	Hs.211440	ESTs
	429670	LD1087	Hs.211593	protein kinase C, theta
	446759	R61463	Hs.16165	expressed in activated TIAK lymphocytes
	402776		0	10.7
	428093	AW594506	Hs.104830	ESTs
	412801	AA121055		gibmZ2b01.r1 Stratagene panomea (937208) Ho
55	440845	AW163201	Hs.190559	ESTs
	434540	NM_015045	Hs.5184	TH1 drosophila homolog
	414273	BE269057		gib501184231F1 NIH_MGC_8 Homo sapiens cDNA cl
	401817		0	10.6
	410423	AA462432	Hs.63469	protein tyrosine phosphatase, non-receptor ty
60	435590	AW363947	Hs.246381	CD58 antigen
	426680	AA320160	Hs.171811	adenylate kinase 2
	445413	AA151342	Hs.12677	Cgi-147 protein
	402947		0	10.8
	457426	AW971119		gibEST383206 MAGE resequencences, MAGL Homo sapi
65	424148	BE242274	Hs.1741	integrin, beta 7
	404944		0	10.6
	405421		0	10.6
	416772	A733872	Hs.79769	protocadherin-1 (cadherin-like 1)
	414191	AW250089	Hs.75807	PDZ and LIM domain 1 (elfin)
70	457988	AS71225	Hs.284171	KIAA1535 protein
	405038	Y14443	Hs.88219	zinc finger protein 200
	404790		0	10.6
	418922	AW555680	Hs.42699	Thrombospondin-1 (hs.B7409)
	425940	AS023184	Hs.163590	KIAA0957 protein
75	448740	AW559678	Hs.21982	Homo sapiens clone 25227 mRNA sequence
	418870	AF147204	Hs.89414	CXCR4; chemokine CXCR receptor 4 (fusin)
	417933	X02308	Hs.82962	thymidylate synthase
	450538	AW297396	Hs.227052	ESTs
	427928	AA417662	Hs.118217	ESTs
80	432721	AL121476	Hs.3132	chromogenic acute regulatory protein
	429267	AA299290	Hs.246857	ESTs, Highly similar to S71100 protein kinase
	439190	AW978693	Hs.238111	ESTs
	408975	AW558993	Hs.43361	hypothetical protein LOC54149
	415130	W65893	Hs.246867	ESTs

	425738	H29630	Hs.159408	Homo sapiens clone 24420 mRNA sequence	10.5
	440232	A1766925	Hs.112554	ESTs	10.5
	425055	AA371906	Hs.294151	ESTs, Moderately similar to KIA0544 protein	10.5
5	426829	AW65612	Hs.221969	ESTs	10.5
	430465	AF032571	Hs.241717	polymerase (DNA directed), theta	10.5
	407771	AL138272	Hs.62713	ESTs	10.5
	444611	AK002180	Hs.11449	DKFZP564C123 protein	10.5
	444665	BE613126	Hs.47763	ESTs, Weakly similar to Y12540 hypothetical p	10.5
10	448630	N33714	Hs.20161	HDCC31P protein	10.5
	438902	AW579101	Hs.291980	ESTs	10.5
	446224	AW455551	Hs.13308	ESTs	10.5
	405108			0	10.5
	436233	WS2448	Hs.56147	ESTs	10.5
	401759			0	10.5
15	454038	X06374	Hs.37040	platelet-derived growth factor alpha polypept	10.5
	414222	AL135173	Hs.878	sorbitol dehydrogenase	10.5
	421626	AW691555	Hs.289109	dimethylarginine dimethylaminohydrolase 1	10.5
	422826	AA344932	Hs.118766	metallothionein 2A	10.5
20	449261	AE637592	Hs.224558	ESTs	10.4
	416218	R21499	Hs.23213	ESTs	10.4
	457848	W26524	Hs.125662	ESTs, Weakly similar to D2692.2 [C.elegans]	10.4
	442577	AA292688	Hs.153900	ESTs	10.4
	406505	AF016272	Hs.115418	cadherin 16, KSP-cadherin	10.4
25	412258	AA376768	Hs.288977	Homo sapiens cDNA: FLJ22622 fs, clone HS1065	10.4
	429224	AB95760	Hs.186272	NADH dehydrogenase (ubiquinone) 1 beta subcom	10.4
	447714	BE018118	Hs.19554	chromosome 1 open reading frame 2	10.4
	403914			0	10.4
	406329			0	10.4
	402423			0	10.4
30	431986	AA536130	Hs.149018	ESTs	10.4
	423145	BE264548	Hs.222190	ESTs, Weakly similar to secretory carrier mem	10.4
	414402	BE294165		gf-60117295F1 NIH_MGC_17 Homo sapiens cDNA c	10.4
	417079	UE5550	Hs.81134	interleukin 1 receptor antagonist	10.4
35	426955	AZ718023	Hs.89986	ESTs	10.4
	434577	R37316	Hs.179769	Homo sapiens cDNA: FLJ22487 fs, clone HRC109	10.4
	442415	A005101	Hs.129550	ESTs	10.3
40	421506	BE302756	Hs.150597	thymidine kinase 1, soluble	10.3
	435084	OT1716	Hs.301607	adenylate cyclase activating polypeptide 1 (p	10.3
	431724	AA514535	Hs.283704	ESTs	10.3
	456798	AJ006422	Hs.135183	centaurin-alpha	10.3
	417370	T28551	Hs.20330	tyrosyl-tRNA synthetase	10.3
45	422356	AF363611	Hs.118633	2-sulfolysyladenylate synthetase-like	10.3
	435226	AU24938	Hs.270106	ESTs	10.3
	433192	AB040680	Hs.225594	ESTs, Moderately similar to KIAA1447 protein	10.3
	419879	T17605	Hs.33554	Homer, neuronal immediate early gene, 2	10.3
	416228	AW505180	Hs.79089	semA domain, immunoglobulin domain (Ig), tran	10.3
	453403	BE465639	Hs.61779	Homo sapiens cDNA FLJ13591 fs, clone PLACE10	10.3
	447905	AL050062	Hs.19999	DNFZP565G023 protein	10.3
50	401762	NM_012434	Hs.117855	solute carrier family 17 (anion/bicarbonate transp	10.3
	453927	AJ062465	Hs.301751	ESTs, Weakly similar to J-protein	10.3
	450737	AW007152	Hs.203330	ESTs	10.3
	421633	AF121860	Hs.106260	sorting nexin 10	10.3
	402681	AF139799	Hs.302630	ESTs	10.3
55	432683	U48936	Hs.3112	sodium channel, nonvoltage-gated 1, gamma	10.3
	440099	AL080058	Hs.6909	DNFZP564G202 protein	10.3
	419024	X56411	Hs.1219	alcohol dehydrogenase 4 (class II), pi polype	10.3
	401835			0	10.3
	408896	AE10447	Hs.48778	niban protein	10.3
60	443120	AW402677	Hs.290801	ESTs	10.2
	400208			0	10.2
	416938	AA333990	Hs.80424	coagulation factor XIII, A1 polypeptide	10.2
	400166			0	10.2
	434642	W25739	Hs.135287	ESTs	10.2
65	424837	BE276113	Hs.153436	N-acetyltransferase, homolog of S. cerevisiae	10.2
	435075	AE10294	Hs.12400	ESTs	10.2
	429512	AL137629	Hs.162189	serine/threonine kinase with Ddb- and pleckst	10.2
	435080	AU31760	Hs.155111	ESTs	10.2
	414958	NM_002543	Hs.77729	acidified low density lipoprotein (lectin-like	10.2
70	410020	T38215	Hs.728	ribonuclease, RNase A family, 2 (liver, eosin	10.2
	411410	R20693	Hs.69954	tannin, gamma 3	10.2
	450294	H42587	Hs.238730	ESTs	10.2
	421154	AA284333	Hs.287631	Homo sapiens cDNA FLJ14269 fs, clone PLACE10	10.2
	414271	AK000275	Hs.75871	protein kinase C binding protein 1	10.2
	400812			0	10.2
75	425843	BE313280	Hs.159627	death associated protein 3	10.2
	449392	Z41609	Hs.26039	Homo sapiens cDNA FLJ13937 fs, clone Y79AA10	10.2
	426069	NM_014761	Hs.50421	KIAA0203 gene product	10.2
	401383			0	10.2
	456855	AF035528	Hs.153663	MAD (mothers against decapentaplegic, Drosoph	10.2
80	424212	A086080	Hs.131450	ESTs	10.2
	400854	C25569	Hs.76325	Homo sapiens cDNA: FLJ23125 fs, clone LNC082	10.2
	401029	BE382701	Hs.25560	v-myc avian myelocytomatosis viral related on	10.2
	416602	NM_006159	Hs.79389	nal (chicken)-like 2	10.2
	421905	AB60247	Hs.32699	ESTs, Weakly similar to LNV-1 protein [Hsapt	10.2

	405094			0	10.2
	453832	AW970602	Hs.105421	ESTs	10.2
	440076	R32052	Hs.178617	ESTs, Weakly similar to AF151840 1 CGI-82 pro	10.2
	447563	BE536115	Hs.160883	ESTs	10.2
5	421238	AB033101	Hs.102796	KIAA1275 protein	10.2
	402682			0	10.2
	415738	BE539367	Hs.295953	ESTs, Weakly similar to AF220049 1 uncharacterized	10.1
	445464	AW172389	Hs.249999	ESTs	10.1
	459042	AW272058	Hs.210338		10.1
10	414469	R31562	Hs.32267	started receptor RNA activator 1 [complexes w	10.1
	434732	A079443	Hs.15151	ghb50505.1 Soares, fetal_liver_spleen, INFLS	10.1
	441030	AW204139	Hs.174424	ESTs, Weakly similar to p140cDis [M.musculus]	10.1
	446855	BE616767	Hs.16269	B-cell CLL lymphoma 78	10.1
	456785	AF151074	Hs.132744	hypothetical protein	10.1
15	404182			0	10.1
	410358	AW957168	Hs.13337	ESTs, Weakly similar to unnamed protein produ	10.1
	430355	NM_005219	Hs.23818	phosphoinositide-3-kinase, catalytic, beta po	10.1
	442162	R32426	Hs.235668	Homo sapiens cDNA FLJ13495 fs, clone PLACE10	10.1
20	436364	A0792522	Hs.15151	Homo sapiens mRNA: cDNA, DNFZp584C2163 (from c	10.1
	426711	AA383471	Hs.180659	conserved gene amplified in osteosarcoma	10.1
	450599	AA460865	Hs.48516	ESTs	10.1
	454393	BE153288		gh-PMO-HT0335-180400-008-e08 HT0335 Homo sapi	10.1
	403383			0	10.1
	415947	U04045	Hs.78934	mutS (E. coli) homolog 2 (colon cancer, nonpo	10.1
25	411773	NM_006799	Hs.72026	protease, serine, 21 (testisin)	10.1
	442116	AW402165	Hs.784	Epstein-Barr virus induced gene 2 (lymphocyte	10.1
	413888	A02097	Hs.182183	coldresonin 1	10.0
	458572	AJ223423	Hs.292794	ESTs	10.0
	403295			0	10.0
30	403910			0	10.0
	453400	A991901	Hs.82590	ESTs, Moderately similar to ALU7_HUMAN ALU GU	10.0
	406602			0	10.0
	404743			0	10.0
35	412517	BE271584		gb501141055F1 NIH_MGC_9 Homo sapiens cDNA cl	10.0
	402678			0	10.0
	455864	BE148970		gh-CMO-HT0245-031199-085-h05 HT0245 Homo sapi	10.0
	425734	AF056209	Hs.159396	peptidylglycine alpha-amidating monooxygenase	10.0
	419280	W07508	Hs.283725	Homo sapiens cDNA FLJ12627 fs, clone NTZPM40	10.0
40	443553	AW645438	Hs.282927	ESTs	10.0
	423165	A937547	Hs.124615	Human DNA sequence from clone 380A1 on chromo	10.0
	450206	AF786450	Hs.201600	ESTs	10.0
	459052	AA298812	Hs.98539	ESTs	10.0
	462246	AL035786	Hs.82425	actin related protein 2/3 complex, subunit 5	10.0
45	428438	NM_001555	Hs.2271	Endothelin 1	10.0
	456525	AW468397	Hs.100000	S100 calcium-binding protein A8 (calgranulin	10.0
	462127	L35963	Hs.167013	dynam2	10.0

TABLE 13B:

Phay: Unique Eos probeset Identifier number
CAT number: Gene cluster number
Accession: Genbank accession numbers

Phay	CAT Number	Accession
50	410696	1226503_1
		AW909357 AW809697 AW810554 AW809707 AW809885 AW810000 AW810068 AW809742 AW809816 AW809748 AW809839 AW809722
		AW909836 AW809774 AW810023 AW810013 AW809813 AW809660 AW809728 AW809768 AW809951 AW809657 AW809954
55	412153	1219701_1
	412241	1284581_1
	412517	130281_1
	412801	132825_1
60	413349	1363598_1
	414273	1431911_1
	414602	1443240_1
	414950	1509777_1
	415789	1556357_1
65	416368	1591066_1
	418464	1789038_2
	418783	1789791_1
	424627	241724_1
	425827	259834_1
70	434371	384638_1
	434414	38585_1
75		
	434732	392447_1
	433052	466554_1
	438336	47467_1
80	447824	73861_1
	450484	83645_1
	451280	835912_1
	451652	885339_1
	452101	898742_1
		AW817705 AW817703 AW817659 BE081531 HS9570
		A078443 AA648102 AT765577 AW974381
		AA30146 AW878407 HB5983 AW503637
		AF086467 WB1444 WB1445
		BE620800
		BE220675 AA345621 AA009092
		AW160733 AT768164
		RS1928 AB206938 AB3360 AB20694
		T60298 AB958257 T69667 T67634 T61224 T71537 T69333

454163	1048369_1	AW175997	AW176000	AW175999	AW175994	AW176004	AW175989
454393	115888_1	BE153288	BE153151	BE152025	AA078302		
455102	1253524_1	BE005498	BE005494	AW863324	AW900199		
455884	1377038_1	BE148970	BE148975	BE148957	BE148537		
455986	1397521_1	BE177736	BE177735	BE177734			
456423	187241_1	AW748920	AA487506	AA248914	AA780494		
457426	336189_1	AW971119	AA574255	AA513268			
457484	342113_1	HS70451	HS0202	AA520703	224851	HS3171	
457705	363883_1	AW974668	AA681959	AA649572	AA540401	AA540402	
459259	966269_1	AJ003294	AJ003315	AJ003293			

TABLE 13C:

Key: Unique number corresponding to an Eos probe set

Ref: Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham I. et al." refers to the publication entitled "The DNA sequence of human chromosome 22" Dunham, et al. (1999) *Nature* 402:488-495

Strand: Indicates DNA strand from which exons were predicted

NL_position: Indicates nucleotide positions of predicted exons

Phy	Ref	Strand	NL_position
400640	8117686	Plus	144324-144429
400666	8118496	Plus	17982-18115,20297-20456
400776	8131651	Plus	103576-103720
400812	8588711	Plus	71705-72153
400881	2842777	Minus	91446-91803,92123-92265
400882	2842777	Minus	110431-110708
400965	7770576	Minus	173043-173564
401010	8117391	Minus	83967-84180
401020	8117458	Minus	59086-60227
401025	8117518	Minus	179287-179483,181044-181166,181844-182039
401047	8705887	Minus	4804-5035,5133-5314
401131	8693812	Minus	94802-94987,95804-95887,96323-96487,97596-97626
401152	9715002	Minus	69559-70101
401220	9525324	Minus	48079-48279
401383	6721135	Minus	155543-157381
401405	7768128	Minus	65276-69452,69548-69958
401519	6645315	Plus	157315-157520
401532	7798785	Plus	124414-124950,125050-125418
401610	7705041	Minus	18921-19505
401714	6715702	Plus	98484-98581
401735	3252819	Plus	217235-217356,217621-217873
401799	7331447	Plus	147802-148251
401817	7417850	Minus	45888-46535
401835	7139700	Plus	142257-142742
401879	8095914	Minus	101054-102027
401888	8516069	Minus	189498-190514
401897	8589218	Plus	604-767
402056	6049289	Plus	135543-136931
402077	8117414	Plus	65014-65195
402104	8119072	Plus	122409-122600
402238	7693126	Plus	24726-24860,26781-27021
402287	4553317	Plus	4081-42647
402388	9883959	Minus	771-972,1571-1683
402408	9796239	Minus	110326-110491
402423	9795344	Minus	62487-62664
402424	9795344	Minus	64925-65073
402486	9797789	Minus	8615-9103
402520	7596899	Minus	171761-171996
402679	8113438	Plus	132079-132216
402840	9389121	Minus	57116-57306
402883	9926552	Plus	38665-38803,38885-39019,39027-39231,39308-39445
402885	9926751	Plus	71919-72049
402926	8217647	Minus	41261-41443
402927	8217647	Minus	47247-47396
402943	8458631	Plus	98467-98668
402944	9358423	Plus	110411-110716,111173-111640
402947	9368458	Minus	101629-101991
402955	9581559	Minus	46855-46941,47032-47148
403022	3132351	Plus	62507-62684
403121	9180223	Plus	4059-4258
403165	9838098	Minus	90959-91848
403295	8066528	Plus	22366-22708
403381	9438267	Minus	26035-26179
403383	9438267	Minus	119837-121197
403398	6862689	Minus	13685-14699
403399	6864178	Plus	6184-62145,62367-62756
403402	9965050	Plus	186864-197135
403485	9566528	Plus	2688-3001,3198-3532,3655-4117
403649	8705159	Minus	27141-27247
403910	7710710	Minus	5761-6188
403912	7710730	Minus	72086-72250,72431-72700,72929-73199
403914	7417588	Minus	7431-8472
404182	4775844	Plus	18163-18444
404502	7225863	Minus	56277-56519
404587	7248189	Minus	101520-101591

	404678	9797204	Plus	115195-115448
	404743	8894169	Minus	120556-120999
	404760	9887810	Minus	175708-175871
	404790	7230968	Plus	38561-30761
5	404931	7342203	Plus	44226-44382
	404944	6899705	Plus	4256-4581
	405024	7107727	Plus	86506-86697
	405069	8072653	Plus	103102-103973
10	405094	8072579	Plus	135587-135758
	405108	7107890	Minus	135020-135472
	405145	9436278	Plus	37863-38052,38138-38332
	405192	7223070	Plus	118525-118671
	405224	6731245	Minus	14413-15979
	405295	3818412	Plus	56933-57059
15	405353	2811095	Plus	118525-118892
	405358	2341017	Minus	18016-18315
	405421	7243869	Minus	97411-97687
	405428	7243500	Minus	37840-37817
	405452	7656538	Minus	93876-94275
20	405484	5922025	Plus	892014-195979,199672-199920,200262-200495
	405552	1552506	Plus	45199-45647
	405570	2808656	Plus	98208-96331
	405626	4508116	Minus	89275-89384,92450-92629,97091-97279,98546-98666
	405699	4165331	Plus	100727-100859
25	405762	5931935	Plus	160602-161110
	405802	5924004	Minus	27743-28264
	405804	7274891	Minus	122557-123551
	406229	6982072	Minus	607903-608271
	406429	9256476	Minus	63206-63365,94051-94193
30	406502	7111350	Minus	63430-63602

Table 14A lists about 955 genes up-regulated in ovarian cancer compared to normal adult tissues. These were selected from 59680 probesets on the Affymetrix/Esu Ho3 GeneChip array such that the ratio of "average" ovarian cancer to "average" normal adult tissues was greater than or equal to 4.0. The "average" ovarian cancer level was set to the 90th percentile amongst various ovarian cancers. The "average" normal adult tissue level was set to the 50th percentile amongst various non-malignant tissues. In order to remove gene-specific background levels of non-specific hybridization, the 15th percentile value amongst various non-malignant tissues was subtracted from both the numerator and the denominator before the ratio was evaluated.

TABLE 14A: ABOUT 955 UP-REGULATED GENES, OVARIAN CANCER VERSUS NORMAL ADULT TISSUES

Play: Primary				
Ex. Accn: Exemplar Accession				
UG ID: UniGene ID				
Title: UniGene title				
ratio: ratio of tumor vs. normal tissues				
Play	Ex. Accn	UG ID	Title	
452338	U50111	Hs.30743	Preferentially expressed antigen in melanoma	
438817	A023799	Hs.163242	ESTs	
432538	T27013	Hs.3132	steroidogenic acute regulatory protein	
421478	A1683243	Hs.97258	ESTs	
413999	A267700	Hs.111128	ESTs	
418179	X51630	Hs.1145	Wilms tumor 1	
449034	A1624049		gb:ta1a09.x1 NCL CGAP_U1 Homo sapiens cDNA clone	
428579	NM_005756	Hs.184942	G protein-coupled receptor 64	
428163	A1653143	Hs.98367	hypothetical protein FLJ22552 similar to SRY-box c	
436982	A0016306	Hs.5379	spondin 1, (F-spondin) extracellular matrix proteol	
427585	D31152	Hs.179729	collagen, type X, alpha 1 (Schmid metaphyseal chon	
435094	A1560129	Hs.277523	EST	
430691	C14187	Hs.103538	ESTs	
430491	AL109791	Hs.241959	Homo sapiens mRNA full length insert cDNA clone EU	
419511	A1732617	Hs.182362	ESTs	
448243	AW369771	Hs.77496	ESTs	
428167	A1687303	Hs.265529	ESTs	
430891	AW451697	Hs.167409	ESTs	
418007	M13509	Hs.83169	Matrix metalloproteinase 1 (interstitial collagenase	
400292	AA250737	Hs.72472	BMPr- β ; bone morphogenetic protein receptor; typ	
422556	BE545072	Hs.122579	ESTs	
413325	AB183318	Hs.48442	ESTs	
423739	AA388155	Hs.97600	ESTs	
410929	H47233	Hs.30643	ESTs	
424066	A351010	Hs.102267	lysyl oxidase	
424605	NM_020497	Hs.153704	NIMA (never in mitosis gene)-related kinase 2	
427356	AW023482	Hs.57949	ESTs	
407168	R45175		gb:gy4001.s1 Soares infant brain 1N8 Homo sapien	
407638	A1404672	Hs.288693	EST	
427469	AA403084	Hs.265347	ESTs	
436993	AA828995		integrin, beta 8	
428664	AK001666	Hs.189095	similar to SALL1 (sal (Drosophila))-like	
439820	A1385204	Hs.283853	Homo sapiens mRNA full length insert cDNA clone EU	
421155	H87879	Hs.102704	lysyl oxidase	
426635	BE395109	Hs.126327	ESTs	
431989	AW972870	Hs.291069	ESTs	
422805	AA436889	Hs.121017	H2A histone family, member A	
444783	AK001468	Hs.52100	ESTs	

424581	MO2602	Hs.150917	catenin (cadherin-associated protein), alpha 2	15.7
453197	A1916269	Hs.109057	ESTs, Weakly similar to ALU5_HUMAN ALU SUBFAMIL	15.7
453525	AW080869	Hs.262184	ESTs	15.7
428376	AL378724	Hs.154695	ras homolog gene family, member 1	15.1
418209	AA236776	Hs.130718	MAD2 (mitotic arrest deficient, yeast), homolog-II	15.0
408660	AA525775	Hs.292523	ESTs	15.0
410247	AF181721	Hs.61345	RU2S	15.0
418738	AW368533	Hs.6582	solute carrier family 7, member 11	15.0
459583	AJ976732	Hs.172834	glt-II-152-080359-004 B152 Homo sapiens cDNA, mR	14.8
413623	AA825721	Hs.246973	ESTs	14.8
439706	AW872527	Hs.59761	ESTs	14.7
408041	AB333025	Hs.55031	KJAA1199 protein	14.7
451110	AB55940	Hs.301594	ESTs	14.5
436775	AA731111	Hs.291891	ESTs	14.3
443211	A1128388	Hs.143655	ESTs	14.3
445258	AB59331	Hs.147613	ESTs	14.3
447350	AJ376572	Hs.172834	ESTs; HERA (c-erb-B4)	14.2
428227	AA321649	Hs.2248	INTERFERON-GAMMA INDUCED PROTEIN PRECURS	14.1
453392	U23752	Hs.32294	SRY (sex determining region Y)-box 11	13.9
447033	AJ357412	Hs.157601	EST - not in UniGene	13.7
423811	AW295958	Hs.50935	homeo box C4	13.7
452461	N78223	Hs.108106	transcription factor	13.7
451106	BE382701	Hs.25590	N-myc	13.6
416208	AW291168	Hs.41295	ESTs	13.5
452249	BE294412	Hs.61352	ESTs	13.4
452055	AJ377431	Hs.293772	ESTs	13.2
439243	AA593254	Hs.191349	ESTs	13.1
420149	AA255320	Hs.89055	ESTs	12.9
429125	AA462854	Hs.271004	ESTs	12.9
413597	AW302885	Hs.117183	ESTs	12.8
416566	NM_003914	Hs.73078	cyclin A1	12.8
442438	AA595998	Hs.28603	s1 NCL_CGAP_J345 Homo sapiens cDNA clone	12.7
407710	AW022727	Hs.23616	ESTs	12.6
416681	AA634543	Hs.79440	IGF-II mRNA-binding protein 3	12.6
428392	H10233	Hs.2265	secretory granule, neuroendocrine protein 1 (7B2 p	12.4
431725	X6374	Hs.2835	Norrie disease (pseudoglioma)	12.4
447700	AJ001013	Hs.171077	ESTs, Weakly similar to similar to surfnin/tenascin	12.2
458027	L49504	Hs.85195	ESTs, Highly similar to (3,5)-(2,5-p34) fusion g	12.2
408460	AA054726	Hs.285574	ESTs	12.2
424735	U31075	Hs.152677	short-chain alcohol dehydrogenase family member	12.2
415263	AA494933	Hs.130653	ESTs	11.9
400298	AA632279	Hs.61635	STEAP1	11.8
452096	BE394901	Hs.226765	ESTs	11.7
421451	AA291377	Hs.50831	ESTs	11.6
453496	AW840171	Hs.255338	ESTs, Weakly similar to transformation-related pro	11.6
443715	AJ583187	Hs.9700	cyclin E1	11.5
402606	R(NOCA1)	Hs.130425	ESTs	11.5
438954	AA740151	Hs.75379	solute carrier family 1 (glut high affinity glut	11.5
413472	BE242870	Hs.75379	ESTs	11.4
410102	AW248508	Hs.279727	ESTs	11.4
408582	AJ436323	Hs.31141	Homo sapiens mRNA for KIAA1588 protein, partial cd	11.4
452030	AL137578	Hs.27667	Homo sapiens mRNA; cDNA DN72p54N2464 (from cbln	11.4
442355	BE378264	Hs.40106	ESTs	11.3
427344	NM_000869	Hs.2142	5-hydroxytryptamine (serotonin) receptor 3A	11.2
453160	AJ253307	Hs.146228	ESTs	11.2
428427	M66699	Hs.169340	TKK protein kinase	11.1
449433	AB672036	Hs.9012	ESTs	11.1
412723	AA648459	Hs.179912	ESTs	11.1
400260			0	11.1
419752	AA246573	Hs.152618	ESTs	11.1
438167	R28363	Hs.24286	ESTs	11.1
434539	AW748078	Hs.214410	ESTs	10.9
429918	AW873986	Hs.119383	ESTs	10.8
450375	AA095647	Hs.8050	a disintegrin and metalloproteinase domain 12 (mel	10.8
400286	X07820	Hs.2259	Matrix Metalloproteinase 10 (Stromelysin 2)	10.8
420900	AL045633	Hs.44269	ESTs	10.8
428758	AA433988	Hs.98502	Homo sapiens cDNA FLJ14303 fs, clone PLACE2000132	10.8
446142	AF754693	Hs.145958	ESTs	10.7
421285	NM_000102	Hs.1363	cytochrome P450, subfamily XVII (steroid 17-alpha-	10.6
434946	AF094254	Hs.49765	VERY-LONG-CHAIN ACYL-CoA SYNTHETASE	10.6
418506	AA084240	Hs.85339	G protein-coupled receptor 39	10.5
433447	U23915	Hs.5281	neuronal pentraxin II	10.4
424188	AW854552	Hs.142634	zinc finger protein	10.4
414245	BE148072	Hs.75850	WAS protein family, member 1	10.3
425462	U59111	Hs.169993	dermatan sulphate proteoglycan 3	10.3
418801	AA279490	Hs.86358	calmagin	10.3
444170	AW513879	Hs.102468	ESTs	10.3
453616	NM_003462	Hs.33846	dynein, axonemal, light intermediate polypeptide	10.2
407378	AA292864	Hs.128612	gh-EST11752 Uterus Homo sapiens cDNA 5' end simila	10.2
409051	AA953356		gh-Homo sapiens c1g33 mRNA, partial sequence.	10.2
407366	AF036342		ESTs	10.2
415227	AW821113	Hs.72402	ESTs	10.2
409269	AA576553	Hs.22972	Homo sapiens cDNA FLJ13352 fs, clone OVARC1002165	10.1
450480	X82125	Hs.25040	zinc finger protein 239	10.1

419088	AIS38323	Hs.77496	ESTs	10.0
453922	AF053308	Hs.36708	binding uninhibited by benzimidazoles 1 (yeast hom)	9.9
429253	AL133540	Hs.153357	Homo sapiens mRNA; cDNA DKFZp584C1021 (from clone)	9.8
426471	M22440	Hs.170009	transforming growth factor, alpha	9.8
407881	AW072003	Hs.40568	heparan sulfate (glucosamine) 3-O-sulfotransferase	9.7
452291	AF015592	Hs.28853	CD7 (cell division cycle 7, S. cerevisiae, homolog)	9.7
445537	AJ245871	Hs.12844	EGF-like domain, multiple 5	9.7
442875	BE623003	Hs.23825	Homo sapiens clone TC02CA0142 mRNA sequence	9.6
423992	AW892092	Hs.137206	Homo sapiens mRNA; cDNA DKFZp554H11663 (from clone)	9.6
412140	AA215991	Hs.23625	RAB6 interacting, kinesin-like (rabkinesin)	9.6
407721	Y12565	Hs.380118	dual-specific tyrosine-TY-phosphatase regu	9.6
438209	AL120659	Hs.61111	KIA0307 gene product	9.5
429782	NM_005754	Hs.220689	Ras-GTPase-activating protein SH3-domain-binding p	9.5
424945	AJ221919	Hs.173438	hypothetical protein FLJ10582	9.5
414972	BE232782	Hs.17695	KIA0008 gene product	9.4
439262	AA832333	Hs.124399	ESTs	9.4
403381	#[NOCAT]		0	9.3
424834	AK001432	Hs.153408	Homo sapiens cDNA FLJ10570 fs, clone NT2RP2003117	9.3
435509	AA58079	Hs.181915	ESTs	9.3
445413	AA151342	Hs.12677	CQI-147 protein	9.2
414083	AL121282	Hs.257786	ESTs	9.2
421373	AA808228	Hs.167771	ESTs	9.2
430510	AW162016	Hs.241576	hypothetical protein PRO2577	9.2
446699	AA151520	Hs.279525	hypothetical protein PRO2805	9.1
459587	AA031955		glb2L15e04.g1 Soares_pregnant_uterus_NbhPuro Homo sa	9.1
414569	AF109298	Hs.118258	Prostate cancer associated protein 1	9.1
405697	M01126	Hs.278200	pregnancy specific beta-1-glycoprotein B	9.0
428479	Y00272	Hs.194572	cell division cycle 2, G1 to S and G2 to M	9.0
408908	BE296227	Hs.48915	serine/threonine kinase 15	9.0
431548	AIB34273	Hs.97111	Homo sapiens cDNA FLJ13018 fs, clone NT2RP2000685	9.0
433764	AW753675	Hs.23082	ESTs	9.0
434636	AA083764	Hs.241334	ESTs	8.9
451807	W52854	Hs.27099	DKFZP564J0663 protein	8.8
437872	AK002915	Hs.3587	RNA binding motif protein 7	8.8
443054	AF145185	Hs.46238	yeast-associated protein 65 kDa	8.8
420032	AA814043	Hs.68045	ESTs	8.8
420159	AIS72490	Hs.59785	ESTs	8.8
447164	AF262941	Hs.17518	Homo sapiens cigs mRNA, partial sequence	8.8
451254	AIS71016	Hs.172587	ESTs	8.7
432677	NM_004482	Hs.278611	UDP-N-acetyl-alpha-D-galactosamine polypeptide N-a	8.7
450434	AA166590	Hs.18845	ESTs, Weakly similar to partial CDS [C.elegans]	8.7
400301	X03635	Hs.1657	Estrogen receptor 1	8.7
408629	NM_000042	Hs.48384	heparan sulfate (glucosamine) 3-O-sulfotransferase	8.7
434891	AA814309	Hs.123583	ESTs	8.7
438812	AW298067		gb.U18-BW0-ajp-g-09-0-ULs1 NCL_OGAP_Sub6 Homo s	8.7
438885	AIB66558	Hs.184987	ESTs	8.7
448765	NB2293	Hs.20832	EST, Moderately similar to ALLUS_HUMAN ALU SUBFAM	8.6
447342	AI199268	Hs.19322	ESTs; Weakly similar to IIII ALU SUBFAMILY J WARM	8.6
434424	AIB11202	Hs.125365	Homo sapiens cDNA: FLJ23523 fs, clone LNG05548	8.6
438078	AF016377	Hs.131693	ESTs	8.6
437212	AF165021	Hs.110775	ESTs	8.5
417728	AW138437	Hs.24790	KIA1573 protein	8.5
438081	HAS546	Hs.298564	ESTs	8.5
411571	AA122393	Hs.70811	hypothetical protein FLJ20516	8.4
435663	AIB23707	Hs.134273	ESTs	8.4
424717	H03754	Hs.152213	wireless-type MMTV integration site family, member	8.4
425734	AF056209	Hs.153996	peptidylglycine alpha-amidating monooxygenase COOH	8.4
453055	NM_004572	Hs.20551	phycophytin 2	8.4
435211	AK001581	Hs.80961	polymersase (DNA directed), gamma	8.3
433639	AI953487	Hs.299112	Homo sapiens cDNA FLJ11441 fs, clone HEMB41001323	8.3
425695	NM_005401	Hs.159238	protein tyrosine phosphatase, non-receptor type 14	8.3
438180	AA008189	Hs.272151	ESTs	8.2
447266	AIS70413	Hs.36563	Homo sapiens cDNA: FLJ22418 fs, clone HRC08590	8.2
433159	AB033599	Hs.150587	kinesin-like protein 2	8.1
400195			0	8.1
424935	AIS55626	Hs.153716	Homo sapiens mRNA for Hmo33 protein, 3' untranslated	8.1
438202	AW185287	Hs.22588	ESTs	8.1
438915	AA280174	Hs.23282	ESTs	8.1
448776	BE302464	Hs.30057	transporter similar to yeast MRS2	8.1
453884	AA335925	Hs.36322	KIA0186 gene product	8.0
420757	XT6592	Hs.89915	androgen receptor (dihydrotestosterone receptor);	8.0
439759	AL355955	Hs.67709	Homo sapiens mRNA full length insert cDNA clone EU	8.0
453102	NM_007197	Hs.31684	frizzled (Drosophila) homolog 10	8.0
424001	W67863	Hs.137476	KIA1051 protein	8.0
434415	BE177494		gb.R05-HT0596-273300-011-CG5 HT0596 Homo sapiens c	8.0
417576	AA339449	Hs.82285	phosphoribosylglycylamide formyltransferase, phosph	7.9
438966	AW973074		gb.EST391184 MAGE resequences, MAGEP Homo sapiens c	7.9
415245	NB5950	Hs.27252	ESTs	7.9
423352	AA765285	Hs.92900	ESTs	7.8
425492	AL021919	Hs.158174	zinc finger protein 184 (Kruppel-2a)	7.8
442655	AW027457	Hs.30323	ESTs	7.8
445857	AW612141	Hs.279375	ESTs	7.8
450221	AA320102	Hs.24641	cytoskeleton associated protein 2	7.8
426320	W47595	Hs.165300	transforming growth factor, beta 2	7.8

	414142	AW368397	Hs.150042	ESTs	7.7
	412170	D16532	Hs.73729	very low density lipoprotein receptor	7.6
	410011	AB02041	Hs.57856	PFT/ARE protein kinase 1	7.5
5	436476	AA326108	Hs.53631	ESTs	7.6
	414132	AB01235	Hs.48480	ESTs	7.6
	437789	AJ581344	Hs.127812	ESTs, Weakly similar to AF141326 1 RNA helicase HD	7.6
	450192	AA263143	Hs.24555	RAD51-interacting protein	7.6
	440328	AB562493	Hs.197647	ESTs	7.5
	440238	AW451970	Hs.155644	paired box gene 2	7.5
10	403657	(NCOAT)			7.5
	408826	AF216077	Hs.48376	Homo sapiens clone H8-2 mRNA sequence	7.5
	418735	AB5769	Hs.44609	ESTs	7.4
	413527	BE182082	Hs.246973	ESTs	7.5
	446293	AA402013	Hs.149722	ESTs	7.4
15	441627	AA594752	Hs.56066	ESTs	7.4
	425465	119594	Hs.1594	protein kinase C; α	7.3
	409242	AL080170	Hs.51692	DKFZP434C091 protein	7.3
	450262	AW405872	Hs.271166	ESTs, Moderately similar to ALU7_HUMAN ALU SUBFA	7.3
	440250	AA876179	Hs.134650	ESTs	7.3
20	451650	BE379761	Hs.14248	ESTs, Weakly similar to ALU8_HUMAN ALU SUBFAMIL	7.3
	458861	AJ630223		gb:ad06g08.r1 Proliferating Erythroid Cells (LCB)	7.3
	435032	AA150797	Hs.105276	lactenin protein	7.2
	407771	AL138272	Hs.82713	ESTs	7.2
	430309	AW043221	Hs.130526	ESTs	7.2
25	444342	NM_014388	Hs.10887	similar to lysosome-associated membrane glycoprote	7.2
	407829	AA045084	Hs.29725	Homo sapiens cDNA FLJ13197 fs, clone NTZRP3004451	7.2
	409731	AA125865	Hs.56145	Thymosin, beta, identified in neuroblastoma cells	7.2
	404253	(NCOAT)			7.1
	424120	T80579	Hs.250270	ESTs	7.1
30	429126	AW172356	Hs.59083	ESTs	7.1
	413573	AJ733659	Hs.140609	ESTs	7.1
	421464	AA291533	Hs.180286	ESTs	7.0
	430386	AA356923	Hs.240770	nuclear cap binding protein subunit 2, 20kD	7.0
	437938	AB50087	Hs.57226	ESTs; Weakly similar to Gag-Pol polyprotein [H.mus	7.0
35	420362	U97934		huntingtin interacting protein 1	7.0
	444743	AA045548	Hs.11817	nucleic acid diphosphate linked moiety X-type	6.9
	415138	C18356	Hs.78045	tissue factor pathway inhibitor 2 (TFPI2)	6.9
	410568	AW162548	Hs.84542	pre-mRNA cleavage factor I (68kD)	6.9
40	429416	AB31028	Hs.95253	ESTs	6.9
	409178	BE303548	Hs.55915	kallikrein 5	6.9
	446608	N75217	Hs.257846	ESTs	6.9
	425905	AB032959	Hs.161700	KIAA1133 protein	6.9
	428532	AF157328	Hs.184786	TBP-interacting protein	6.9
	433426	H81125	Hs.133525	ESTs	6.9
45	431322	AW970622	Hs.222194	gb:EST382704 MAGIE resequences, MAGK Homo sapiens	6.8
	437960	AJ659586	Hs.222194	ESTs	6.8
	423244	AL039379	Hs.208032	ESTs, Weakly similar to ubiquitous TPR motif, Y is	6.8
	424085	NM_002914	Hs.139226	replication factor C (activator 1) 2 (40kD)	6.8
50	448674	W31178	Hs.154140	ESTs	6.8
	438122	AJ620270	Hs.129837	ESTs	6.8
	440046	AJ697451	Hs.158459	ESTs, Weakly similar to envelope protein [H.sapien	6.7
	418478	U39945	Hs.1174	cyclin-dependent kinase inhibitor 2A (melanoma, p1	6.7
	407162	N53855	Hs.142634	zinc finger protein	6.7
	410804	U64820	Hs.65521	Machado-Joseph disease (spinocerebellar ataxia 3,	6.7
55	424630	AB17404	Hs.131329	ESTs	6.7
	432415	T16971	Hs.289014	ESTs	6.7
	421470	R27496	Hs.1378	annexin A3	6.7
	444549	AM78629	Hs.159465	ESTs	6.7
	418203	X54942	Hs.83768	CD28 protein kinase 2	6.6
60	432809	AA555509	Hs.131703	ESTs	6.6
	409234	AB78419	Hs.27206	ESTs	6.6
	433594	BE375623	Hs.27693	CSG-124 protein	6.6
	423007	AB002694	Hs.27916	ADAM-TS3 ; a disintegrin-like and metalloproteas	6.6
	453745	AA952989	Hs.63908	Homo sapiens HSPC316 mRNA, partial cds	6.6
65	414136	AA812434	Hs.178227	ESTs	6.6
	423248	AA380177	Hs.125845	ribulose-5-phosphate-3-epimerase	6.6
	454016	AW010282	Hs.241652	ESTs	6.6
	452281	T33500	Hs.26792	ESTs	6.5
	424620	AA101043	Hs.151254	kallikrein 7 (chymotryptic; stratum corneum)	6.5
70	452594	AL070405	Hs.29391	solute carrier family 26 (sulfate transporter), ma	6.5
	424149	Z43829	Hs.19374	ESTs, Weakly similar to keratin g80 subunit [H.sap	6.4
	425776	U25128	Hs.159499	parathyroid hormone receptor 2	6.4
	418577	S53308	Hs.87224	SRY (sex determining region Y)-box 5	6.4
	409517	X50780	Hs.44658	troponin I, cardiac	6.4
75	423696	AWC04089	Hs.128220	ESTs, Weakly similar to unnamed protein product [H	6.4
	448706	AW291035	Hs.21814	class II cytokine receptor ZCYTOR7	6.4
	429163	AA844766		gban:20a10s.1 Soares_NFL_T_GBC_S1 Homo sapiens cDN	6.4
	413692	AA929547	Hs.71331	Homo sapiens cDNA: FLJ21971 fs, clone HEP05790	6.4
	419171	AA320681	Hs.83768	Homo sapiens mRNA: cDNA DKFZp434E232 (from clone	6.4
80	424153	AA451737	Hs.141456	MAGE-like 2	6.4
	434265	AA648811	Hs.130554	Homo sapiens cDNA: FLJ23089 fs, clone LING07061	6.4
	435882	AA694373	Hs.186104	Homo sapiens cDNA FLJ13803 fs, clone THYR01000187	6.4
	441081	AJ584019	Hs.161806	ESTs, Moderately similar to pleckstrin 2b [H.sapi	6.4
	443539	AJ076182	Hs.134074	ESTs	6.4

	443830	A1142095	Hs.143273	ESTs	6.4
	452606	N45202	Hs.90012	Homo sapiens cDNA: FLJ23441 fs, clone HS100612	6.4
	418394	AW140266	Hs.25130	ESTs	6.3
	425371	D49441	Hs.155981	mesothelin	6.3
5	429441	AJ224172	Hs.204096	lipophilin B (ultrapolin family member), prostate	6.3
	449048	Z45051	Hs.22520	similar to S65401 (catlin) glucose induced gene	6.3
	437117	AL049256	Hs.122593	ESTs	6.3
	448579	AW207260	Hs.134014	prostate cancer associated protein 6	6.3
10	433370	AI47023	Hs.182356	ESTs, Moderately similar to translation Initiation	6.3
	426514	BE516633	Hs.301122	bone morphogenetic protein 7 (osteogenic protein 1	6.3
	415076	NM_000857	Hs.177890	guanylate cyclase 1, soluble, beta 3	6.2
	408155	AB014528	Hs.43133	KIA00620 gene product	6.2
	423504	AL157581	Hs.209587	Homo sapiens mRNA; cDNA DKFZp434E0626 (from clone	6.1
15	439138	AF742605	Hs.159396	ESTs	6.2
	457030	AJ031740	Hs.173381	dihydropyrimidinase-like 2	6.2
	436281	AW411194	Hs.120051	ESTs	6.1
	407385	AA501050	Hs.273272	ESTs, Moderately similar to ALU7_HUMAN ALU SUBFA	6.1
	406815	AA833930	Hs.288036	RNA isopentoylpyrophosphate transferase	6.1
20	430437	AI768801	Hs.169943	Homo sapiens cDNA FLJ13569 fs, clone PLACE1008369	6.1
	428743	AL080500	Hs.301549	Homo sapiens mRNA; cDNA DKFZp434E1172 (from clone	6.1
	415138	AW675942	Hs.46824	ESTs	6.1
	417404	NM_007350	Hs.82101	pleckstrin homology-like domain, family A, member	6.1
	433527	AW235613	Hs.133020	ESTs	6.1
25	449448	D60730	Hs.57471	ESTs	6.1
	457733	AF5974812	Hs.251971	ESTs	6.1
	457978	AA776955	Hs.270942	ESTs	6.1
	428867	L32137	Hs.1584	cartilage oligomeric matrix protein	6.0
	423554	M50516	Hs.1674	glutamine-fructose-6-phosphate transaminase 1	6.0
30	421502	AF111856	Hs.105939	solute carrier family 34 (sodium phosphate), member	6.0
	412733	AA984472	Hs.74554	KIAA0080 protein	6.0
	422065	AI868872	Hs.288968	ceruloplasmin (ferroxidase)	6.0
	449347	AW457436	Hs.259501	ESTs	6.0
	440870	AB607254	Hs.150338	Homo sapiens cDNA FLJ13793 fs, clone THYRC1000085	6.0
35	434748	AL359172	Hs.118811	Homo sapiens cDNA	6.0
	411598	BE366554	Hs.70937	H3 histone family, member K	6.0
	418134	AA397769	Hs.86617	ESTs	6.0
	418845	AA552985	Hs.80232	chromobox homolog 5 (Drosophila HP1 alpha)	6.0
	452039	AB223988	Hs.172510	ESTs	6.0
	410555	U92649	Hs.64311	a disintegrin and metalloproteinase domain 17 (tum	5.9
40	412719	AW018610	Hs.129911	ESTs	5.9
	410566	AA373210	Hs.43947	Homo sapiens cDNA FLJ13585 fs, clone PLACE1009150	5.9
	437099	N77793	Hs.48659	ESTs, Highly similar to LMA1_HUMAN LAMININ ALPH	5.9
	453431	AF094754	Hs.32373	glycine receptor, beta	5.9
	408520	AL120071	Hs.48938	tuberculin leucine rich transmembrane protein 2	5.9
45	417866	AW007503	Hs.82772	"collagen, type XI, alpha 1"	5.9
	420440	NM_024047	Hs.97644	mammaglobin 2	5.9
	430291	AV560345	Hs.238126	CGI-49 protein	5.9
	465547	#NCCA1		0	5.9
50	427510	Z67542	Hs.175312	small nuclear RNA activating complex, polypeptide	5.9
	435793	AB037734	Hs.4993	ESTs	5.8
	427975	AI536265	Hs.122460	ESTs	5.8
	428949	AA442153	Hs.104744	ESTs, Weakly similar to AF208855 1 BM-013 [H.sapi	5.8
	428933	T8163	Hs.48389	zinc finger protein 228	5.8
	440138	AB033023	Hs.6582	hypothetical protein FLJ10201	5.8
55	421246	AW982862	Hs.300561	ESTs, Highly similar to AF151905 1 CGI-47 protein	5.8
	445424	AB028945	Hs.12595	cardiac SH3 domain-binding protein	5.8
	448186	AA252105	Hs.4094	Homo sapiens cDNA FLJ14209 fs, clone NT29P3003264	5.7
	426154	NM_001851	Hs.154550	collagen, type IX, alpha 1	5.7
	419335	AW950146	Hs.284137	Homo sapiens cDNA FLJ12888 fs, clone NT29P2004081	5.7
60	426357	AW761553	Hs.43124	gEESTB8062 MAGC nascent, MAGN Homo sapiens	5.7
	431924	AW001860	Hs.272203	Homo sapiens cDNA FLJ20543 fs, clone ACDKA01954	5.7
	448688	AV680737	Hs.135100	ESTs	5.7
	452971	AB873878	Hs.91789	ESTs	5.7
	426927	AA441637	Hs.90020	huntingtin interacting protein 2	5.7
65	423282	AW153518	Hs.155465	fragile X mental retardation 1	5.7
	419247	SE5791	Hs.89764	ESTs, Weakly similar to KIAA0227 [H.sapiens]	5.7
	445640	AW959626	Hs.31704	ESTs	5.6
70	422338	NM_001869	Hs.301570	ESTs	5.6
	447078	AW955727	Hs.102910	general transcription factor IIIH, polypeptide 4 (5	5.6
	421247	BE391727	Hs.41154	Zic family member 1 (odd-paired Drosophila homolog	5.6
	407896	D76435	Hs.41572	ESTs	5.6
	436556	AB344987	Hs.132808	epithelial cell transforming sequence 2 oncogene	5.6
	417530	AW564786	Hs.132808	ESTs	5.6
	429826	N93266	Hs.40747	ESTs	5.6
75	432030	AB084000	Hs.143789	ESTs	5.6
	443270	NM_004272	Hs.5192	Homer, neuronal immediate early gene, 1B	5.5
	432900	AW033592	Hs.226414	ESTs, Weakly similar to ALU8_HUMAN ALU SUBFAMIL	5.5
	411598	U80034	Hs.65853	mitochondrial intermediate peptidase	5.5
	419558	AW533679	Hs.278394	ESTs	5.5
80	427388	AW536261	Hs.177465	amyloid beta (A4) precursor protein (protease nexi	5.5
	427561	AW531865	Hs.143134	ESTs	5.5
	404561	#NCOAT		0	5.5
	429682	NM_006306	Hs.211602	SMC1 (structural maintenance of chromosomes 1, yea	5.5
	407216	NR1773	Hs.102267	lysyl oxidase	5.5

	10658	AW105231	Hs.192035	ESTs	5.5
	113930	M86153	Hs.75618	RAB11A, member RAS oncogene family	5.5
	14315	Z24878		gb:45865052 STRATAGENE Human skeletal muscle cD	5.5
	427878	C25765	Hs.181022	Ccd-47 protein	5.5
5	431041	AA490967	Hs.105276	ESTs	5.5
	441645	AZ22279	Hs.201555	ESTs	5.5
	428071	AF212848	Hs.182339	transcription factor ESE-38	5.4
	435406	AW102723	Hs.125345	ESTs	5.4
10	429181	AW579104	Hs.294009	ESTs	5.4
	410509	AW681861	Hs.53112	ESTs, Weakly similar to ALU8_HUMAN ALU SUBFAMIL	5.4
	423435	AK001380	Hs.145479	Homo sapiens cDNA FLJ10518 fs, clone NTZRP2000814	5.4
	451956	AW614291	Hs.245510	ESTs	5.4
	449318	AW235021	Hs.106788	ESTs, Weakly similar to zeste [D.melanogaster]	5.4
	441433	AA933809	Hs.42746	ESTs	5.4
15	445495	BE52641	Hs.38489	ESTs	5.4
	410153	BS131926	Hs.15830	Homo sapiens cDNA FLJ12691 fs, clone NTZRM4002571	5.4
	442611	BE077155	Hs.177537	ESTs	5.4
	452401	NM_007115	Hs.25352	tumor necrosis factor, alpha-induced protein 6	5.4
20	453161	AA628608	Hs.61656	ESTs	5.4
	419948	AB941535	Hs.53847	NAOPH oxidase 4	5.3
	427718	AT98680	Hs.25933	ESTs	5.3
	453867	AJ929383	Hs.108196	HSPC037 protein	5.3
	422634	NM_016010	Hs.118621	CSG-62 protein	5.3
	444478	W07318	Hs.240	M-phase phosphoprotein 1	5.3
25	428002	AA18703		gb:zv985d3.1 Soares, NhlhMpu_S1 Homo sapiens cDNA c	5.3
	443486	NM_003428	Hs.9450	zinc finger protein 84 (HPF2)	5.3
	451177	AJ989716	Hs.13034	ESTs	5.3
	406288	AT45325	Hs.271923	ESTs, Moderately similar to III ALU SUBFAMILY S82	5.3
	435687	AA954229	Hs.114062	ESTs	5.3
30	423698	AA327996	Hs.1098	DKFZp434J1813 protein	5.3
	448543	AW957741	Hs.21380	Homo sapiens mRNA; cDNA DKFZp566P1124 (from clone	5.3
	427660	AT414320	Hs.114121	Homo sapiens cDNA: FLJ23228 fs, clone CAE06854	5.3
	450345	AK000282	Hs.236681	hypothetical protein FLJ20275	5.3
	432222	AW514472	Hs.238415	ESTs, Moderately similar to ALU8_HUMAN ALU SUBFA	5.3
35	449532	W74653	Hs.271893	ESTs	5.3
	452822	Z55689	Hs.20861	Homo sapiens cDNA: FLJ22621 fs, clone HSI05658	5.2
	437641	AA811452	Hs.291911	ESTs	5.2
	418379	AA218940	Hs.137516	ldgulin-like 1	5.2
40	416530	US2801	Hs.79381	Kat5/krelin 5 (neurosin, zyme)	5.2
	433889	AA895530	Hs.188912	ESTs	5.2
	409143	AW025980	Hs.138955	ESTs	5.2
	410303	AA324597	Hs.21851	Homo sapiens cDNA FLJ12900 fs, clone NTZRP2004321	5.2
	413384	NM_000401	Hs.75334	exonuclease (multiple) 2	5.2
	424698	AA164366	Hs.151973	hypothetical protein FLJ10378	5.2
45	431229	AA495479		gb:zv97065.1 Soares ovary tumor NBHOT Homo sapien	5.2
	433377	AT52713	Hs.43845	ESTs	5.2
	445236	AK001676	Hs.12457	hypothetical protein FLJ10814	5.2
	406367	BNOC241		0	5.2
50	442500	AJ819058	Hs.209122	ESTs	5.2
	450101	AV649983	Hs.24385	Human hbc647 mRNA sequence	5.2
	419140	AB882647	Hs.215725	ESTs	5.2
	411078	AZ222020	Hs.183264	ESTs, Weakly similar to 25 kDa trypsin inhibitor I	5.2
	423020	AA383092	Hs.1608	replication protein A3 (14kD)	5.2
	427061	AB032871	Hs.173392	KIAA1145 protein	5.2
55	439542	AW979172		gk:EST391282 MAGE nonsequences, MA3P Homo sapiens c	5.2
	452200	AW185286	Hs.194097	ESTs	5.1
	417791	AW653339	Hs.111471	ESTs	5.1
	433277	W27268	Hs.151010	ESTs	5.1
	447835	AW691623	Hs.164129	ESTs	5.1
60	434041	AA54131	Hs.71119	Potential prostate cancer tumor suppressor	5.1
	437496	AA452378	Hs.170144	Homo sapiens mRNA; cDNA DKFZp547J125 (from clone D	5.1
	418849	AW474547	Hs.53565	ESTs, Weakly similar to B0491.1 [C.elegans]	5.1
	428093	AW934506	Hs.104630	ESTs	5.1
	408821	AT970672	Hs.46538	chromosome 11 open reading frame 8; fetal brain I	5.1
65	453096	AW294631	Hs.11325	ESTs	5.1
	418852	BE537037	Hs.273294	hypothetical protein FLJ20089	5.1
	436787	AA506554	Hs.192759	ESTs	5.1
	446577	AB940633	Hs.15420	KIAA1500 protein	5.1
	437267	AW511443	Hs.258110	ESTs	5.1
70	419423	D26488	Hs.90315	KIAA0007 protein	5.0
	404539			0	5.0
	439392	AF085917	Hs.37921	ESTs	5.0
	447020	T27308	Hs.16985	hypothetical protein FLJ11046	5.0
75	453878	AW954440	Hs.19025	ESTs	5.0
	410824	AW954813	Hs.33284	ESTs	5.0
	427701	AA411101	Hs.221750	ESTs	5.0
	424602	AK020255	Hs.301129	Homo sapiens clone Z3859 mRNA sequence	5.0
	430044	AA464510	Hs.152812	EST cluster (not in UniGene)	5.0
	417423	AA197341	Hs.111164	ESTs	5.0
80	421477	AJ904743	Hs.104650	hypothetical protein FLJ10232	5.0
	433384	AJ021992	Hs.124244	ESTs	5.0
	434160	BE551196	Hs.114275	ESTs	5.0
	443555	N71710	Hs.21398	ESTs, Moderately similar to GNP1_HUMAN GLUCOSAM	5.0
	416198	W27332	Hs.99598	ESTs	4.9

424538	L02911	Hs.150402	activin A receptor, type I	4.9
436545	AW023424	Hs.156520	ESTs	4.9
417251	AW015242	Hs.95488	ESTs; Weakly similar to ORF YKR074e [S.cerevisiae]	4.9
447207	AA442233	Hs.17731	hypothetical protein FLJ12892	4.9
416585	AW002960	Hs.44970	ESTs	4.9
425292	NM_008024	Hs.155545	37 kDa leucine-rich repeat (LRR) protein	4.9
435420	AJ508513	Hs.59203	ESTs	4.9
435532	AW291488	Hs.117305	ESTs	4.9
443268	AB002071	Hs.129445	hypothetical protein FLJ12496	4.9
446140	AA356170	Hs.287670	Homo sapiens cDNA: FLJ11908 fs, clone HEP03830	4.9
452881	N75692	Hs.121875	ESTs; Weakly similar to KIAA0357 [H.sapiens]	4.9
431130	NM_006103	Hs.2719	epididymis-specific; whey-acidic protein type; Iou	4.9
408938	AA059013	Hs.22507	ESTs	4.9
432842	AW674093	Hs.273525	hypothetical protein PRO2805	4.9
433754	AB011288	Hs.133437	ESTs; Moderately similar to gonadotropin inducible	4.9
442573	H93366	Hs.7567	Branched chain aminotransferase 1, cytosolic, U215	4.9
409049	AA23132	Hs.145343	ESTs	4.9
422475	AL359938	Hs.117313	Mdm (mouse) homolog 3	4.9
447112	H17800	Hs.7154	ESTs	4.9
458627	AW086642	Hs.97984	ESTs; Weakly similar to WASP-family protein [H.sap	4.8
431689	AA305688	Hs.267695	UDP-Galactase/Cdc4c beta 1,3-galactosyltransferase,	4.8
410530	M25069	Hs.64173	ESTs; Highly similar to VAD1_HUMAN VACUOLAR AT	4.8
429414	AJ735355	Hs.202095	empty spiracles (Drosophila) homolog 2	4.8
418882	NM_004996	Hs.69433	ATP-binding cassette, sub-family C (CFTR/MRP), mem	4.8
422505	AL120862	Hs.124165	ESTs; (HS4)PAP protein (programmed cell death 9;	4.8
425977	R15136	Hs.163570	Homo sapiens clone 25052 mRNA sequence	4.8
428555	NM_002214	Hs.184908	integrin, beta 8	4.8
452909	NM_015368	Hs.30385	pannexin 1	4.8
449535	W15267	Hs.23572	low density lipoprotein receptor-related protein 6	4.8
452232	AW020603	Hs.271698	ESTs	4.8
409732	NM_016122	Hs.55148	NY-REN-58 antigen	4.8
415115	AA214226	Hs.127751	hypothetical protein	4.7
423161	AL049227	Hs.124776	Homo sapiens mRNA; cDNA DKFZp564N1116 (from clon	4.7
441085	AW138551	Hs.181245	Homo sapiens cDNA FLJ12322 fs, clone NT20M4000200	4.7
423575	CH833	Hs.163443	ESTs	4.7
415211	RF64730.comp	Hs.155986	ESTs; Highly similar to SPERM SURFACE PROTEIN SP1	4.7
418804	AA020532		glnr217h04.1 NCL_CGAP_GCB1 Homo sapiens cDNA do	4.7
428405	Y00762	Hs.2286	cholinergic receptor, nicotinic, alpha polypeptide	4.7
432885	AJ737078	Hs.152484	ESTs	4.7
433330	AW207084	Hs.132816	ESTs	4.7
453047	AW023798	Hs.286025	ESTs	4.7
421308	AA587322	Hs.192843	ESTs	4.7
452273	AF154946	Hs.1148	zinc finger protein	4.7
443933	AJ051831	Hs.135501	Homo sapiens two pore potassium channel KT3.3	4.7
434551	BE387162	Hs.280858	ESTs; Highly similar to XPB_HUMAN DNA-REPAIR PRO	4.7
440351	AF300333	Hs.7179	RAD1 (S. pombe) homolog	4.7
425300	U19979	Hs.169228	delta-like homolog (Drosophila)	4.7
453775	NM_002916	Hs.35120	replication factor C (activator 1) 4(37kD)	4.7
446102	AW160067	Hs.252956	ESTs	4.7
420547	AF155140	Hs.98738	gonadotropin-regulated testicular RNA helicase	4.7
429486	AF156827	Hs.203863	hypothetical protein FLJ10339	4.7
429944	R13949	Hs.226440	Homo sapiens clone 24881 mRNA sequence	4.7
433042	AW193534	Hs.281895	Homo sapiens cDNA FLJ11660 fs, clone HEMBA1004610	4.7
434988	AJ180655	Hs.161160	ESTs	4.6
452671	W31618	Hs.34665	ESTs	4.6
434351	AF129755	Hs.117772	ESTs	4.6
406400	#(NOCAT)		0	4.6
410227	AB020284	Hs.61152	enoxonases (multiple)-like 2	4.6
418945	AW250375	Hs.118923	ESTs	4.6
428301	AW628666	Hs.58440	ESTs	4.6
430153	AW981828	Hs.156942	gbcEST380338 MAGE resequences, MAGJ Homo sapiens c	4.6
431349	AA530363	Hs.156942	ESTs; Moderately similar to ALJ22_HUMAN ALU SUBFA	4.6
446254	BE178928	Hs.175852	Homo sapiens cDNA FLJ11932 fs, clone NT2RP22003137	4.6
447505	AL049266	Hs.18724	Homo sapiens mRNA; cDNA DKFZp564F093 (from clone	4.6
448027	AS45437	Hs.177224	ESTs	4.6
449511	AS702694	Hs.187075	ESTs	4.6
459574	AF171122	Hs.101810	Homo sapiens cDNA FLJ14232 fs, clone NT2RP40000335	4.6
409928	AL137163	Hs.57549	hypothetical protein dJ473B4	4.6
405387	AW384900	Hs.123265	ESTs	4.6
424078	AB060625	Hs.139033	paternally expressed gene 3	4.6
435244	NT7221	Hs.187324	ESTs	4.6
404996	#(NOCAT)		0	4.6
407995	AW103655	Hs.252905	ESTs	4.6
411580	AW051186		gbc-EST380338 MAGE resequences, MAGJ Homo sapiens c	4.6
424341	AA365074	Hs.118923	gbc-EST38873 Thyroid Homo sapiens cDNA S' end simil	4.6
441675	AJ914329	Hs.5461	ESTs	4.6
452172	H00797	Hs.133007	Homo sapiens mRNA for KIAA1230 protein, partial cd	4.6
420276	AA328838	Hs.190561	ESTs; Highly similar to mosaic protein LR11 [H.sap	4.6
402820	#(NOCAT)		0	4.6
419899	AA248998	Hs.31246	ESTs	4.5
422529	AW015128	Hs.256703	ESTs	4.5
428018	AK001160	Hs.5999	hypothetical protein FLJ10298	4.5
441828	AW053600	Hs.122915	phosphotransferase related	4.5
453931	AL121278	Hs.25144	ESTs	4.5

	435538	AB011540	Hs.4830	low density lipoprotein receptor-related protein 4	4.5
	457465	AW301344	Hs.185969	ESTs	4.5
	418848	AB20961	Hs.193465	ESTs	4.5
5	428221	AW05882	Hs.44205	corfalsin	4.5
	447459	AW62550	Hs.147874	KIA1621 protein	4.5
	424513	BE358564	Hs.149894	mitochondrial translational initiation factor 2	4.5
	432731	R31178	Hs.287820	fibronectin 1	4.5
	448275	BE51434	Hs.20830	synaptic Ras GTPase activating protein 1 (homolog	4.5
10	433371	D97466	Hs.240112	KIA0276 protein	4.5
	448653	AW004854	Hs.228230	Homo sapiens cDNA: FLJ23537 fs, clone LNC07690	4.5
	407289	AA135159	Hs.203349	Homo sapiens cDNA: FLJ12149 fs, clone MAMMA100042	4.4
	448141	AA11558	Hs.197531	ESTs	4.4
	434659	AA545807	Hs.149425	Homo sapiens cDNA FLJ11980 fs, clone HEMBB1001304	4.4
15	417718	T8540	Hs.193981	ESTs	4.4
	436464	A016176	Hs.269783	ESTs, Weakly similar to ALU1_HUMAN ALU SUBFAMIL	4.4
	427528	AU077143	Hs.179565	mitochondosome maintenance deficient (S. cerevisiae)	4.4
	403992	AT73253	Hs.172608	ESTs	4.4
	416241	N52639	Hs.32683	ESTs	4.4
20	432005	AA524190	Hs.120777	ESTs, Weakly similar to ELI2_HUMAN RNA POLYMER	4.4
	440234	AW117254	Hs.126252	ESTs	4.4
	448743	AB032522	Hs.21856	KIA11336 protein	4.4
	451389	N73222	Hs.21738	KIAA1008 protein	4.4
	453331	AI240655	Hs.8895	ESTs	4.4
	454036	AA374756	Hs.93550	ESTs, Weakly similar to unnamed protein product [H	4.4
25	448133	AA721157	Hs.173709	folate receptor 1 (beta)	4.4
	429557	NM_003816	Hs.2442	a disintegrin and metalloproteinase domain 9 (mult	4.4
	453279	AW853940	Hs.59998	ESTs	4.4
	409458	D85407	Hs.54481	low density lipoprotein receptor-related protein 8	4.4
30	431708	AIB01338	Hs.108873	ESTs	4.4
	433906	AI167816	Hs.43355	ESTs	4.4
	437958	BE139550	Hs.121668	ESTs	4.4
	441423	AI793299	Hs.126877	ESTs	4.4
	428076	AB028977	Hs.152574	KIAA1054 protein	4.4
	445770	AW660309	Hs.154596	ESTs, Weakly similar to AF137386 1 plasmidom [H.	4.3
35	412078	X69559	Hs.73149	paired box gene 8	4.3
	422093	AF161852	Hs.111449	CGI-84 protein	4.3
	422123	NM_012247	Hs.124027	SELENOGRAPHY SYNTHETASE ; Human selenium	4.3
	448390	AL035414	Hs.21066	hypothetical protein	4.3
	453628	AW243307	Hs.170187	ESTs	4.3
40	440722	BE26074	Hs.23390	cyclin B1	4.3
	458675	AI121483	Hs.120451	ESTs, Weakly similar to unnamed protein product [H	4.3
	431592	R63016	Hs.293871	ESTs, Weakly similar to ALU1_HUMAN ALU SUBFAMIL	4.3
	432383	AK000144	Hs.274449	Homo sapiens cDNA FLJ20137 fs, clone COL07137	4.3
45	419926	AW905992	Hs.83758	DKFZ58602223 protein	4.3
	453357	U71207	Hs.29279	eyes absent (Drosophila) homolog 2	4.3
	401644	#(NOCAT)	0		4.3
	410044	BE56742	Hs.58169	highly expressed in cancer, rich in leucine heptad	4.3
	413775	AW409934	Hs.73528	nucleolar GTPase	4.3
50	424296	AB31874	Hs.163391	ESTs	4.3
	431118	BE264901	Hs.250502	carbonic anhydrase VIII	4.3
	432201	AB38613	Hs.135657	TNFRSS3a mRNA for serine protease (ECHOS 1) (TAGD-1	4.3
	451073	AI758905	Hs.206583	ESTs	4.3
	451892	AB05416	Hs.213897	ESTs	4.3
55	452453	AI902519	Hs.35952	gbc-IV-BT009-101 198-051 BT009 Homo sapiens cDNA, m	4.2
	441020	W79283	Hs.35558	ESTs	4.2
	439024	R96636	Hs.33922	H.sapiens novel gene from PAC 117P20, chromosome 1	4.2
	453619	H87648	Hs.257789	ESTs	4.2
	453459	BE047032	Hs.177236	ESTs	4.2
60	408427	AW194270	Hs.177236	gbcw66a12.1 NCL CGAP CG91 Homo sapiens cDNA do	4.2
	419311	AA68599	Hs.183702	Homo sapiens cDNA FLJ11752 fs, clone HEMBA1035582	4.2
	444540	AB93927	Hs.265165	ESTs	4.2
	452943	BE247449	Hs.31062	hypothetical protein FLJ10525	4.2
	453913	AW004683	Hs.233502	ESTs	4.2
65	417847	AI251568	Hs.288312	Homo sapiens cDNA: FLJ22316 fs, clone HRC05282	4.2
	428856	AA436735	Hs.183711	Homo sapiens cDNA: FLJ22002 fs, clone HEP06638	4.2
	428679	AA431785	Hs.254020	gbcw60c03.a1 Soares_testis_NHT Homo sapiens cDNA	4.2
	441006	AW852527	Hs.7627	CGI-80 protein	4.2
	436209	AW850417	Hs.47314	ESTs, Moderately similar to unnamed protein produc	4.2
70	446936	HI10207	Hs.137011	ESTs	4.2
	405076	AL390179	Hs.138514	Homo sapiens mRNA; cDNA DKFZ547P134 (from clone	4.2
	428919	AL135623	Hs.235754	KIA0675 gene product	4.2
	406871	AA125547	Hs.85112	met proto-oncogene (hepatocytic growth factor recep	4.2
	418432	M14156	Hs.55498	Insulin-like growth factor 1 (somatomedin C)	4.2
75	417048	AO88775	Hs.263705	geranylgeranyl diphosphate synthase 1	4.2
	431750	AA514586	Hs.178144	ESTs	4.2
	433014	AA382413	Hs.94812	ESTs	4.2
	448582	AI530880	Hs.59982	ESTs	4.2
	449554	AA682382	Hs.59982	ESTs	4.2
80	455700	BE088115	Hs.27379	gbc-IV-BT0358-061299-050-g07 BT0358 Homo sapiens c	4.1
	409373	AA053458	Hs.7369	gbc271a07.a1 Soares_pituit_gland_N3HPG Homo sapie	4.1
	433929	AB375459	Hs.28313	ESTs	4.1
	415457	AW081710	Hs.28313	ESTs, Weakly similar to ALU1_HUMAN ALU SUBFAMIL	4.1
	444381	BE387335	Hs.28313	ESTs	4.1

451024	AA442176		gbzw63068.1 Sources_total_telus_Hb2HF8_3w Homo sa	4.1
415539	AT33881	Hs.72472	MAPK8, bone morphogenetic protein receptor, typ	4.1
421515	Y11339	Hs.105352	GalNAc alpha-2, 6-sylactransferase 1, long form	4.1
426736	A263022	Hs.82204	ESTs	4.1
453293	AA382267	Hs.10553	ESTs	4.1
405554	AA345857	Hs.54943	trachea callos 1 (rat) homolog	4.1
418378	AW82281		gbtEST374154 MAGE resequences, MAGG Homo sapiens	4.1
429628	H09604	Hs.13268	ESTs	4.1
439635	AA472788	Hs.94891	Homo sapiens cDNA: FLJ22729 fs, clone H8115685	4.1
440452	A0925136	Hs.55153	ESTs, Weakly similar to CAPP, HUMAN CALCYPHOSIN	4.1
443595	AW304993	Hs.112759	ESTs, Weakly similar to AF1267801 refseq short-c	4.1
446816	AB033052	Hs.22151	KIAA1226 protein	4.1
452795	AW392555	Hs.18878	hypothetical protein FLJ21620	4.1
443717	BE281128	Hs.9930	TORCU	4.1
425322	U63630	Hs.105637	protein kinase; DNA-activated; catalytic polypept	4.1
442717	R88382	Hs.180591	ESTs, Weakly similar to R06G6.5b (C elegans)	4.1
414747	U30872	Hs.77204	centromere protein F (350/400KD, mitotin)	4.1
417300	A765227	Hs.55610	solute carrier family 30 (anion transport), membe	4.1
417389	BE26544	Hs.82045	Midline (neurofilament growth-promoting factor 2)	4.1
448105	AW591433	Hs.170675	ESTs, Weakly similar to TMS2, HUMAN TRANSMEMBR	4.1
419131	AA06293	Hs.301622	ESTs	4.1
408348	R(NC0A1)		0	4.0
419750	AL079141	Hs.183114	Homo sapiens cDNA FLJ14236 fs, clone NT2RP4000515	4.1
419790	U79250	Hs.93201	glycerol-3-phosphate dehydrogenase 2 (mitochondria	4.1
420908	AL049974	Hs.100281	Homo sapiens mRNA; cDNA DKFZp5646222 (from clone	4.1
421039	NM_003478	Hs.101259	cutin 5	4.1
425990	AA033167	Hs.41124	ESTs	4.1
428571	NM_006531	Hs.2291	Probe Hg737 (polycystic kidney disease, autosomal	4.1
452834	A063827	Hs.105685	ESTs	4.0
428771	AB028992	Hs.183143	KIAA1069 protein	4.1
437849	U78119	Hs.41654	ESTs	4.0
450568	AL050078	Hs.25159	Homo sapiens cDNA FLJ10784 fs, clone NT2RP4000448	4.0
424081	NM_006413	Hs.139120	ribonuclease P (30KD)	4.0
418375	NM_003081	Hs.84389	synaptonemal-associated protein, 25KD	4.0
447204	AW56811	Hs.157897	ESTs, Moderately similar to ALUIC, HUMAN III ALU CL	4.0
407910	AA650274	Hs.41256	fibronectin leucine rich transmembrane protein 3	4.0
412314	AA822247	Hs.250899	heat shock factor binding protein 1	4.0
435291	BE568432	Hs.5101	ESTs, Highly similar to protein regulating cytokin	4.0
453554	AJ245547	Hs.25375	Kruppel-type zinc finger protein	4.0
425991	AK001536	Hs.285803	Homo sapiens cDNA FLJ18852 fs, clone NT2RP2003445	4.0
409355	AA702376	Hs.226440	Homo sapiens clone 24881 mRNA sequence	4.0
410784	AW603201		gblc2-LIM0077-07505-080-ES6 LIM0077 Homo sapiens c	4.0
413374	NM_001034	Hs.75319	ribonucleotide reduction N2 polypeptide	4.0
413425	F20956		gblc3HSPD05390 HK3 Homo sapiens cDNA clone Q32-X4-1	4.0
417655	AA780791	Hs.14014	ESTs, Weakly similar to KIAA0873 protein (H sapiens)	4.0
424783	AA913909	Hs.153096	TATA box binding protein (TBP)-associated factor,	4.0
425024	R09235	Hs.12407	ESTs	4.0
445941	AJ267371	Hs.172636	ESTs	4.0
448595	AB014544	Hs.21572	KIAA0644 gene product	4.0
453448	AL038710	Hs.209527	ESTs	4.0
458944	N53227	Hs.59403	ESTs	4.0
400284			Estrogen receptor 1	4.0
441134	W25092	Hs.7678	cellular retinoic acid-binding protein 1	4.0
408796	AA658292	Hs.118553	ESTs	4.0
408286	AL117452	Hs.44155	DKFZP586G1517 protein	4.0
438913	AL360429	Hs.172445	ESTs	4.0
402408			0	4.0
411630	U24249	Hs.71119	Putative prostate cancer tumor suppressor	4.0
450701	H09960	Hs.289467	Homo sapiens cDNA FLJ12280 fs, clone MAMMA100174	4.0
439780	AL109688		gblcHomo sapiens mRNA full length insert cDNA clone	4.0
418301	AW976201	Hs.187618	ESTs	4.0
420077	AW512280	Hs.87787	ESTs	4.0
425572	AB037783	Hs.170623	hypothetical protein FLJ11183	4.0
403721			0	4.0
411945	AL033527	Hs.92137	v-myc avian myelocytomatosis viral oncogene homolo	4.0
408554	R51377	Hs.12727	hypothetical protein FLJ21610	4.0
414689	AA157291	Hs.72163	ESTs	4.0
437980	R50393	Hs.278436	KIAA1474 protein	4.0
451050	AW937420	Hs.69662	ESTs	4.0

TABLE 14b:

Key: Unique Eos probe/seq identifier number
 CAT number: Gene cluster number
 Accession: Genbank accession numbers

Key	CAT Number	Accession
409073	109851_1	AA063458 AA063018 AH448822
410784	1221005_1	AW603201 BE079700 BE032940
411580	1305441_1	AW651186 AW656967 BE143456
413425	136885_1	F20956 AA12374 AA133740 AW619878
414315	143512_1	Z24878 AA454098 F13654 AA634040 AA143127
418378	174656_1	AW52081 AA218925 AA354357
418804	179138_1	AA089532 AS172745 A071732 AA229406
419311	183793_1	AA689591 AW974261 AA236240 AJ077451 AA631399 AW974262

420637	195241_1	AW576153 AA278945 AA747881
424341	238294_1	AA385074 AA339054 AA339115 AW956369
428002	285602_1	AA418703 AA418711 BE071915 BE071920 BE071912
428679	294049_1	AA437165 AA432015
429163	305643_1	AA884766 AW574271 AA592975 AA447312
430153	313709_1	AW568128 AA468102 AA468165
431229	330060_1	AA496479 T85859 AW002056 AW135251 A1221100 AA628705 A1263148 T75074
431322	331543_1	AW570622 AA533059 AA502989 AA502989 AA502986 T92168
434415	369351_1	BE177484 AW276599 AW532849
436812	427323_1	AW258087 AA731645 AA810101 AW194180 A1890673 AW978773
437938	44573_2	A1950807 N70208 R37040 N36809 A1308119 AW597677 N33200 A1251473 H59397 AW571973 R37278 W01059 AW567671 AA065958
		AA21875 A1825501 A1820332 W47891 T45504 U71458 T82291 BE20871 T75102 R34725 AA884922 BE238517 A1218708 AA884444 N92578
		F13493 AA277794 A1560251 AW874058 AL134043 AW235353 AA663345 AA000282 AA488964 AA283144 A1890387 A1950344 A714346
		A1889062 AA282915 AW102898 A1872193 A1763273 AW173586 AW150329 A1653632 A1762688 AA598777 AA408892 A1356394 AW103813
		A1539642 AA642789 AA858975 AW505512 A1361530 AW529870 BE612881 AW276997 AW513681 AW512943 AA044209 AW565538
		AA100009 AA337499 AW561101 AA251688 AA251874 A1819125 AW205862 A1863338 A1856509 AW576095 A1853006 AA572584 AA592841
		AW072526 AW133986 AA2353273 AA569759 W75288 N22388 H84729 H60052 T92487 A1022058 AA780419 AA551005 W08701 AW613456
		A1373032 A1564269 F00531 H83488 W37181 W78802 R65056 A1002839 R67840 AA302207 AW595881 T63226 F04005
		AW579074 AA834841 AA822850
		AA828955 AA834878 A1925361
		AW579172 AA829585 R55050
		AL109688 R23665 R26578
		A1953598 A1916584 R81871 T77332 F07756 F08149 F07647
		A824049 AW117770 A1858360
		AA442176 AA289101
		A1902519 A1902518 A1902516
		BE068115 BE068104 BE068102 BE068096 BE068103 BE068154 BE068198
		AW58601 799055_1
		A1930222 A1930470

TABLE 14C:

Phy: Unique number corresponding to an Eos probe set

Ref: Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham I. et al." refers to the publication entitled "The DNA sequence of the human chromosome 22" Dunham, et al. (1999) Nature 393: 489-495

Strand: Indicates DNA strand from which exons were predicted

N_positoin: Indicates nucleotide positions of predicted exons

Phy	Ref	Strand	N_positoin
401644	8576138	Plus	82655-83599
402408	9796239	Minus	110326-110491
402506	9959429	Minus	81747-82094
402320	6458653	Minus	82274-82443
403381	9438267	Minus	26009-28178
403657	8843996	Minus	156223-156370
403721	7529046	Minus	156947-157358
404253	9367202	Minus	55875-55925
404561	9795980	Minus	69039-70100
404939	6882897	Plus	175318-175476
404996	9007850	Plus	37995-38145,38652-38998,39727-39872,40557-40674,42351-42450
405547	1054740	Plus	124361-124520,124914-125050
406348	9255985	Minus	71764-71944
406367	9256128	Minus	58313-58489
406400	9256258	Plus	1553-1712,1878-2140,4252-4385,5932-6077

55 Table 15A lists about 499 genes up-regulated in ovarian cancer compared to normal adult tissues that are likely to be extracellular or cell-surface proteins. These were selected as for Table 14A, except that the ratio was greater than or equal to 3.0, and the predicted protein contained a structural domain that is indicative of extracellular localization (e.g., Ig, FN3, epf, Tm domains). Predicted protein domains are noted.

60 TABLE 15A: ABOUT 499 UP-REGULATED GENES ENCODING EXTRACELLULAR/CELL SURFACE PROTEINS, OVARIAN CANCER VERSUS NORMAL ADULT TISSUES
Phy: Phylokey
UG ID: UniGene ID
Title: UniGene title
Prot. Dom.: Predicted protein structural domains
ratio: ration tumor vs normal tissues

Phy	Ex. Acct	UG ID	Title	Prot. Dom.	ratio
415989	A1267700	Hs.111128	EST6	TM	42.7
428579	NM_005765	Hs.194942	G protein-coupled receptor 64	TM	30.5
429163	AW513143	Hs.58367	similar to SRY-box containing gene 17	TM	30.1
436982	AB018205	Hs.5378	spondin 1, (F-spondin) extracellular matrix	SS	29.4
427535	C11152	Hs.179729	collagen, type X, alpha 1 (Schmid metaph	C1q,Collagen	27.0
430891	C14187	Hs.1835338	EST5	TM	26.2
418007	M13559	Hs.83169	Matrix metalloproteinase 1 (interstitial collag	SS,Peptidase_M10	20.6
400292	AA250737	Hs.72472	BMPLR-1, bone morphogenetic protein rec	TM	20.6
424086	A1351010	Hs.102267	lysyl oxidase	Lysyl_oxidase	17.7
424095	NM_002497	Hs.153704	NIMA (never in mitosis gene a)-related kin	phos,kinase	17.4
427356	AW023482	Hs.97849	EST6	TM	17.1
407638	AJ404672	Hs.288603	EST5	TM	17.1
427469	AA403084	Hs.269347	EST5	TM	17.0
432693	AA428995	Hs.1033338	integrin beta 8	SS,Integrin_B	16.7
421155	H87879	Hs.102267	lysyl oxidase	SS	16.1
431989	AW972870	Hs.291069	EST5	SS	15.9
428976	AL037824	Hs.194895	ras homolog gene family, member 1	ras	15.1
416209	AA236776	Hs.79078	MD2 (mucic acid deficient, yeast, hom	TM	15.0

5	413623	AA825721	Hs.246973	ESTs	TM	14.8
	447350	A0375572	Hs.172634	ESTs; HERA (p-erbB-64)	SS, TM, Furin-like, kinase	14.2
	482827	AA321649	Hs.2248	INTERFERON-GAMMA INDUCED PRO	IL8	14.1
	452461	N78223	Hs.108106	transcription factor	G9a, PHD	13.7
	451106	BE382701	Hs.2550	N-my	hsc_N_term	13.6
10	416208	AW291168	Hs.41295	ESTs	TM	13.5
	452249	BE384412	Hs.61252	ESTs	homeobox	13.4
	416566	NM_003914	Hs.79378	cyclin A1	cyclin	12.6
	416661	AA54543	Hs.7340	IGF-II mRNA-binding protein 3	TM	12.6
	431725	X85774	Hs.2639	Norrie disease (retinopathy)	SS, Ops_knot	12.3
15	458027	LK6054	Hs.85195	ESTs, Highly similar to (3-5)-(25,1-234) f	TM	12.2
	406460	AA054726	Hs.285574	ESTs	TM	12.2
	415263	AA948033	Hs.130653	ESTs	histone	11.9
	400296	AA002279	Hs.61636	STEAP1	TM	11.8
	421451	AA291377	Hs.50831	ESTs	TM	11.6
20	443715	AS583187	Hs.9700	cyclin E1	TM, SOF	11.5
	413472	BE242870	Hs.75379	adult carrier family 1 (glial high affinity gl	SS	11.4
	410102	AW246558	Hs.279727	ESTs	TM	11.2
	408562	AA436323	Hs.31141	Homo sapiens mRNA for KIAA1568 prote	TM	11.4
	442353	BE379594	Hs.49136	ESTs	TM	11.3
25	427344	NM_000659	Hs.2142	5-hydroxytryptamine (serotonin) receptor 3	TM, neur_chan	11.2
	453160	AA263307	Hs.146228	ESTs	histone	11.2
	412723	AA648459	Hs.179912	ESTs	TM	11.1
	400250			0	Hist_deacetyl-F105	11.1
	438167	R28363	Hs.24286	ESTs	TM, L1	11.1
30	424329	AW748078	Hs.214410	ESTs	TM	10.9
	450375	AA009647	Hs.8850	a disintegrin and metalloproteinase domain	TM	10.8
	400289	X07820	Hs.2258	Matrix metalloproteinase 10 (Stromelysin 2	SS, homeobox	10.8
	446142	A0754693	Hs.145588	ESTs	Cadherin_C_term	10.7
	421285	NM_000102	Hs.1363	cyclochrome P450, subfamily XVII (steroid	TM, p450	10.6
35	433496	AF064254	Hs.49765	VERY-LONG-CHAIN ACYL-COA SYNT	SS, TM	10.6
	418506	AA084248	Hs.85339	G protein-coupled receptor 39	TM	10.5
	443243	U29195	Hs.3281	neuronal pentraxin II	SS	10.4
	414245	BE148072	Hs.75829	WASP protein family, member 1	TM	10.3
	426452	U59111	Hs.169993	dermatan sulphate proteoglycan 3	SS, LRRT	10.3
40	418801	AA279490	Hs.86358	calretinin	SS	10.3
	415227	AW821113	Hs.72402	ESTs	TM	10.2
	429259	A076983	Hs.22972	Homo sapiens cDNA FLJ13352 f5, clone O	TM	10.1
	426471	M22440	Hs.170009	transforming growth factor, alpha	SS, EGF	9.8
	407881	AW072003	Hs.40958	heparan sulfate (glucosamine) 3-O-sulfotran	SS	9.7
45	445337	AJ246571	Hs.12844	EGF-like domain; multiple 6	SS, EGF	9.7
	414972	BE283782	Hs.77695	KIAA0068 gene product	TM	9.4
	435509	AA586679	Hs.181915	ESTs	TM	9.3
	445413	AA151342	Hs.12677	CGI-147 protein	UPF0099	9.2
	446999	AA151520	Hs.279525	hypothetical protein PRO2605	TM	9.1
50	414569	AF109298	Hs.116258	Prostate cancer associated protein 1	TM	9.1
	406687	M31126	Hs.272620	pregnancy specific beta-1-glycoprotein 9	hemopexin	9.0
	408908	BE296227	Hs.48916	serine/threonine kinase 15	phos, TM	9.0
	451807	W52854	Hs.27069	DKFZ006470663 protein	TM	8.9
	429159	AJ72490	Hs.89785	ESTs	TM	8.9
55	432677	NM_004482	Hs.278611	UDP-N-acetyl-alpha-D-galactosaminopol	TM, Aldin_B_lectin	8.7
	408829	NM_006042	Hs.48394	heparan sulfate (glucosamine) 3-O-sulfotran	TM	8.7
	438885	AJ885658	Hs.184987	ESTs	TM	8.7
	447242	A1199268	Hs.8322	ESTs; Weakly similar to III ALU SURFAM	TM	8.6
	437212	A1765021	Hs.210975	ESTs	UDPGT	8.5
60	427417	H03754	Hs.152213	wingless-type MMTV integration site fami	wnt	8.4
	455055	NM_004572	Hs.26061	pleiophelin 2	TM	8.4
	435938	AJ983487	Hs.299112	Homo sapiens cDNA FLJ11441 f1, clone H	wnt	8.3
	425695	NM_005401	Hs.159238	protein tyrosine phosphatase, non-receptor	Y_phosphatase	8.3
	447268	AJ370413	Hs.36563	Homo sapiens cDNA: FLJ22416 f5, clone O	Ribosomal_S8	8.2
65	400195				TM	8.1
	424906	AJ566086	Hs.153716	Homo sapiens mRNA for Hmo33 protein,	TM	8.1
	438202	AW169287	Hs.22588	ESTs	TM	8.1
	439759	AL259055	Hs.67709	Homo sapiens mRNA full length insert cDN	TM	8.0
	453102	NM_001197	Hs.31654	Fizzled (Drosophila) homolog 10	TM, Fz, Fizzled	8.0
70	424001	W57883	Hs.137476	KIAA1051 protein	TM	8.0
	426655	AW027457	Hs.30323	ESTs	TM	7.8
	446567	AW612141	Hs.279575	ESTs	TM, L1	7.8
	426320	W47155	Hs.163300	transforming growth factor, beta 2	SS, TGF-beta	7.8
	412170	D16532	Hs.73729	very low density lipoprotein receptor	TM, LDL_recept_b, EGF	7.6
75	436476	AA326108	Hs.53631	ESTs	TM	7.6
	414132	AJ801235	Hs.48480	ESTs	TM	7.6
	437789	AJ581344	Hs.127812	ESTs; Weakly similar to AF141326 1 RNA	TM	7.6
	450192	AA63143	Hs.24596	RAD51-interacting protein	TM	7.6
	408826	AF216077	Hs.48378	Homo sapiens clone HB-2 mRNA sequence	TM	7.5
80	413827	BE182082	Hs.246973	ESTs	TM	7.4
	446293	AA20213	Hs.149122	ESTs	TM, homeobox	7.4
	490242	AL080170	Hs.51692	DKFZP434C091 protein	TM, TM, L1	7.3
	450262	AW409872	Hs.271156	ESTs; Moderately similar to ALU7_HUMA	TM	7.3
	451659	BE379761	Hs.14248	ESTs; Weakly similar to ALU8_HUMAN A	TM	7.3
	444342	NM_014308	Hs.10887	similar to lysosome-associated membrane g	TM	7.2
	429126	AW172356	Hs.90803	ESTs	TM, L1	7.1
	421464	AA291553	Hs.190086	ESTs	TM	7.0
	420362	U79734	Hs.97206	huntingtin interacting protein 1	TM	7.0

	447473	AA045548	Hs.11817	nudix (nucleoside diphosphate linked moiety) factor pathway inhibitor 2	TM	7.0
	415108	C18356	Hs.78045	ESTs	Kuntz1, BPTI, G-gamma	6.9
	429416	A3301028	Hs.35283	ESTs	AAA	6.9
	409178	BE339348	Hs.52915	kallikrein 5	SS,lysozin	6.9
5	425905	AB032599	Hs.161700	KIAA1133 protein	TM	6.9
	428532	AF157326	Hs.184786	TBP-interacting protein	TM	6.9
	433426	H89125	Hs.133525	ESTs	TM	6.8
	448674	W31178	Hs.154140	ESTs	TM	6.8
	432415	T16971	Hs.283014	ESTs	TM	6.7
10	418203	X54942	Hs.83758	CDC28 protein kinase 2	TM	6.6
	438394	BE378623	Hs.27693	CGI-124 protein	pro_3amomerase	6.6
	425057	AA022354	Hs.27916	ADAM-TS1: a disintegrin-like and metal	Regulatory	6.6
	453745	AA952589	Hs.63908	Homo sapiens HSPC316 mRNA, partial of	TGF-beta_propeptide	6.6
	423248	AA380177	Hs.125845	ribulose-5-phosphate-3-epimerase	flament	6.6
15	422281	T35500	Hs.28792	ESTs	TGF-beta	6.5
	424520	AA101043	Hs.151222	kallikrein 7 (hymenotrophic; stratum corneum	SS,lysozin	6.5
	452594	AJ076405	Hs.29391	solute carrier family 26 (sulfate transporter)	TM,Sulfate_transp	6.5
	434149	Z43829	Hs.19574	ESTs, Weakly similar to katanin p80 subunit	kinase,fn3	6.5
	425776	U28128	Hs.159499	parathyroid hormone receptor 2	TM,7m_2	6.4
20	409517	X30780	Hs.54568	Immunin L, cardiac	Y_phosphatase	6.4
	432656	AW204069	Hs.129250	ESTs, Weakly similar to unnamed protein p	TM	6.4
	448706	AW291095	Hs.21814	class II cytokine receptor ZCYTOR	SS	6.4
	413582	AW295647	Hs.71331	Homo sapiens cDNA: FLJ21971 fls, clone	TM	6.4
	421453	AA651737	Hs.141496	MADE-like 2	TM	6.4
25	441081	AF584019	Hs.169006	ESTs, Moderately similar to plakophilin 2b	PAX	6.4
	443639	A076182	Hs.134074	ESTs	TM	6.4
	418394	AW149268	Hs.25130	ESTs	TM	6.3
	425371	C19441	Hs.155591	mesothelin	SS	6.3
	449048	Z45051	Hs.22920	similar to 988A01 (cattle) glucose induced g	SS	6.3
30	437117	AL048256	Hs.122593	ESTs	TM	6.3
	453370	AA709523	Hs.182356	ESTs, Moderately similar to translation init	ABC_tran	6.3
	426514	BE510633	Hs.301122	bone morphogenetic protein 7 (osteogenic p	SS,TGF-beta	6.3
	452904	AL157581	Hs.30957	Homo sapiens mRNA: cDNA DKFZ434E	TM	6.2
	457030	A301740	Hs.173381	dihydropyrimidinase-like 2	TM	6.2
35	456281	AW411194	Hs.120051	ESTs	TM	6.1
	415139	AW975842	Hs.48524	ESTs	TM	6.1
	449448	D60730	Hs.57471	ESTs	TM	6.1
	457979	AA176655	Hs.270942	ESTs	TM	6.1
40	422857	L32157	Hs.15584	cartilage oligomeric matrix protein	SS,EGF,asp_3	6.0
	421502	AF111856	Hs.105339	solute carrier family 34 (sodium phosphate)	TM	6.0
	412733	AA984472	Hs.74554	KIAA0080 protein	C2	6.0
	422095	AJ868872	Hs.289566	ceruloplasmin (ferroxidase)	SS	6.0
	418845	AA52585	Hs.89322	chromobox homolog 5 (Drosophila HP1 alp	Chromo_shadow	6.0
	410555	U32548	Hs.54311	a disintegrin and metalloproteinase domain	TM,disintegrin,Reprolysin	5.9
45	437099	W77793	Hs.48659	ESTs, Highly similar to LMA1_HUMAN	laminin_EGF	5.9
	453431	AF094754	Hs.32873	glycine receptor, beta	TM,neur_chan	5.9
	417856	AK067563	Hs.62772	"collagen, type XI, alpha 1"	TSPN,Collagen,COLFI	5.9
	430291	AV593045	Hs.236126	CGI-45 protein	TM	5.9
	405547	#(NOCAT)	0		TM,ABC_membrane	5.9
50	435793	AB037734	Hs.4993	ESTs	TM	5.8
	440138	A3033023	Hs.6982	hypochlorite protein FLJ10201	TM	5.8
	423154	NM_001851	Hs.154650	collagen, type IX, alpha 1	SS,Collagen,TSPN	5.7
	419335	AW590146	Hs.284137	Homo sapiens cDNA FLJ12888 fls, clone N	TM	5.7
	452971	A873878	Hs.91789	ESTs	TM	5.7
55	428827	AA418137	Hs.90250	ESTs	TM	5.7
	419247	S65791	Hs.80784	fragile X mental retardation 1	TM	5.7
	445640	AW959526	Hs.31704	ESTs, Weakly similar to KIAA0227 (H.sap	TM	5.7
	447078	AW885727	Hs.301570	ESTs	kazal	5.6
	421247	BE391727	Hs.102910	general transcription factor IIF, polypeptide	TM	5.6
60	432030	AW934400	Hs.143789	ESTs	TM	5.6
	433270	NM_004272	Hs.91192	Homer, neuronal immediate early gene, 1B	TM	5.5
	411099	U80034	Hs.65853	mitochondrial intermediate peptidase	Peptidase_M3	5.5
	418559	AW536379	Hs.273694	ESTs	TM	5.5
	427386	AW833261	Hs.177466	amyloid beta (A4) precursor protein (prote	TM	5.5
65	427961	AW293155	Hs.143134	ESTs	TM	5.5
	407216	N91773	Hs.102267	lysyl oxidase	TM	5.5
	413550	M65153	Hs.75618	RAB11A, member RAS oncogene family	TM	5.4
	414315	Z44678	Hs.201555	glb4SBS6D562 STRATAGENE Human sk	TM	5.5
	416145	A1222279	ESTs	SS	SS	5.5
70	449318	AW236021	Hs.106788	ESTs, Weakly similar to zeste [D.melanoga	TM	5.4
	441453	AA533805	Hs.42746	ESTs	TM	5.4
	445495	BE822541	Hs.35469	ESTs	L_LWEQ,ENTH	5.4
	410153	BE311926	Hs.15830	Homo sapiens cDNA FLJ12691 fls, clone N	Glycos_transf_2	5.4
	442611	BE077155	Hs.177537	ESTs	TM	5.4
75	452401	NM_007115	Hs.29352	tumor necrosis factor, alpha-induced protein	TM	5.4
	419948	AB041035	Hs.53847	NADPH oxidase 4	XMRK,CUB	5.3
	427718	AJ798580	Hs.25933	ESTs	histone	5.3
	453867	AJ929383	Hs.106196	HSPC037 protein	TM	5.3
	402898	AJ745235	Hs.271923	ESTs, Moderately similar to IRII ALU SUB	SS,Glycos_transf_2,DSPC	5.3
80	448543	AW597741	Hs.21380	Homo sapiens mRNA: cDNA DKFZ586P	TM	5.3
	433222	AW514472	Hs.238415	ESTs, Moderately similar to ALU8_HUMA	TM	5.3
	449532	W74653	Hs.271593	ESTs	TM	5.3
	452822	X05689	Hs.288617	Homo sapiens cDNA: FLJ2621 fls, clone	TM,EGF,fn3	5.3
	418579	AA218940	Hs.137616	EdgR-like 1	AAA	5.2

116530	U62801	Hs.79361	katzirelin 6 (neurosin, zymo)	TM, trypsin	5.2
413384	NM_000401	Hs.75334	exostoses (multiple) 2	TM	5.2
445226	AK001676	Hs.12457	hypothetical protein FLJ10814	TM	5.2
406367	#(NOCAT)	0	0	proteasoma, trypsin	5.2
442500	AJ819068	Hs.209122	ESTs	SS	6.2
450101	AV64989	Hs.24385	Human hbc547 mRNA sequence	TM	5.2
419140	U58247	Hs.215725	ESTs	TM	5.2
417791	AW66335	Hs.111471	ESTs	AK1_Xen_gu_C	5.3
437496	AA452378	Hs.170144	Homo sapiens mRNA; cDNA DKFZp47J1	TSPN, Folate_carrier	5.1
418849	AW474547	Hs.433565	ESTs, Weakly similar to B0491.1 [Colegan]	TM	5.1
428053	AK594506	Hs.104830	ESTs	TM	5.1
409621	AF97072	Hs.46538	chromosome 11 open reading frame 6; beta	SS, Adhivin_recpt, plasminase	4.9
418852	BE537037	Hs.273294	hypothetical protein FLJ20069	TM	5.1
404939		0	0	TM	5.0
447020	T27368	Hs.16996	hypothetical protein FLJ11046	TM	5.0
410824	AW594913	Hs.33264	ESTs	TM	5.0
417423	AA197341	Hs.111164	ESTs	TM	5.0
421477	AY04743	Hs.104650	hypothetical protein FLJ10292	TM	5.0
443555	N71710	Hs.21398	ESTs, Moderately similar to GNP1_HUMA	Glucosamine_ase	5.0
424539	U02011	Hs.150402	activin A receptor, type I	SS, Adhivin_recpt, plasminase	4.9
416565	AW000560	Hs.44970	ESTs	TM	4.9
431130	NM_006103	Hs.2719	epididymis-specific; whey-acidic protein ly	SS	4.9
408938	AK059013	Hs.22607	ESTs	TM	4.9
436764	AW61288	Hs.133437	ESTs, Moderately similar to gonadotropin I	TM	4.9
409049	AA23132	Hs.146343	ESTs	TM	4.9
458627	AW088642	Hs.97984	ESTs; Weakly similar to WASP-family pro	TM	4.8
418882	NM_004996	Hs.89433	ATP-binding cassette, sub-family C (CFTR	TM, ABC_membrane	4.8
425505	AL120862	Hs.124165	ESTs; (RISAPAP protein (programmed on	SS, Integrin_B	4.8
428555	NM_002214	Hs.184908	Integrin, beta 8	SS, Integrin_B	4.8
452909	NM_015368	Hs.30985	paxillin 1	TM	4.8
448535	W15667	Hs.23872	low density lipoprotein receptor-related pro	SS, Idl_recept_a, EGF	4.8
452232	AW020603	Hs.271098	ESTs	TM	4.8
423161	AL049227	Hs.124778	Homo sapiens mRNA; cDNA DKFZp564N	Catheherin_C_term	4.7
428405	Y00762	Hs.2266	cholinergic receptor, nicotinic, alpha potype	TM, near_chan	4.7
433330	AW207094	Hs.132816	ESTs	TM	4.7
443033	AF016311	Hs.13550	Homo sapiens two pore potassium channel	TM	4.7
440351	AF030933	Hs.7179	RAD1 (S. pombe) homolog	TM	4.7
453700	U15979	Hs.169228	delta-like homolog (Drosophila)	TM, EGF	4.7
437375	NM_002918	Hs.35120	replication factor C (activator 1) 4 (37kD)	AAA, DEAD, helicase_C	4.7
429944	AW1949	Hs.239440	Homo sapiens clone 24681 mRNA sequenc	TM	4.6
434988	AA18065	Hs.161160	ESTs	TM	4.6
406400	#(NOCAT)	0	0	trypsin, TM	4.6
426301	AW52666	Hs.38440	ESTs	TM	4.6
446224	BE178029	Hs.178582	Homo sapiens cDNA FLJ12832 fls, clone N	TM	4.6
459674	AY741122	Hs.107810	Homo sapiens cDNA FLJ14232 fls, clone N	TM	4.6
409928	AL137163	Hs.57549	hypothetical protein dJ47384	TM	4.6
435244	N7221	Hs.187624	ESTs	phosphatase, h3	4.6
404996	#(NOCAT)	0	0	Peptidase_C1	4.6
407905	AW103655	Hs.252905	ESTs	SS, Ephrin	4.6
441675	AW914329	Hs.5461	ESTs	TM	4.6
420276	AW249038	Hs.190551	ESTs, Highly similar to mosaic protein LR1	TM, h3, Idl_recept_Ls	4.5
422523	AW015128	Hs.250703	ESTs	TM	4.5
438018	AK021160	Hs.5599	hypothetical protein FLJ10288	TM	4.5
457465	AW301344	Hs.195699	ESTs	Phosphotyran	4.5
418446	AK020961	Hs.193455	ESTs	TM, phase	4.5
447459	AW262580	Hs.147574	KIAA1621 protein	TM	4.5
432731	K31178	Hs.287820	Strocnocin 1	SS	4.5
434699	AA643687	Hs.149425	Homo sapiens cDNA FLJ11980 fls, clone H	Nucleoside_tra2	4.4
427626	AK071143	Hs.176565	mitochondrion maintenance deficient (S.	TM	4.4
409032	AT75263	Hs.175038	ESTs	TM	4.4
451389	N73222	Hs.21738	KIAA1008 protein	TM	4.4
453331	AK240565	Hs.8895	ESTs	TM	4.4
448133	AA723157	Hs.73769	folate receptor 1 (arcti)	TM	4.4
429597	NM_003816	Hs.2442	a disintegrin and metalloproteinase domain	TM	4.4
453279	AW893940	Hs.59698	ESTs	TM	4.4
409459	D86407	Hs.54481	low density lipoprotein receptor-related pro	TM, EGF, Idl_recept_Ls	4.4
431708	AW86138	Hs.108073	ESTs	TM	4.4
433906	AL167816	Hs.43335	ESTs	TM	4.4
441423	AY933299	Hs.126877	ESTs	TM	4.4
446770	AV650309	Hs.154986	ESTs, Weakly similar to AF137386 1 plasm	TM	4.3
412076	AK58599	Hs.73149	paired box 1	TM	4.3
432123	NM_012247	Hs.124027	SELENOPHOSPHATE SYNTHETASE; H	AIRS	4.3
448380	AL035414	Hs.21068	hypothetical protein	TM	4.3
453628	AW243307	Hs.170187	ESTs	TM	4.3
452387	UT1207	Hs.25279	eyes absent (Drosophila) homolog 2	TM	4.3
413775	AW409334	Hs.75528	nuclear GTPase	NMR, HSR1	4.3
451592	AW805416	Hs.213897	ESTs	TM	4.3
419311	AA685991		gbuv66at12a1 NCL_OGAP_GC81 Homo s	TM	4.2
452943	BE247449	Hs.31082	hypothetical protein FLJ16525	TM	4.2
428679	AA431765		gbzw6920.0.1 Soarac, beta, NHT Homo s	TM	4.2
436209	AW850417	Hs.254020	ESTs, Moderately similar to unnamed prote	TM	4.2
406076	AL1360179	Hs.137011	Homo sapiens mRNA; cDNA DKFZp47P	TM	4.2
428819	AL135623	Hs.193914	KIAA2575 gene product	TM	4.2
406671	AA129547	Hs.285754	mol proto-oncogene (hepatocyte growth fac	F-actin_cap_A	4.2

	431750	AA514986	Hs.283705	ESTs	TM	4.2
	449554	AA682382	Hs.59882	ESTs	TM	4.2
	480873	AA063456		glc2zf1a07.s1 Soares_pineal_gland_K3HP	TM	4.1
	433929	AW37499	Hs.27379	ESTs	TM	4.2
5	415457	AW081710	Hs.7369	ESTs, Weakly similar to ALU1_HUMAN A	TM	4.1
	444381	BE387335	Hs.283713	ESTs	TM	4.1
	415539	AT32681	Hs.72472	BMFR-1b, bona morphogenetic protein roc	TM	4.1
	421515	Y11339	Hs.100352	GaINac alpha-2, 6-sialyltransferase 1, lung	TM	4.1
	453293	AA382267	Hs.10053	ESTs	TM	4.1
10	409564	AA045857	Hs.54943	fracture callus 1 (rat) homolog	TM	4.1
	426028	H09564	Hs.13268	ESTs	TM	4.1
	440452	AA25136	Hs.55150	ESTs, Weakly similar to CAYP_HUMAN	TM	4.1
	443695	AW204099	Hs.112759	ESTs, Weakly similar to AF126760.1 retina	TM	4.1
	425322	U63630	Hs.155637	protein kinase, DNA-activated; catalytic po	TM	4.1
15	417300	AT765227	Hs.55610	solute carrier family 30 (zinc transporter), m	TM	4.1
	417389	BE220664	Hs.62045	Midline (neurile growth-promoting factor 2	SS, TM	4.1
	452834	AB36527	Hs.105085	ESTs	TM	4.1
	428771	AB028992	Hs.193143	KIAA1069 protein	PI-PLC-X, PI-PLC-Y	4.0
	412314	AA625247	Hs.250689	heat shock factor binding protein 1	TM	4.0
20	435291	BE588452	Hs.5101	ESTs, Highly similar to protein regulating c	TM	4.0
	450564	AJ245587	Hs.25275	Kruppel-type zinc finger protein	KRAB	4.0
	409365	AA702376	Hs.226440	Homo sapiens clone 24881 mRNA sequenc	TM	4.0
	413374	NM_001034	Hs.75319	ribonucleotide reductase M2 polypeptide	ribonuc_red	4.0
	417655	AA702791	Hs.14014	ESTs, Weakly similar to KIAA0973 protein	TM	4.0
25	445941	AT257371	Hs.172636	ESTs	TM, Ucdin_c	4.0
	441134	Y92092	Hs.7678	cellular retinoic acid-binding protein 1	lipocalin	4.0
	411630	U02439	Hs.71119	Putative prostate cancer tumor suppressor	TM	4.0
	118301	AA076201	Hs.187618	ESTs	TM	4.0
30	411945	AL033527	Hs.92137	v-myc avian myelocytomatous viral onco	TGF-beta, Myc_N_term	4.0
	408684	R51377	Hs.12727	hypothetical protein FLJ21610	TM	4.0
	414869	AA157291	Hs.72163	ESTs	TM	4.0
	420201	BE225983	Hs.191533	ESTs	TM	4.0
	416658	U03272	Hs.79432	fibrillin 2 (congenital contractual arachnoid	EGF, TB	3.9
	411274	NM_002776	Hs.69423	kalikrein 10	trypsin, TM	3.9
35	427222	AL117988	Hs.239953	ESTs	TM	3.9
	431858	X53529	Hs.2857	Cadherin 3, P-cadherin (placental)	TM, cadherin,	3.8
	430634	AB060651	Hs.26585	ESTs	TM	3.9
	415716	N59294	Hs.301141	Homo sapiens cDNA FLJ11689 fs, clone H	NAP_family	3.9
	420179	J074530	Hs.21168	ESTs	TM	3.8
40	451280	AA411275	Hs.233840	Homo sapiens cDNA FLJ12542 fs, clone N	TM	3.8
	429496	AA453800	Hs.192793	ESTs	TM	3.8
	421764	AB81535	Hs.99342	ESTs, Weakly similar to KCCL1_HUMAN C	TM	3.8
	447197	R50575		glycylserine 1.1 Soares placenta N2HP Hom	TM, SDF	3.8
45	422939	BE294055	Hs.98427	ESTs	TM	3.8
	414737	AI160386	Hs.125087	ESTs	TM	3.8
	411773	NM_006799	Hs.72028	protease, serine, 21 (testisin)	SS, trypsin	3.7
	425247	NM_005940	Hs.155324	matrix metalloproteinase 11 (stromelysin 3)	SS, Peptidase_M10	3.7
	424433	H04067	Hs.9216	ESTs	TM	3.7
	431846	BE019924	Hs.271580	Uroplakin 1B	TM, transmembrane4	3.7
50	407792	AD077715	Hs.33384	putative secreted ligand homologous to fxl1	SS	3.7
	417531	NM_003157	Hs.1087	serine/threonine kinase 2	SS, protein_kinase	3.7
	434836	AA621629	Hs.118068	ESTs	TM	3.7
	439810	AL106710	Hs.85568	EST	TM	3.7
55	418593	AT750978	Hs.87409	thrombospondin 1	SS, EGF, TSPN	3.7
	427854	AF089251	Hs.40539	chromosome 8 open reading frame 1	TM	3.7
	435304	AA339622	Hs.108897	ESTs	TM	3.7
	425259	AA317439	Hs.28707	signal sequence receptor, gamma (transferr	TM	3.7
	453468	W00712	Hs.32290	DKFZP566F084 protein	TM	3.6
	425943	AA086180	Hs.37636	ESTs, Weakly similar to KIAA1392 protein	TM	3.6
60	411402	BE297855	Hs.65855	NRAS-related gene	CSD, ras, CSD	3.6
	425176	AW015544	Hs.301430	ESTs, Moderately similar to TEF1_HUMA	TM	3.6
	402096	AA305627	Hs.139336	ATP-binding cassette, sub-family C (CFTR	ABC_tran	3.6
	407340	AA310168	Hs.85769	ESTs	TM	3.6
	418524	AA300576	Hs.85769	acidic 82 kDa protein mRNA	TM	3.6
65	438279	AA805165	Hs.165165	ESTs, Moderately similar to ALUR_HUMA	TM	3.6
	439453	BE284974	Hs.6566	thyroid hormone receptor interactor 13	AAA, AAAA	3.6
	441111	AB06667	Hs.126594	ESTs	TM	3.6
	431865	NM_003729	Hs.27076	RNA 3-terminal phosphate cyclase	TM	3.6
	409542	AA503020	Hs.36563	ESTs	Ribosomal_S8	3.6
70	425441	AA449644	Hs.133063	Homo sapiens cDNA FLJ14201 fs, clone N	Aa_trans	3.6
	428137	AA421732	Hs.176959	ESTs	AAA	3.6
	435302	AB058860	Hs.208675	ESTs, Weakly similar to neuron thread pr	TM	3.6
	436689	AW129261	Hs.250656	ESTs	TM	3.6
	443341	AW631480	Hs.8688	ESTs	TM	3.6
75	446261	AA315883	Hs.13399	hypothetical protein FLJ12615 similar to m	ATP-synt_D, PH	3.6
	414345	AL038166	Hs.75914	control vesicle membrane protein	TM	3.5
	414842	X77755	Hs.77367	monokine induced by gamma interferon	SS, IL8	3.5
	410361	BE291804	Hs.62661	guanylate binding protein 1, interferon-indu	TM	3.5
	415796	AA181916	Hs.257924	ESTs	TM	3.5
80	427177	AA055537	Hs.173980	interleukin 1 receptor accessory protein	TM, Iq	3.5
	427687	AW003867	Hs.112403	ESTs	7m1_1	3.5
	444619	BE538082	Hs.8172	ESTs	TM	3.5
	447336	AW135063	Hs.245437	ESTs	AhpC-TSA	3.5
	412519	AA186241	Hs.73980	tropotin T1, skeletal, slow	TM	3.5

418792	AB037805	Hs.88442	KIAA1394 protein	TM	3.5
408031	AA081395	Hs.42173	Homo sapiens cDNA FLJ10356 fs, clone N	TM	3.5
416852	L24498	Hs.80409	growth arrest and DNA-damage-inducible,	TM	3.5
418783	AW382387	Hs.88474	prostaglandin-endoperoxide synthase 1 (pro	EGF	3.5
446080	AA67945	Hs.173696	ESTs	SS	3.5
422278	AF072873	Hs.114218	ESTs	TM,Fz,Fizzled	3.5
442133	AW674138	Hs.128017	ESTs	TM	3.5
410088	AA121686	Hs.100622	ESTs	TM	3.5
452198	AA097560	Hs.61210	ESTs	TM	3.5
408730	AV660717	Hs.47144	DKFZP586N0819 protein	kinase	3.4
436488	BE629509	Hs.261023	hypothetical protein FLJ20958	TM	3.4
409745	AA077391	Hs.145404	gb:7814512 Chromosome 7 Fetal Brain cd	TM	3.4
445870	AW410053	Hs.134005	syntactin 18	TM	3.4
451743	AW074266	Hs.23071	ESTs	TM	3.4
407846	AA426262	Hs.40403	Cop9p300-interacting transactivator, with G	TM	3.4
423250	NM_005665	Hs.274407	proteinase, serine, 16 (thymus)	SS	3.4
412848	AA121514	Hs.70832	ESTs	TM	3.4
413625	AW451103	Hs.71371	ESTs	TM	3.4
417801	AA417383	Hs.82582	Integrin, beta-like 1 (with EGF-like repeat d	SS	3.4
422972	NS9319	Hs.145404	ESTs	TM	3.4
429170	NM_0010394	Hs.2359	dual specificity phosphatase 4; MAP kinase	TM	3.4
450377	AB033091	Hs.24935	ESTs	TM	3.4
443475	AA066470	Hs.134482	ESTs	TM	3.4
419452	US3355	Hs.90572	PTK protein tyrosine kinase 7	TM	3.4
409744	AW575258	Hs.56265	Homo sapiens mRNA: cDNA DKFZp586P	TM	3.4
422789	AK001113	Hs.120842	hypothetical protein FLJ10251	TM	3.4
404440	BNQCAT	0	0	TM,neur_chan	3.4
417412	U16899	Hs.82112	interleukin 1 receptor, type 1	SS,TRILg	3.4
411828	AW161449	Hs.72280	wingless-type MMTV integration site farr	wnt	3.4
417177	NM_004458	Hs.81452	fatty-acid-Coenzyme A ligase, long-chain 4	SS	3.4
421013	M62397	Hs.1345	mutated in colorectal cancers	TM	3.4
427072	U38046	Hs.1345	gb:55610.1 Soares fetal liver spleen INF	Ribosomal_L22e	3.4
433703	AA210863	Hs.3532	ramo-like kinase	kinase	3.4
434254	AJ271379	Hs.21175	ESTs	TM	3.4
444188	AJ393185	Hs.19175	ESTs	TM	3.4
445109	N67953	Hs.145920	ESTs	TM	3.4
400981	0	0	0	Asparaginase_2	3.3
450236	AW162998	Hs.24684	KIAA1376 protein	TM	3.3
419836	AW65439	Hs.167172	ESTs	TM	3.3
437951	T34520	Hs.4210	Homo sapiens cDNA FLJ13059 fs, clone N	TM	3.3
446996	T15757	Hs.22452	Homo sapiens cDNA FLJ21084 fs, clone	TM	3.3
430687	BE274217	Hs.249247	heterogeneous nuclear protein similar to rat	am	3.3
410080	NM_001448	Hs.58367	glycylserine	SS	3.3
415546	AA244189	Hs.210863	glucocorticoid-induced NCL-CCAP_Py1 Homo sapi	TM	3.3
429509	AF022246	Hs.210863	cell adhesion molecule with homology to L	TM	3.3
413289	AA128061	Hs.114992	ESTs	TM	3.3
440006	AK000517	Hs.6844	hypothetical protein FLJ20510	TM	3.3
401435	BNQCAT	0	0	TM	3.3
420072	AW961196	Hs.207725	ESTs	TM	3.3
421426	AA291101	Hs.33020	Homo sapiens cDNA FLJ20434 fs, clone K	TM	3.3
425851	NM_001490	Hs.15942	glucosaminyl (N-acetyl) transferase 1, core	SS	3.3
443255	AA049783	Hs.241294	ESTs	TM	3.3
453116	AJ276690	Hs.146086	ESTs	Ribosomal_L5_C	3.2
456546	AE90321	Hs.203845	ESTs. Weakly similar to TWIK-related acid	TM	3.2
430106	NM_004736	Hs.227656	xenotropic and polytropic retrovirus recepto	TM	3.2
416281	U05559	Hs.1154	oxidized glycoprotein 1, 120kD (muslin b)	arg,Glyco_hydro_18	3.2
433800	AA034361	Hs.135150	lung type I cell membrane-associated glyco	TM	3.2
425159	NM_004341	Hs.154868	carbamoyl-phosphate synthetase 2, separata	TM	3.2
428882	AA430915	Hs.131748	ESTs. Moderately similar to ALU1_HUMA	carb_anhydase	3.2
409533	AW069443	Hs.21291	mitogen-activated protein kinase kinase kin	TM	3.2
411248	AA551538	Hs.69521	KIAA1358 protein	TM	3.2
421379	Y15221	Hs.103982	small inducible cytokine subfamily B (Cys-	SS,IL8	3.2
403029	BE550182	Hs.127826	RafG1-like protein 3, mouse homolog	TM	3.2
414945	BE078358	Hs.77667	lymphocyte antigen 6 complex, locus E	SS	3.2
444471	AB020684	Hs.11217	KIAA0877 protein	TM	3.2
421674	T10707	Hs.296355	neuronal PAS domain protein 2	Ribosomal_L31e	3.2
434163	AW974720	Hs.25208	ESTs	TM	3.2
421991	NM_014918	Hs.110468	KIAA0690 protein	SS	3.2
409589	AW439930	Hs.256914	ESTs	TM	3.2
414147	BE091834	Hs.121929	gb:IL2-BT0731-240400-069-003 BT0731	TM	3.2
414661	T97401	Hs.121417	ESTs. Weakly similar to unnamed protein p	TM	3.2
437537	AA258674	Hs.134182	ESTs	A2M	3.1
439702	AW065525	Hs.134182	ESTs	TM	3.1
420552	AK000492	Hs.98908	hypothetical protein	ICE_p20,CARD	3.1
441028	AK333660	Hs.17558	ESTs	SS	3.1
425264	AA333553	Hs.203969	ESTs. Weakly similar to gonadotropin indu	SS,Bornesin	3.1
421209	S73265	Hs.1473	gastin-releasing peptide	TM	3.1
441859	AW194364	Hs.128022	ESTs. Weakly similar to FIG1 MOUSE FIG	TM	3.1
415451	H19415	Hs.286720	ESTs. Moderately similar to ALU1_HUMA	SS,Ephrtn	3.1
447886	AW444754	Hs.211517	ESTs	homeobox	3.1
419978	NM_001454	Hs.93974	forkhead box J1	Fork_head	3.1
446219	AZ87344	Hs.149827	ESTs	MIP	3.1
448428	AF282874	Hs.21201	nectin 3; DKFZP568B0846 protein	TMlg	3.1
407615	AW753085	0	gb:FM1-CT0247-151299-005-003 CT0247	TM	3.1

410518	AW976443	Hs.285655	ESTs	RasGEF, PH, RhoGEF	3.1	
418396	A765805	Hs.26691	ESTs	TM	3.1	
427855	R61263	Hs.98265	ESTs	TM	3.1	
423272	W26140	Hs.110667	ESTs	TM	3.1	
450711	AL133661	Hs.24583	hypothetical protein DKFZp434C0328	TM	3.1	
414774	X02419	Hs.77274	plasminogen activator, urokinase	SS, kringle, hypoxin	3.1	
422363	T63979	Hs.115474	replication factor C (activator 1) 3 (38kD)	TM	3.1	
423622	AW411096	Hs.94785	hypothetical protein LOC57163	TM	3.1	
428698	AA852773	Hs.297839	ESTs; Weakly similar to neogenin [H]Laake	TM	3.1	
427051	BE178110	Hs.173374	ESTs	TM	3.1	
428422	H55709	Hs.2250	leukemia inhibitory factor (cholesterol; di	SS	3.1	
425906	BE207039	Hs.75621	serine (or cysteine) proteinase inhibitor, dif	TM	3.1	
428626	AB023226	Hs.202276	KIAA1009 protein	TM	3.1	
417517	AF001176	Hs.82238	POP4 (processing of precursor, S. cerevisia	TM	3.1	
406137	BC00CAT	Hs.153203	MyoD family inhibitor	TM	3.1	
424680	AL035588	Hs.61418	microtubule-associated protein 1	TM	3.1	
410252	AW021182	Hs.97393	KIAA0328 protein	SS	3.1	
420392	A242930	Hs.18612	Homo sapiens cDNA: FLJ21909 fs, clone	voltage_CLC, CBS	3.1	
423629	AW021173	Hs.18618	Homo sapiens cDNA: FLJ22398 fs, clone	Glyco_hydro_2	3.1	
423334	DE3078	Hs.23584	fibroblast activation protein; alpha	SS, Peptidase_S9	3.1	
449802	AW011804	Hs.418	ESTs	TM	3.1	
450506	NM_004460	Hs.280728	signal transducer and activator of transcript	SH2, STAT	3.1	
411584	NM_004419	Hs.72988	bone marrow stromal cell antigen 2	TM	3.1	
422530	AW072300	Hs.118110	gk-QV-OT0033-010400-182-407 OT0033	TM	3.1	
422128	AW081145	Hs.123114	cystatin SN	SS, cystatin	3.1	
409767	NM_001898	Hs.94634	ESTs	TM	3.1	
419727	AA227609	Hs.113503	keratophen (importin) beta 3	TM	3.1	
42244	Y08990	Hs.152981	CDP-diacylglycerol synthase (phosphatidat	TM	3.1	
456844	A264155	Hs.72830	ESTs	SS	3.1	
423258	A093491	Hs.5638	KIAA1572 protein	BTB	3.1	
416896	A712662	Hs.36938	activating transcription factor 1	TM	3.1	
447312	AK34346	Hs.12251	Homo sapiens cDNA FLJ11163 fs, clone P	TM	3.1	
445021	AK002025	Hs.118722	flucosyltransferase 8 (alpha (1,6) fucosyltran	SS	3.1	
422611	AA158177	Hs.33713	myo-inositol 1-phosphate synthase A1	TM	3.1	
453597	BE281130	Hs.151787	US snRNP-specific protein, 116 kD	0	arEts	3.1
401187	BE247275	Hs.151787	glucocorticoid 12- α Stratiagene pancreas (3720	TM, FG-GAP	3.1	
410008	AA075552	Hs.75256	regulator of G-protein signalling 1	RGS	3.1	
413268	AL039079	Hs.47783	ESTs; Weakly similar to 112540 hypotheti	TM	3.1	
414080	AA116267	Hs.97365	ESTs	TM	3.1	
426882	AA383108	Hs.18498	Homo sapiens cDNA FLJ12277 fs, clone M	TM	3.1	
427651	AW405731	Hs.54578	ESTs	TM	3.1	
439444	A2271652	Hs.279905	clone HQ0310 PROQ301p1	TM	3.1	
453001	AF217513	Hs.301192	EST cluster (not in UniGene)	TM, ASC	3.1	
444895	A074383	Hs.289008	Homo sapiens cDNA FLJ21814 fs, clone	TM	3.1	
441992	AW972542	Hs.123335	Homo sapiens cDNA FLJ13148 fs, clone M	TM, 7tm_1	3.1	
414725	AA763971	Hs.263607	hypothetical protein PROQ3077	SS	3.1	
434241	AF115913	Hs.153954	TRAM-like protein	TM	3.1	
424882	NM_012288	Hs.183380	ESTs; Moderately similar to ALU7_HUMA	TM	3.1	
411997	AA375975	Hs.110165	ribosomal protein L23 homolog	TM	3.1	
421977	W94187	Hs.5199	HSPC150 protein similar to ubiquitin-conju	TM	3.1	
436481	AA379567	Hs.40735	frizzled (Drosophila) homolog 3	TM, 7tm_2, Frizzled	3.1	
407872	AB039723	Hs.163900	ESTs	TM	3.1	
442677	AA292998	Hs.204732	gkyl4M02.41 Soares adult brain N2bSHB5	TM	3.1	
416130	H40739	Hs.204732	matrix metalloproteinase 26	TM, Peptidase_M10, 7tm_1	3.1	
434775	AF291664	Hs.66295	Homo sapiens HSPC311 mRNA, partial cd	TM	3.1	
414664	AA587775	Hs.5378	spondin 1, (I-spondin) extracellular matrix	SS	3.1	
457590	A012809	Hs.132103	ESTs	TM	3.1	
116946	A785641	Hs.30445	Homo sapiens mRNA full length insert cDN	TM, SPRY, 7tm_1	3.1	
60	457940	AL380159	Hs.30445			3.1

TABLE 19B:

Phay: Unique Eos probaset identifier number
CAT number: Gene cluster number
Accession: Genbank accession numbers

Phay	CAT Number	Accession
70	407615	1005404_1
	409073	108951_1
	409745	115237_1
	410026	116812_1
	414147	142127_1
	414315	143512_1
75	416120	1571266_1
	419311	182791
	419546	185766_1
	422128	211994_1
	427072	274884_1
80	426679	294046_1
	438593	467661_1
	447197	711623_1
	AW753085	AW753082 AW054744 AW753107 AW753087
	AA063458	AA063018 AA44822
	AA077391	AA077318 AA068754 AA07451 AW069012 AA921874 AA286833 AA150722 BE152353 AW188822 BE152450
	AA076552	BE142525 BE142527
	BE091634	
	Z24878	AA494098 F13654 AA494040 AA413127
	H46739	H51513 H15979
	AA065591	AW074261 AA26240 AW07451 AA631399 AW974262
	AA244199	AA244272 H57440
	AW681145	AA490718 MB5637 AA304375 T06057 AA331991
	H35048	W68645 AA397668 H36047
	AA431765	AA432015
	AA828995	AA834279 AA926361
	R36075	AA366546 R36167

TABLE 15C:

Play: Unique number corresponding to an Ecos probe set

Ref: Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham L. et al." refers to the publication entitled "The DNA sequence of human chromosome 22" Dunham, et al. (1999) Nature 393:402-499

Strand: Indicates DNA strand from which exons were predicted

NI_position: Indicates nucleotide positions of predicted exons

Play	Ref	Strand	NI_position
420681	2842777	Minus	91446-91003,92123-92265
401197	9719705	Plus	176341-176452
401435	8217934	Minus	54508-55233
404440	7528051	Plus	80430-81581
404339	6862697	Plus	175316-176476
404596	6007899	Plus	37999-38145,38652-38958,39727-39872,40557-40674,42351-42450
405547	1054740	Plus	124361-124520,124914-125050
406137	9166422	Minus	30487-31058
406357	9255126	Minus	58313-58499
406400	9256298	Plus	1553-1712,1876-2140,4252-4385,5922-6077

Table 16A lists about 92 genes up-regulated in mucinous-type ovarian cancer compared to normal adult tissues. These were selected as for Table 14A, except that the "average" ovarian cancer level was set to the 75th percentile amongst various mucinous-type ovarian cancers, and the tumor/normal tissue ratio was greater than or equal to 2.5.

TABLE 16A: ABOUT 92 UP-REGULATED GENES, MUCINOUS OVARIAN CANCER VERSUS NORMAL ADULT TISSUES

Play: Primary

Ex_Accn: Exemplar Accession

UG ID: UniGene ID

Title: UniGene title

Prot. Dom.: Predicted protein domain structure

ratio: ratio tumor vs. normal tissues

Play	Ex_Accn	UG ID	Title	Prot. Dom.	ratio
432981	C14187	Hs.103538	ESTs		34.9
432938	T27013	Hs.3132	steroidogenic acute regulatory protein		28.0
418007	M13509	Hs.83169	Matrix metalloproteinase 1 (interstitial collag	SS,Peptidase_M10	22.3
451181	A755330	Hs.207461	ESTs		10.8
422838	U55511	Hs.30743	Preferentially expressed antigen in melanom		10.0
407638	AJ404672	Hs.286693	EST		9.3
450159	AJ02416	Hs.200771	ESTs, Weakly similar to CAN2_HUMAN		9.2
426890	AJ353167	Hs.41294	ESTs		9.1
421155	H87975	Hs.102287	lysozyme	SS,Lysyl_oxidase	8.9
437099	N77793	Hs.48659	ESTs, Highly similar to LMA1_HUMAN L	laminin_EGF	7.6
453866	AW291498	Hs.200557	ESTs		7.6
438496	AW840171	Hs.265398	ESTs, Weakly similar to transformation-rel		7.4
418738	AW398533	Hs.6692	soluble carrier family 7, member 11		7.2
431956	AJ002032	Hs.272245	Homo sapiens cDNA FLJ11170 fs, clone P	RA	7.0
449579	AW207260	Hs.134014	prostate cancer associated protein 6		6.7
424586	NM_003401	Hs.150930	X-ray repair complementing defective repa		6.7
445891	AW261342	Hs.189460	ESTs		6.2
424717	H03754	Hs.152213	wingless-type MMTV integration site fami	wnt	6.1
452705	H48905	Hs.246005	ESTs		6.1
421265	NM_005102	Hs.1360	cytochrome P450, subfamily XVII (steroid	TM,p450	5.5
408562	AJ435323	Hs.31141	Homo sapiens mRNA for KIAA1568 prote		5.3
420159	AJ572450	Hs.99785	ESTs		5.3
451105	A761324	Hs.146343	gb-w60b11.x1 NCL_CGAP_Co16 Homo s		5.2
409049	AJ423132	Hs.146343	ESTs		5.0
448574	WQ1178	Hs.154140	ESTs	TM	5.0
423811	AW295698	Hs.50395	homeo box C4		4.9
427469	AA403084	Hs.269347	ESTs		4.9
447033	AJ357412	Hs.157691	EST - not in UniGene	PH	4.9
424433	H04607	Hs.9218	ESTs		4.9
448811	AJ590371	Hs.174759	ESTs	TM	4.8
444330	AJ597655	Hs.49265	ESTs		4.8
409041	AJ503325	Hs.50391	KIAA1199 protein		4.7
418735	N48789	Hs.44609	ESTs		4.5
416661	AA634543	Hs.79440	IGF-1 mRNA-binding protein 3	IGF-domain	4.5
430073	U06136	Hs.232070	telomerase-associated protein 1	WD40	4.4
407581	AW072003	Hs.40958	heparan sulfate (glycosaminoglycan) 3-O-sulfotran		4.4
422260	AJ319993	Hs.105484	ESTs, Weakly similar to LITHOSTATHIN		4.4
421110	AJ250717	Hs.1355	cathelin E	SS,asp	4.3
445676	AJ247763	Hs.16928	ESTs		4.2
430704	AW133091	Hs.16928	gb-RC2-ST0186-240400-111-407 ST0186		3.8
414569	AF109298	Hs.118258	Prostate cancer associated protein 1	TM	3.8
438078	AO16377	Hs.131693	ESTs		3.7
434032	AW009951	Hs.206892	ESTs		3.7
445557	AW612141	Hs.278575	ESTs	7tm_1	3.7
439759	AL359055	Hs.67709	Homo sapiens mRNA full length insert cDN		3.6
456666	BE065813	gb-RC2-BT0318-110100-012-408 BT0318			3.6
448844	AJ581519	Hs.177164	ESTs		3.5
448946	Z45051	Hs.22920	similar to S69A01 (cat) glucose induced g	SS	3.5
438018	AQ021160	Hs.5599	hypothetical protein FLJ10298	TM	3.4
458123	AW892676	gb-CM3-NN0004-280000-131-c12 NN0004			3.4
407385	AA610150	Hs.272072	ESTs, Moderately similar to ALLU7_HUMA		3.4
424894	H83520	Hs.153678	reproduction 8	SS,UBX	3.3

	424639	A1917494	Hs.131329	ESTs		3.3
	414083	AL121262	Hs.257786	ESTs		3.2
	426471	M22440	Hs.170009	transforming growth factor, alpha	SS,EGF	3.2
5	428527	A4441837	Hs.90250	ESTs		3.1
	406126	#(NOCAT)	0		TM,cNMP_binding	3.1
	452699	AW265380	Hs.213062	ESTs		3.1
	425842	A1587490	Hs.159523	HK-2 (Drosophila) homolog B	homeobox	3.1
	428576	AL037624	Hs.194695	ras homolog gene family, member 1	ras	3.1
10	436396	A583467	Hs.295112	Homo sapiens cDNA FLJ114411, clone H	wnt	3.0
	454077	AC005952	Hs.37062	insulin-like 3 (Leydig cell)	SS,insulin_kinase	3.0
	404253	#(NOCAT)	0		histone	2.9
	452461	N78221	Hs.108106	transcription factor	GSA,PHO	2.9
	429597	NM_103816	Hs.2442	alpha disintegrin and metalloprotease domain	TM	2.8
15	413289	AA128061	Hs.114992	ESTs		2.9
	429703	T93154	Hs.28705	ESTs		2.9
	407629	AA045084	Hs.29725	Homo sapiens cDNA FLJ13197 fs, clone N		2.8
	424706	AW298244	Hs.293507	ESTs		2.8
	424086	AC351010	Hs.102267	lysyl oxidase	Lysyl_oxidase	2.8
	408427	AW194270	Hs.177236	ESTs		2.7
20	450375	AA005647	Hs.8850	alpha disintegrin and metalloprotease domain		2.7
	440899	AA161520	Hs.279525	hypothetical protein PR02605		2.7
	428819	AL135623	Hs.193914	KIA00575 gene product		2.7
	422556	BE545072	Hs.122579	ESTs		2.7
	428549	AA442153	Hs.104744	ESTs, Weakly similar to AF208555.1 BM-0		2.7
25	423200	UI1879	Hs.169228	delta-like homolog (Drosophila)	TM,EGF	2.7
	402380	AA643981	Hs.102406	ESTs		2.6
	428651	AF196478	Hs.188401	annexin A10	TM,annexin	2.6
	417649	AW291587	Hs.82733	Mdogen 2	EGF,IGF_recept_Lb	2.6
	433700	AE029426	Hs.550	hypothetical protein B mRNA editing enzyme, ca	TM	2.6
30	417975	AA641836	Hs.300385	Homo sapiens cDNA: FLJ23186 fs, clone		2.6
	448756	AT739241	Hs.171480	ESTs		2.6
	425087	R52424	Hs.126509	ESTs		2.5
	444153	AK001610	Hs.10414	hypothetical protein FLJ10748	Kalch	2.5
	443211	AI128368	Hs.143655	ESTs		2.5
35	415263	AA948033	Hs.130853	ESTs	histone	2.5
	428867	AW016936	Hs.233064	ESTs	GSHPx	2.5
	438839	AE278038	Hs.31409	ESTs		2.5
	455386	AW935875	gbt-QV3-DT0019-120100-055-005 DT0019			2.5
40	419952	J05581	Hs.89603	mucin 1, transmembrane	TM,SEA	2.5
	452055	A1377431	Hs.293772	ESTs		2.5

TABLE 16B:

Pkey: Unique Eos probe/identifier number
 CAT number: Gene cluster number
 Accession: Genbank accession numbers

	Pkey	CAT Number	Accession
	430704	322217_1	AW613091 AW206555 AA634443
50	451105	859053_1	AT761324 AW880941 AW880937
	455396	1287756_1	AW935875 BE068116 BE160251
	455666	1349545_1	BE065813 BE065788 BE065889 BE065832
	458123	479942_1	AW692676 AA653877 D44747

TABLE 16C:

Pkey: Unique number corresponding to an Eos probe/identifier
 Ref: Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham L. et al." refers to the publication entitled "The DNA sequence of human chromosome 22" Dunham, et al. (1995) Nature 402:489-495
 Strand: Indicates DNA strand from which exons were predicted
 NL_position: Indicates nucleotide positions of predicted exons

	Pkey	Ref	Strand	NL_position
	404253	9367202	Minus	55975-59055
	406129	9160131	Plus	2567-3056

Table 17A lists about 183 genes up-regulated in endometrioid-type ovarian cancer compared to normal adult tissues. These were selected as for Table 14A, except that the "average" ovarian cancer level was set to the 75th percentile amongst various endometrioid-type ovarian cancers, and the tumor/normal tissue ratio was greater than or equal to 2.5.

TABLE 17A: ABOUT 183 UP-REGULATED GENES, ENDOMETRIOID OVARIAN CANCER VERSUS NORMAL ADULT TISSUES

	Pkey	Ref	Strand	NL_position	Ex. Accn	UG ID	Title	Prot. Dom.	ratio
	452838	U65011	Hs.30743				Preferentially expressed antigen in melanoma		38.9
	435094	AS661129	Hs.277523						28.9
	428153	AW513143	Hs.95357				hypothetical protein FLJ22252 similar to SR		24.1
	428187	A587303	Hs.285529				ESTs		23.9
	449034	A626049					gbt41 a09.x1 NCL_CGAP_U11 Homo sapi		19.2
80	433102	NM_007197	Hs.31664				fizzled (Drosophila) homolog 10	TM,Fz,Fizzled	15.7

142925	A089319	Hs.179243	EST6		15.7
438817	A023799	Hs.163242	ESTs		13.6
447033	A1387412	Hs.157601	EST - not in UniGene	PH	13.5
433222	AW514472	Hs.228415	ESTs, Moderately similar to ALU8_HUMA		13.1
422856	BE548972	Hs.152279	ESTs		12.9
450451	AW591528	Hs.262072	ESTs		11.9
453964	A561466	Hs.127144	ESTs	homeobox	11.5
442438	A555559		gb262603.s1 NCL_CGAP_K05 Homo sa		11.4
413623	AW972870	Hs.291069	ESTs	SS	10.3
440501	A505358	Hs.128612	ESTs		9.7
416681	A153453	Hs.79440	IGF-II mRNA-binding protein 3	KH-domain	9.6
421478	A083204	Hs.972528	class II cytokine receptor ZCYTOR7	SS,Tissuun_fac	9.6
448706	AW291095	Hs.21814	Homo sapiens cDNA FLJ13585 fs, clone P		9.2
410566	AA373210	Hs.43047	Integrin beta 8	SS,Integrin_B	8.7
435933	A582895		KIAA0041 protein	homeobox	8.4
427121	A272815	Hs.173656	distal-less homeo box 5		8.1
420610	A1683183	Hs.99348	ESTs		8.0
427356	AW023482	Hs.97849	KIAA1500 protein		8.0
446577	A504053	Hs.15420	carbonic anhydrase VIII	carb_anhydrase	7.5
431118	BE354901	Hs.255502	ESTs, Weakly similar to ALUB_HUMAN	HLH,Myo_N_term	6.9
448112	AW245919	Hs.301018	N-myc		6.6
451106	BE382701	Hs.25960	ESTs		6.3
448433	A072096	Hs.9012	ESTs		6.1
432922	A053306	Hs.36708	budding uninhibited by benzimidazoles 1 (y		6.3
434636	AA033764	Hs.241334	ESTs		6.1
453688	AW381270	Hs.194110	Homo sapiens mRNA; cDNA DKFZp434C		5.9
422605	AA436989	Hs.121017	H2A histone family, member A	histone	5.8
402932	A4250737	Hs.72472	SMFPR, bone morphogenetic protein rec		5.7
447179	A1528402	Hs.5933	Homo sapiens cDNA FLJ12684 fs, clone N		5.6
418134	AA337769	Hs.86617	ESTs		5.5
452449	BE394412	Hs.61252	ESTs	homeobox	5.5
402689	A457693	Hs.223972	Homo sapiens cDNA FLJ13352 fs, clone O	TUUPF0016	5.5
413335	A1613318	Hs.48442	ESTs		5.5
441081	A584019	Hs.169006	ESTs, Moderately similar to plakophilin 2b	PAX	5.4
428029	H05940	Hs.253071	ESTs		5.3
419183	L06669	Hs.89563	cytochrome P450, subfamily XOV (vitamin	p450	5.3
409094	AW337237		gb262201.s1 NCL_CGAP_Pan1 Homo sa		5.2
432938	T27013	Hs.3132	steroidogenic acute regulatory protein	START	5.1
410102	AW248508	Hs.279727	ESTs		5.0
447835	AW59123	Hs.164129	ESTs	SS	5.1
438202	AW169287	Hs.22588	ESTs		5.0
423992	AW598292	Hs.137206	Homo sapiens mRNA; cDNA DKFZp564H		5.0
425906	A5032559	Hs.161700	KIAA1133 protein	TM	5.0
452461	A78223	Hs.108106	transcription factor	GSA,PHD	4.9
430691	C14187	Hs.103538	ESTs		4.8
441675	A1914329	Hs.5481	ESTs		4.7
425695	NM_005401	Hs.159238	protein tyrosine phosphatase, non-receptor	Band_41_Y_phosphatase	4.6
460340	AW565593	Hs.126276	ESTs		4.5
428579	NM_005756	Hs.184942	G protein-coupled receptor 64	TM	4.5
444783	A0201468	Hs.62180	ESTs	PH	4.4
451489	A797515	Hs.270550	ESTs, Moderately similar to ALU7_HUMA		4.4
413395	A1266507	Hs.145689	ESTs		4.3
415263	AA948033	Hs.130853	ESTs	histone	4.2
413988	M81893	Hs.75668	glutamate decarboxylase 1 (brain, 67kD)	pyridoxal_deC	4.2
432030	AL137878	Hs.27607	Homo sapiens mRNA; cDNA DKFZp564N		4.1
418852	BE32037	Hs.272294	hypothetical protein FLJ20059		4.1
446431	R45852	Hs.153486	ESTs		4.1
434891	A4814309	Hs.123583	ESTs		4.0
415138	AW973942	Hs.46524	ESTs	G-patch	4.0
451897	A1516289	Hs.109057	ESTs, Weakly similar to ALU5_HUMAN A		4.0
447112	H17800	Hs.7154	ESTs		3.9
420833	NM_014581	Hs.99526	odorant-binding protein 2b	TM,lipocalin	3.9
458574	A741182	Hs.101818	Homo sapiens cDNA FLJ14233 fs, clone N		3.9
415138	C18356	Hs.78045	tissue factor pathway inhibitor 2 TFPI2	Kunitz_BPTL-G-gamma	3.7
414083	AL121282	Hs.257766	ESTs		3.7
442006	AW975193	Hs.282663	ESTs		3.7
402731	AA125885	Hs.58145	Thymosin, beta, identified in neuroblastoma	Thymosin	3.7
424906	A1556086	Hs.153716	Homo sapiens mRNA for Hmnc33 protein,		3.7
456552	NM_002448	Hs.1494	mch (Drosophila) homeo box homolog 1 (fo	homeobox	3.6
429125	AA446854	Hs.271004	ESTs		3.6
435538	A5011540	Hs.45330	low density lipoprotein receptor-related pr		3.7
458861	A1530223		gb245059.s1 Proliferating Erythroid Cells	PHD	3.5
418506	AA084248	Hs.85339	G protein-coupled receptor 39		3.5
423123	NM_012247	Hs.124027	SELENOPHOSPHATE SYNTHETASE; H	AIRS,AIRS	3.4
437960	A1556986	Hs.222194	ESTs		3.4
402099	AA032279	Hs.616035	STEAP1	TM	3.4
407162	N63855	Hs.142634	zinc finger protein		3.4
429219	A1970672	Hs.48638	chromosome 11 open reading frame 8: beta		3.3
445929	A452487	Hs.145526	ESTs		3.3
405262	AW409872	Hs.271168	ESTs, Moderately similar to ALU7_HUMA		3.3
457979	AA776655	Hs.270942	ESTs	TM	3.3
402606	R(NOCAT)			SS,EGF	3.2
426471	M22440	Hs.170009	transforming growth factor, alpha		3.2

5	430294	AI538226	Hs.135184	ESTs	polyprony_Lynt	3.2
	448027	A458437	Hs.177224	ESTs		3.2
	432619	AW291722	Hs.278526	related to the N terminus of tre	TBC	3.2
	413527	BE162682	Hs.246973	ESTs		3.2
	441377	BE219239	Hs.202556	ESTs		3.2
10	441085	AW136551	Hs.181245	Homo sapiens cDNA FLJ12532 fis, clone N		3.2
	433527	AW235613	Hs.133020	ESTs		3.2
	450171	AL133661	Hs.24593	hypothetical protein DKFZp434C0328	TM	3.2
	419807	RT7402		ghy7f11.1 Scores placenta Nb2HP Hom		3.1
	418867	DS1771	Hs.89404	msl (Drosophila) homoio box homolog 2	homeobox	3.1
15	419335	AW950146	Hs.284137	Homo sapiens cDNA FLJ12888 fis, clone N		3.1
	450480	X32125	Hs.25040	zinc finger protein Z39	zf-C2H2	3.1
	420149	AA255320	Hs.89265	ESTs		3.1
	413415	AA625282	Hs.34569	ESTs		3.1
	438966	AW979074		glo:EST391184 MAGE resequences, MAGP		3.1
20	413041	AA493557	Hs.105276	ESTs	Oxysterol_BP	3.1
	415245	NS9559	Hs.27252	ESTs		3.1
	412140	AA219691	Hs.73525	RAB6 interacting, kinesin-like (rabkinesin6	kinesin	3.0
	431707	R21328	Hs.267905	hypothetical protein FLJ10422		3.0
	448816	AB033352	Hs.22151	KIAA1226 protein		3.0
25	447885	AW444754	Hs.211517	ESTs	homeobox	3.0
	450221	AA326102	Hs.24541	cytoskeleton associated protein 2		3.0
	406997	U07807	Hs.194762	Human metallothionein IV (MTIV) gene, c		3.0
	434266	H59125	Hs.133525	ESTs	TM	3.0
	420440	NM_002407	Hs.97564	mannosylglucosyl 2	Uteroglobulin	3.0
30	420181	AI330089	Hs.158951	ESTs		3.0
	458627	AW088842	Hs.97984	ESTs; Weakly similar to WASP-family pro		2.9
	452055	AI371431	Hs.293772	ESTs		2.9
	429563	A68874	Hs.211587	Human phosphatidylcholine 2-acylhydrolase	C2,PLA2_B	2.9
	415125	AF061198	Hs.301941	Homo sapiens mRNA for norepinephrine tr	TM,SNF	2.9
35	412708	R26830	Hs.108137	ESTs	TM,7bL_2,Rho_GDI	2.9
	451389	N73222	Hs.21738	KIAA1008 protein		2.9
	423537	NM_004655	Hs.127137	cell 2 (conductin, cell)		2.9
	435185	AA659490	Hs.189109	dimethylarginine dimethylaminohydrolase	DDX,RGS	2.9
	428054	AF948685	Hs.265619	ESTs		2.9
40	448243	AW369771	Hs.77435	ESTs		2.9
	425723	NM_014420	Hs.153311	disclasp (Planopus laevis) homolog 4	SS	2.9
	432415	T16971	Hs.285014	centromere protein F (350/400kd, mitosi)		2.9
	414747	U30872	Hs.77204	0		2.9
	409195			ESTs		2.9
45	449674	AA133588	Hs.10053	eyes absent (Drosophila) homolog 2	Hydrolase	2.8
	452367	U71207	Hs.29279	ESTs		2.8
	428093	AW594506	Hs.104630	ESTs		2.8
	409640	U78722	Hs.55481	zinc finger protein 165	TM,zf-C2H2,SCAN	2.8
	424169	AA338339	Hs.153797	ESTs	mllo_carr	2.8
50	409638	AW150420	Hs.21335	ESTs		2.8
	440048	AA897461	Hs.158469	ESTs; Weakly similar to envelope protein (2.8
	426990	AA353157	Hs.41254	ESTs		2.8
	452771	T05477		ghc:ST03366 Fetal brain, Stratagene (cal93		2.8
	422505	AL120862	Hs.124165	ESTs; (HS)APAP protein (programmed os		2.8
55	416524	H55044		ghy77705.1 Scores fetal liver spleen 1NF	zf-C3HC4	2.8
	445870	AW410053	Hs.13405	synthase 18	TM	2.7
	441952	AW972542	Hs.289308	Homo sapiens cDNA: FLJ21814 fis, clone		2.7
	447342	AI199288	Hs.19322	ESTs; Weakly similar to IIII ALU SUBFAM		2.7
	421247	BE361727	Hs.102910	general transcription factor IIB, polypeptid		2.7
60	415752	AA349573	Hs.152618	ESTs		2.7
	410658	AW105231	Hs.192035	ESTs		2.7
	437698	RS1837	Hs.7990	ESTs		2.7
	450027	L49504	Hs.85195	ESTs; Highly similar to (U35)(q25.1;p4)		2.7
	435889	AW129261	Hs.252055	ESTs		2.7
65	438676	AI376278	Hs.100921	ESTs; Weakly similar to ALU7_HUMAN A	SCAN	2.7
	428479	Y00272	Hs.184572	cell division cycle 2, G1 to S and G2 to M	pl kinase	2.7
	438406	AW105723	Hs.125346	ESTs		2.7
	437938	A350087		ESTs; Weakly similar to Gag-Pol polypro		2.7
	419917	AA320068	Hs.93701	Homo sapiens mRNA; cDNA DKFZp434E		2.7
70	434836	AA651629	Hs.118088	ESTs		2.7
	448404	BE069973		ghc:RC6-BT0709-013030-021-G07 BT0709		2.7
	444078	BE246910	Hs.10209	US mRNAP-specific 40 kDa protein (HnpB	WD40	2.7
	409575	NM_001089	Hs.123114	cystatin SN	SS,cystatin	2.6
	443775	AF251664	Hs.204732	matrix metalloproteinase 26	TM,Peptidase_M10,7m_1	2.6
75	427961	AW293165	Hs.143134	ESTs		2.6
	426568	AW135534	Hs.97162	ESTs		2.6
	424717	H03754	Hs.152213	wingless-type MMTV integration site fami	wnt	2.6
	434669	AF151534	Hs.92023	core histone macroH2A.2	Histone_A1pp,DUF27	2.6
	417369	BE250564	Hs.82045	Mdkine (neurot growth-promoting factor 2	SS,TM,PTN_MK	2.6
80	451009	A4013140	Hs.115707	ESTs		2.6
	429774	AI522215	Hs.60883	ESTs	pl kinase	2.6
	439951	AI347067	Hs.124636	ESTs	TM	2.6
	417576	AA339449	Hs.82285	phosphoribosylglycinamide formyltransfera	ARS,formyl_transf	2.5
	416806	NM_000286	Hs.76993	peroxisomal biogenesis factor 7	WD40	2.5
	429800	AL045633	Hs.44269	ESTs	AW_Xan_oth_C	2.5
	457300	AI301740	Hs.173381	dhcydroprymidine-like 2	dhcydroxylase	2.5
	459583	AI907673		ghc:IL-BT152-080399-004 BT152 Homo sa		2.5
	440870	AI687284	Hs.150539	Homo sapiens cDNA FLJ15793 fs, clone T	PAX,	2.5

446693	AW750373	Hs.42315	Homo sapiens cDNA FLJ13036 fs, clone N	TM	2.5
407289	AA135159	Hs.203349	Homo sapiens cDNA FLJ12149 fs, clone M		2.5
409882			0		2.5
431322	AW970622		gb:EST382704 MAGE resequences, MARG		2.5
424081	NM_005413	Hs.139120	30kD		2.5
451996	AW514021	Hs.245510	ESTs		2.5
403381	#(NOCAT)		0		2.5
419488	AK316241	Hs.90691	nucleoschism/nucleoplasm 3	SS	2.5
419882	NM_004595	Hs.89433	ATP-binding cassette, sub-family C (CFTR)	TM,ABC_membrana	2.5

TABLE 17B:

Play: Unique Eos probe/identifier number

CAT number: Gene cluster number

Accession: Genbank accession numbers

Play	CAT Number	Accession
409304	1038811_1	AW861542 AW861555 AW858006 AW857990 AW858007
416624	1604694_1	H59044 T47567 H57691 T50292
419807	188252_1	R77402 AA262462 AA250988 R06794
431322	331543_1	AW970622 AA503089 AA502956 AA502969 AA502985 T32188
437936	44573_2	AA503087 NT0208 R07040 N38819 A308119 AW957577 H03200 A1251473 H53937 AW971573 R73728 W01059 AW957671 AA908695 AA9251875
		AJ202001 A120532 W87891 T85004 U71456 T83291 BE328571 T75102 R34725 AA884922 BE328517 A1219788 AA884444 N82578 F13493
		AA527794 A1560251 AW874058 AL134043 AW253363 AA563345 AW008282 AA488964 AA283144 A1890387 A1950344 A1741345 A1689052
		AA282915 AW102898 A1872193 A1763273 AW173586 AW150329 A1653632 A1762688 AA368777 AA468892 A1356394 AW100813 A1539942
		AA642785 AA505575 AA505512 A1361530 AW029370 BC512881 AW720897 AW513501 AW510843 AA041029 AW655538 AA160029 AA337489
		AW951101 AA216689 AA2181874 A1819225 AW250562 A1683338 A1858506 AW276905 A1832006 AA397284 AA508741 AW072629 AW513596
		AA253274 AA569789 H56288 N22288 H84729 H60052 T92487 A1022058 AA780419 AA551005 W08071 AW513456 A1373032 A1562499 F00531
		H83488 W37181 W78622 R56566 A002839 R67840 AA300207 AW959581 T63226 F04005
		AW970074 AA324941 AA328650
		AA628955 AA348793 AA526381
		AA959598 A1916584 R61781 T77332 F07756 F08149 F07647
		BE089973 AA498612 AW985032
		794817_1 A024048 AW1117770 A558350
		T05477 T07855 A1917711
		A0330223 A630470

TABLE 17C:

Play: Unique number corresponding to an Eos probe/seq

Ref: Sequence source. The 7 digit numbers in this column are Genbank identifier (GI) numbers. "Dunham I. et al." refers to the publication entitled "The DNA sequence of human chromosome 22" Dunham, et al. (1999) *Hum. Genet.* 102:469-495

Strand: indicates DNA strand from which exons were predicted

N_positlon: indicates nucleotide positions of predicted exons

Play	Ref	Strand	N_positlon
403882	2847777	Minus	110431-110708
402606	9509429	Minus	81747-82094
403381	9438267	Minus	26009-26178

Table 18 lists lists 178 genes up-regulated in ovarian cancer compared to normal adult tissues that are likely to encode proteins that are secreted into blood, lymph, or other bodily fluids. These genes, and/or their protein products, in combination or alone, are ideal candidates for the early diagnosis of ovarian cancer. These were selected from 59860 proteins on the Affymetrix/Exon Array chip array such that the ratio of "average" ovarian cancer to "average" normal adult tissues was greater than or equal to 2.4, and that are likely to encode secreted or extracellularly-coded proteins. The "average" ovarian cancer level was set to the 50th percentile amongst various ovarian cancer samples. The "average" normal adult tissue level was set to the 50th percentile amongst various non-malignant tissues. In order to remove gene-specific background levels of non-specific hybridization, the 15th percentile value amongst various 149 non-malignant tissues was subtracted from both the numerator and the denominator before the ratio was evaluated.

TABLE 18: ABOUT 178 UP-REGULATED GENES ENCODING SECRETED PROTEINS, OVARIAN CANCER VERSUS NORMAL ADULT TISSUES

Play: Primekey

Ex Acc: Exon/Accession

UG ID: UniGene ID

Title: UniGene title

ratio: ratio tumor vs. normal tissues

Play	Ex Acc	UG ID	Title	ratio
428579	NM_005756	Hs.184942	G protein-coupled receptor 64	30.6
435982	AB018305	Hs.5378	spondin 1, (I-spondin) extracellular mat	29.4
427365	D31162	Hs.178729	integrin, type X, alpha 1 (Schmid metaph	27.0
423736	AA588155	Hs.8760	ESTs	22.7
418007	M13509	Hs.83169	Matrix metalloproteinase 1 (interstitial c	20.6
438993	M73780	Hs.52620	Integrin, beta 8	16.7
428654	AK601668	Hs.169895	similar to SALL1 (sal (Drosophila)-like	16.5
438920	AL350104	Hs.283553	Homo sapiens mRNA full length insert cDN	16.5
400289	X07820	Hs.2258	Matrix Metalloproteinase 10 (Stromelysin	16.2
421155	H87879	Hs.102267	lysyl oxidase	16.1
431989	AW972876	Hs.291668	ESTs	15.9
426335	BE306109	Hs.125027	ESTs	15.9
424581	M62062	Hs.150917	caterin (cadherin-associated protein), a	15.7
428976	AL037824	Hs.194695	ras homolog gene family, member 1	15.1
416209	AA238776	Hs.78078	MAO2 (mitotic arrest deficient, yeast, h	15.0
433706	AW872627	Hs.5761	ESTs	14.7
452065	A137431	Hs.293772	ESTs	13.2
410102	AW248508	Hs.279727	ESTs	12.5
426392	H10233	Hs.2265	secretory granule, neuroendocrine protai	12.4

5	402605	AA434329	Hs.36563	hypothetical protein FLJ22418	11.5
	443715	AS63187	Hs.9700	cyclin E1	10.7
	433496	AF064254	Hs.49765	VLCG-H1 protein	10.6
	418601	AA279490	Hs.86388	calnegin	10.3
	409289	AA576953	Hs.22972	Homo sapiens cDNA FLJ13352 fls.	10.1
	446537	AJ245671	Hs.12844	EGF-like-domain, multiple 6	9.9
	427344	NM_000869	Hs.2142	5-hydroxytryptamine (serotonin) receptor	9.7
	428479	U00272	Hs.184572	cell division cycle 2, G1 to S and G2 to	9.7
	429782	NM_003754	Hs.22669	Ras-GTPase-activating protein SHC-domain	9.5
	412240	AA219691	Hs.73625	RAB6 interacting, kinesin-like (rabkines)	9.4
10	407881	AW072003	Hs.40968	heparan sulfate (glucosamine)-3-O-sulfate	9.4
	435509	AA68679	Hs.181915	ESTs	9.3
	408008	BE258227	Hs.48815	serine/threonine kinase 15	9.0
	433764	AW753678	Hs.39582	ESTs	9.0
	445413	AA151342	Hs.12677	CGI-147 protein	8.7
	438078	AB016377	Hs.131693	ESTs	8.6
	447342	AI195260	Hs.15322	ESTs; Weakly similar to III ALU SURFA	8.1
	415138	C18356	Hs.78045	tissue factor pathway inhibitor 2 TFP2	7.7
	418478	U38945	Hs.1174	cyclin-dependent kinase inhibitor 2A (me)	7.5
	426320	W47595	Hs.185300	transforming growth factor, beta 2	7.5
20	424001	W67893	Hs.137476	KIAA1051 protein	7.4
	458881	NM_007358	Hs.31016	DNA-BINDING PROTEIN M96	7.3
	425465	L18954	Hs.1904	protein kinase C, beta	7.2
	425776	U25128	Hs.159499	parathyroid hormone receptor 2	7.1
	424620	AA101043	Hs.151254	kallikrein 7 (chymotryptic; elastom com)	7.0
	409178	BE333948	Hs.50915	kallikrein 5	6.8
	433159	AB035988	Hs.150587	kinesin-like protein 2	6.6
	410630	U25009	Hs.84173	ESTs; Highly similar to VAB1	6.5
	449348	Z45051	Hs.22220	similar to S6801 (cathe) glucose induc	6.5
	422995	AB68872	Hs.288965	carboxylase (ferroxidase)	6.4
30	425371	D49441	Hs.155981	mesothelin	6.4
	448706	AW291095	Hs.21814	class II cytokine receptor ZCYTOR7	6.3
	441081	AS64015	Hs.182008	ESTs; Moderately similar to placophilin	6.4
	447207	AA442333	Hs.17731	hypothetical protein FLJ12892	6.3
	420440	NM_002407	Hs.97644	mammaglobin 2	6.2
	457030	AB01740	Hs.173381	dihydropyrimidinase-Dco 2	6.2
	415139	AW175942	Hs.48824	ESTs	6.0
	40870	AB687284	Hs.150539	Homo sapiens cDNA FLJ13793 fls, clone TH	6.0
	417866	AW067903	Hs.82772	"collagen, type XI, alpha 1"	6.0
	437960	AB69586	Hs.222194	ESTs	6.0
40	410555	U72649	Hs.64311	a disintegrin and metalloproteinase doma	5.9
	433447	U29195	Hs.3281	neuronal pentonin II	5.9
	437099	N77793	Hs.48659	ESTs; Highly similar to LMA1	5.9
	427510	Z47542	Hs.178312	small nuclear RNA activating complex, po	5.9
	422867	L32137	Hs.1584	cartilage oligomeric matrix protein	5.8
	444478	W07318	Hs.240	M-phase phosphoprotein 1	5.7
	445640	AW969626	Hs.31704	ESTs; Weakly similar to KIAA0227 [Hsap]	5.7
	453775	NM_002916	Hs.35120	replication factor C (activator 1) 4 (7)	5.6
	419971	AA320068	Hs.53701	Homo sapiens mRNA; cDNA DKFZp434E232	5.6
	424539	LD2911	Hs.150402	activin A receptor, type 1	5.5
50	418455	AA222279	Hs.201555	ESTs	5.5
	424345	AK001380	Hs.145479	Homo sapiens cDNA FLJ10518 fls, clone NT	5.4
	426514	BE510633	Hs.301122	bone morphogenetic protein 7 (osteogenic)	5.4
	425154	NM_001851	Hs.154850	collagen, type IX, alpha 1	5.4
	416530	U62801	Hs.79361	kallikrein 6 (neurosin, zyme)	5.3
	445238	AK001676	Hs.12457	hypothetical protein FLJ10814	5.2
	425230	AW195285	Hs.194097	ESTs	5.1
	431130	NM_006103	Hs.2719	epididymis-specific; whey-acidic protein	5.1
	411571	AA122393	Hs.70811	hypothetical protein FLJ20516	5.1
	432158	W33165	Hs.55548	ESTs; Weakly similar to unknown protein	5.0
60	447020	T73208	Hs.16968	hypothetical protein FLJ11946	4.9
	443268	AB000271	Hs.129445	hypothetical protein FLJ12496	4.9
	448133	AA723157	Hs.73759	folate receptor 1 (adult)	4.9
	418682	NM_004996	Hs.89433	ATP-binding cassette, sub-family C (CFTR)	4.8
	428568	NM_002214	Hs.194098	Integrin, beta 8	4.8
	427528	AB077143	Hs.179565	mitochondrion maintenance deficient (S.	4.7
	406400	AA343629	Hs.104570	kallikrein 8 (neurotensin)rasin	4.7
	439324	R66696	Hs.35398	ESTs	4.6
	426300	U15978	Hs.168228	delta-like homolog (Drosophila)	4.6
	448027	AA58437	Hs.177224	ESTs	4.6
70	404995	NM_001333	Hs.87417	Cathepsin L2	4.6
	443633	AB051631	Hs.135501	ESTs	4.5
	409450	DB6407	Hs.54461	low density lipoprotein receptor-related	4.5
	414747	U30872	Hs.77204	centromere protein F (350/400kd, mitosis	4.3
	423123	NM_012247	Hs.124027	SELENOPHOSPHATE SYNTHETASE 4	4.3
	448275	BE314434	Hs.20630	synaptic Ras GTPase activating protein 1	4.2
	419528	AW930992	Hs.93786	DNFZP58602223 protein	4.1
	420736	AB263022	Hs.82204	ESTs	4.1
	419790	U79250	Hs.93201	glyoxal-3-phosphate dehydrogenase 2 (mi	4.1
	414343	ALJ36166	Hs.75914	coated vesicle membrane protein	4.0
80	430654	AJ245537	Hs.25276	Kruppel-type zinc finger protein	3.9
	445808	AB555234	Hs.298083	ESTs	3.9
	417389	BE260984	Hs.82045	Mitkino (neurite growth-promoting factor	3.8
	425247	NM_005940	Hs.155324	matrix metalloproteinase 11 (stromelysin	3.8

	430634	AI806051	Hs.26685	ESTs	3.8
	431846	BE019924	Hs.271580	Urokinase 1B	3.7
	416558	U03272	Hs.79432	fibronin 2 (congenital contractual ara	3.7
5	407792	AD077115	Hs.35384	putative secreted ligand homologous to 1	3.7
	420585	AW505139	Hs.279844	hypothetical protein FLJ10033	3.7
	407756	AA116021	Hs.38260	ubiquitin specific protease 18	3.6
	411773	NM_005799	Hs.72026	protease, serine, 21 (testis)	3.6
	421928	AF015758	Hs.108643	polyadenylation binding protein-interactin	3.5
	431958	X63829	Hs.2877	Cadherin 3, P-cadherin (placental)	3.5
10	410467	AF102546	Hs.63331	dachshund (Drosophila) homolog	3.5
	418753	AW382887	Hs.88474	prostaglandin-endoperoxide synthase 1 (p	3.4
	422278	AF072873	Hs.114218	ESTs	3.4
	431840	AK534842	Hs.2890	PCNA domain, class 5, transcription facto	3.4
	408730	AV650717	Hs.47144	DKFZ568N0819 protein	3.4
	419452	U33635	Hs.90572	PTK7 protein tyrosine kinase 7	3.3
	421841	AA030187	Hs.108650	KIA0936 protein	3.3
	430884	AT720078	Hs.291197	ESTs	3.3
	456546	AI690321	Hs.203845	ESTs, Weakly similar to TWIK-related ac	3.2
	410587	U24389	Hs.65436	lysyl oxidase-like 1	3.2
20	414774	X02419	Hs.77274	plasminogen activator, urokinase	3.2
	420552	AK000492	Hs.98306	hypothetical protein	3.1
	421991	NM_014918	Hs.110488	KIA0990 protein	3.1
	418140	BE813836	Hs.83551	microtubular-associated protein 2	3.1
	458924	BE242158	Hs.24427	DKFZ56601648 protein	3.1
25	411789	AF245305	Hs.72157	Ucma sapiens mRNA: cDNA DKFZp564119	3.1
	434241	AF119913	Hs.283507	hypothetical protein PRO3077	3.1
	422611	AA158177	Hs.118722	fluoroyltransferase 8 (alpha 1,6) fuosy	3.1
	409533	AW989543	Hs.21291	mitogen-activated protein kinase kinase	3.1
	416391	AJ878827	Hs.79284	mesoderm specific transcript (mouse) hom	3.1
30	412604	AW578234	Hs.47144	DKFZ568N019 protein	3.1
	425851	NM_001490	Hs.159542	glucosaminyl (N-acetyl) transferase 1, c	3.0
	431259	NM_006580	Hs.251391	claudin 16	3.0
	418557	BE143802	Hs.246645	ESTs	3.0
35	428242	H55709	Hs.2250	leukemia inhibitory factor (cholinergic	3.0
	418359	AL043202	Hs.50073	chromosome segregation 1 (yeast homolog)	3.0
	407590	A612608	Hs.5378	spondin 1, [I-spondin] extracellular mat	2.9
	415741	NM_007019	Hs.93022	ubiquitin carrier protein E2-C	2.9
40	428330	L22524	Hs.2256	matrix metalloproteinase 7 (matlyshn,	2.9
	417315	AI080042	Hs.180450	ribosomal protein S24	2.9
	438777	AA825487	Hs.142179	ESTs, Weakly similar to ORF2 [Musculus	2.9
	442286	AB27249	Hs.224388	ESTs	2.9
	428248	AI126772	Hs.40479	ESTs	2.9
45	430319	AA834826	Hs.66718	RAD54 (S.cerevisiae)-like	2.8
	436252	AJ395519	Hs.120969	Homo sapiens cDNA FLJ11592 fs	2.8
	419488	AJ316241	Hs.89891	nucleoside/nucleosidephosphate 3	2.8
	434288	AW189075	Hs.116265	ESTs	2.7
	407872	AB039723	Hs.40735	frizzled (Drosophila) homolog 3	2.7
	431611	U58766	Hs.264428	tissue specific transplantation antigen	2.7
50	433981	BS4512	Hs.22746	Homo sapiens cDNA FLJ14224 fs, clone NT	2.7
	453779	N35187	Hs.43368	ESTs	2.7
	433968	NM_006456	Hs.288215	sialyltransferase	2.7
	428641	A052358	Hs.183725	ESTs	2.7
	428778	A0000230	Hs.183326	fibroblast growth factor receptor-like 1	2.7
55	415346	NM_006338	Hs.26312	geloma amplified on chromosome 1 protein	2.6
	433883	AA114212	Hs.9530	serine (or cysteine) proteinase inhibitor	2.6
	420162	BE378432	Hs.96577	cyclin-dependent kinase 4	2.6
	447149	BE295857	Hs.339	TAR (HIV) RNA-binding protein 2	2.6
	433656	AW974941	Hs.292385	ESTs	2.6
60	408210	N61189	Hs.43104	ESTs	2.6
	430551	A4951854	Hs.185187	kinase protein 9 gene	2.5
	422599	BE387202	Hs.118638	non-melanocytic cells 1, protein (NM23A)	2.5
	421802	BE261450	Hs.108408	CG-78 protein	2.5
	446211	A021993	Hs.14331	S100 calcium-binding protein A13	2.5
	404022	W73781	Hs.265470	prothymosin beta 2	2.5
65	453012	TG5504	Hs.31334	putative mitochondrial outer membrane pr	2.5
	419581	AA897581	Hs.128773	ESTs	2.5
	448153	Y10605	Hs.20621	HMT1 (hRNP methyltransferase, S. cerevi	2.5
	418220	AA811838	Hs.281759	ESTs	2.5
	432180	Y18418	Hs.272622	RuvB (E.coli homolog)-like 1	2.4
70	406850	AI624300	Hs.172928	collagen, type I, alpha 1	2.4
	429893	AW247090	Hs.57101	minichromosome maintenance deficient (S.	2.4
	421654	AW163267	Hs.165469	suppressor of var1 (S.cerevisiae) 3-like	2.4
	409956	AW103364	Hs.77	H.sapiens actinin beta-A subunit (exon 2	2.4
	407584	W25945	Hs.18745	ESTs	2.4
75	448796	AA147829	Hs.33193	ESTs, Highly similar to AC007228 3 BC372	2.4

Table 19 lists about 17 genes up-regulated in ovarian cancer compared to normal adult tissues that are likely to encode proteins that are secreted into blood, lymph, or other body fluids. These genes, and/or their protein products, in combination or alone, are ideal candidates for the early diagnosis of ovarian cancer. These were selected from 59660 proteins on the Affymetrix/Exon Hu3d GeneChip array such that the ratio of "average" ovarian cancer to "average" normal adult tissues was greater than or equal to 2.4, and that are likely to encode secreted or extracellularly-local proteins. The "average" ovarian cancer level was set to the 50th percentile amongst various ovarian cancer samples. The "average" normal adult tissue level was set to the 90th percentile amongst various non-malignant tissues. In order to remove gene-specific background levels of non-specific hybridization, the 15th percentile value amongst various non-malignant tissues was subtracted from both the numerator and the denominator before the ratio was evaluated.

TABLE 19: ABOUT 17 GENES, AND COMBINATIONS THEREOF, USEFUL FOR DIAGNOSIS OF OVARIAN CANCER

UG ID: UniGene ID

Title: UniGene Title

% tumors: percent of tumors detected expressing gene

Single genes:

UG ID	Title	% tumors
Hs.5378	spondin 1, (I)-spondin extracellular matrix protein	77
Hs.12844	EGF-like-domain 6	85
Hs.151254	kallikrein 7 (chymotrypsin; stratum corneum)	66
Hs.59764	mammaglobin 2	73
Hs.155591	mesothelin (lysofollin)	57
Hs.2258	Matrix Metalloproteinase 10 (Stromelysin 2)	21
Hs.50915	kallikrein 5	27
Hs.301122	bone morphogenetic protein 7 (osteogenic protein 1) (BMP7)	54
Hs.73551	collase 6 (neumatin, tyms)	38
Hs.83169	MMP 1 (interstitial collagenase)	23
Hs.72026	protease, serine, 21 (testisin)	16
Hs.39384	putative secreted ligand homologous to tly1	46
Hs.2719	epithelial-specific, whey-acidic protein type; four-disulfide core	91
Hs.155324	matrix metalloproteinase 11 (stromelysin 3)	11
Hs.15584	cartilage oligomeric matrix protein	25
Hs.169300	TGF beta 2	21
Hs.2250	leukemia inhibitory factor (cholinergic differentiation factor)	23

Exemplary Combinations:

EGF-like-domain 6 + mammaglobin 2	93
kallikrein 7 + mesothelin	71
mammaglobin 2 + bone morphogenetic protein 7	88
EGF-like-domain 6 + bone morphogenetic protein 7	91
kallikrein 7 + bone morphogenetic protein 7 + testisin	75
kallikrein 7 + mammaglobin 2 + mesothelin	84
mammaglobin 2 + bone morphogenetic protein 7 + TGF beta 2	91
EGF-like-domain 6 + bone morphogenetic protein 7 + MMP 1	95

Table 20A lists about 1025 genes up-regulated in ovarian cancer compared to normal adult tissues. Genes associated with ovarian cancer were selected from the 53462 probesets such that the ratio of "average" ovarian cancer to "average" normal adult tissues was greater than or equal to 5.0. The "average" ovarian cancer level was set to the 50th percentile value amongst various ovarian cancer specimens; the "average" normal adult tissue level was set to the 50th percentile value amongst various non-malignant tissues. In order to remove gene-specific background levels of non-specific hybridization, the 15th percentile value amongst various non-malignant tissues was subtracted from both the numerator and the denominator before the ratio was evaluated.

Tables 20B-24B list accession numbers for Phyx's lacking UniGene/ID's for tables 20A-24A. For each probe set is listed a gene cluster number from which oligonucleotides were designed. Gene clusters were compiled using sequences derived from Genbank ESTs and mRNAs. These sequences were clustered based on sequence similarity using Clustering and Alignment Tools (DoubleTwist, Oakland California). Genbank accession numbers for sequences comprising each cluster are listed in the "Accession" column.

Tables 20C-24C list genomic positioning for Phyx's lacking UniGene ID's and accession numbers in tables 20A-24A. For each predicted exon is listed genomic sequence source used for prediction. Nucleotide locations of each predicted exon are also listed.

TABLE 20A:

Phyx: Unique Eca probe set Identifier number

ExAccn: Exemplar Accession number, Genbank accession number

UniGene/ID: UniGene number

UniGene Title: UniGene title

Pred. Protein Dom.: Predicted protein domain

Rt: Ratio of tumor to normal body tissue

Phyx	ExAccn	UniGene ID	UniGene Title	Pred. Protein Dom.	Rt
421296	NM_002666	Hs.103253	perlepin	perlepin_SS	32.5
453028	AB056532	Hs.31442	RecC protein-like 4	DEAD,hefcase_C_Fork_head	27.6
422310	AA316622	Hs.98370	cyclochrome P450, subfamily IIS	SS,TM,kinase,h3lg	26.5
437897	AA770361	Hs.145170	hypothetical protein FLJ22968	SS,TM,4-DHHC	26.3
445374	AA523256	Hs.24756	ESTs, Moderately similar to al	SS,kinase,PMP22_Claudin	22.6
441021	AWS78716	Hs.7644	H1 histone family, member 2	SS	22.3
405518	BE384836	Hs.3454	KIAA1821 protein	SS	21.3
413436	AF236018	Hs.58051	sphingosine kinase 1	DAGic	21.2
424420	BE514743	Hs.146688	prostaglandin E synthase	MAPEGS,SS,TM,MAPEG	20.7
422645	LA5027	Hs.118890	glycogen synthase kinase 3 alp	kinase,SS,Es	20.7
422098	HD3117	Hs.111497	similar to mouse neuronal prot	TM	20.2
423556	AW139588	Hs.36986	ESTs	SS,kinase,PMP22_Claudin	20.1
436485	X59135	Hs.156110	Immunoglobulin kappa constant	SS,ss	19.9
423552	AF052122	Hs.130712	Homo sapiens clone 23929 mRNA	ABCI,SS,PID,PID	19.3
431773	BE409442	Hs.268557	pleckstrin homology-like domain	PH,SS,LIM,Tropotin	19.4
422178	AF291918	Hs.112657	dymch, anosomal, intermediate	WD40,SS	18.5
420839	A179252	Hs.282950	hypothetical protein MGC10870	SS,DS,UPF0139,Glyco_hydro	18.4
441356	BE384061	Hs.182885	ESTs, Weakly similar to JC5024	SS,TM,ark	18.5
424659	AW891298	Hs.331601	Homo sapiens, Similar to cyste	SS,Fork_head	18.1
428924	AB65858	Hs.125283	ESTs	SS	17.5
458914	A488957	Hs.170861	ESTs, Weakly similar to Z195_H	SS,TM,ld_recept,ldf,le	17.2
451643	M54437	Hs.234799	breakpoint cluster region	RhoGEF,RhoGAP,PH,C2	17.5
439108	AW163034	Hs.6467	synaptogrin 3	Synaptogrin,SS,TM,POZ,WD	16.9
432945	ALP43683	Hs.6467	hypothetical protein FLJ10803	SS	16.8

110418	D31382	Hs.63325	transmembrane protease, serine	SS,TM,ld_recept_Ln,lypsl	16.8
438424	A912458	Hs.25955	hypothetical protein FLJ14996	SS,TM	16.7
409435	A910721	Hs.59424	ESTs	SS	16.4
415969	W33191	Hs.26297	hypothetical protein FLJ20258	SH3,G13	16.2
421612	AF161254	Hs.106195	BCL antigen	ld_recept_Ln,SS,TM	16.0
458177	NM_012391	Hs.79414	prostate epithelium-specific E	Ets,SAM_PNT	15.7
414837	U24266	Hs.77448	aldehyde dehydrogenase 4 family	aldohd	15.8
432631	H8379	Hs.165563	hypothetical protein DKFZp434N	TM,DnaJ,UBA,AhGag,homocB	15.5
454017	AW052317	Hs.347130	hypothetical protein FLJ22709	SS,TM,mypsin_head,RA,DAGL	15.5
401278			Target Exon	Band_41	15.4
446404	A084452	Hs.22158	hypothetical protein FLJ21988	SS	15.4
412259	A080337	Hs.61465	hypothetical protein	GFO_DH,MocA,GFO_JDH,MocA	15.4
406220	W81105	Hs.146520	myosin, heavy polypeptide 9, n	myosin_head,Myosin_tail	15.1
423081	AF262992	Hs.123159	sperm associated antigen 4	TM	14.9
421495	A553067	Hs.149152	ESTs, Weakly similar to RHOP M	SS,rm,SS	14.7
418923	A445558	Hs.62408	hypothetical protein FLJ22573	SS,TM,BTB_Pep_M129_propesp	14.6
413244	AWS55951	Hs.152625	kruppel-related zinc finger pr	E1_dehydrog	14.7
406901	M14624		gloHuman 4-beta-galactosyltran	DNAI,SS	14.6
416006	A4324251	Hs.78950	branched chain keto acid dehyd	Metallophos	14.6
436185	BE350717	Hs.5074	similar to S. pombe dmi1	SS	14.4
455557	AW95839		gloCVA-BN004-110209-108-N07 B	SS,PL-PLC-X,PI-PLC-Y,C2	14.2
434518	H56995	Hs.37372	Homo sapiens DNA binding pep1	SS	14.1
421489	A922821	Hs.32433	ESTs	SS,PL-PLC-X,PI-PLC-Y,C2	14.2
444441	AW613541	Hs.301394	hypothetical protein MGC3101	SS	14.0
432017	A433632	Hs.12854	thymosin α_1 , type 1 recepto	SS	13.9
446572	AV659151	Hs.282961	ESTs	SS	13.7
434058	AA97935	Hs.127274	ESTs	SS,Collagen,COLP,TSPN	13.6
432481	AW61845	Hs.151504	Homo sapiens cDNA FLJ11973 fs	SS,Prothymosin_C2	13.6
447304	Z89093	Hs.18079	phosphatidylinositol glycan, c	SS,Topoisomerase_I,Topois	13.3
421182	A0284855	Hs.104480	ESTs	SS,rf-COOH	13.3
407767	W15398	Hs.36628	hypothetical protein	SS	13.3
456942	AW61823	Hs.105752	putative c-Myc-responsive	SQS_PSY	13.2
437457	A472790	Hs.270923	ESTs, Weakly similar to S65657	SS	13.1
430178	AW449612	Hs.152475	ESTs	Sac7PH	12.9
430399	A916284	Hs.199671	ESTs	SS,TM,Ooductin,BIR	12.7
416219	BE465223	Hs.136912	hypothetical protein MGC10796	SS,RNA_pol_K	12.7
410219	T83226	Hs.171552	occludin	rf-C3Hc1,TM,Sulfate_trans	12.7
426220	C00138	Hs.8535	Homo sapiens mRNA for KIAA1668	rf-C2H2,LIM,SS,Exo_endo_p	12.6
439233	AA831993	Hs.292767	hypothetical protein FLJ23109	SS,C2H2,SH3,PH	12.6
425010	BE465277	Hs.154195	E4F transcription factor 1	SS,cadherin,Cadherin_C,le	12.6
423801	NM_015071	Hs.152442	GTPase regulator associated wt	SS,TM,SS,TM	12.5
417626	T85105	Hs.15471	ESTs	SS,TM,SS,TM	12.5
409261	BE315042	Hs.19210	hypothetical protein MGC11308	SS,TM,SS,TM	12.5
426568	F09247	Hs.247735	protocadherin alpha 10	SS,TM,SS,TM	12.5
411570	BE144884	Hs.314341	ESTs	SS,TM,SS,TM	12.5
430397	A924533	Hs.105607	bicarbonate transporter relate	HCO3_cotransp,SS,TM	12.5
423767	H18283	Hs.132753	F-box only protein 2	F-box,SS,F-box,HORMA	12.4
441805	AA255136	Hs.301914	neuronal specific transcripto	LIM,SS,LIM	12.3
402365			Target Exon	SS,SS,TM,lg	12.2
414371	A905865		thymosin, beta 4, X chromosome	Thymosin	12.2
445780	R31107		glybH1g01.1 Soares placenta	SS,TM,ln,3lg,SS,TM	12.1
428782	X12630	Hs.183400	interleukin 6 receptor	SS	12.1
427695	R88483	Hs.172862	intron of Elicadid D homolog 1	SS	12.1
400460			CT1002253*gt[12909]ppgP23267	SS,TM,SCAN,rf-C2H2,KRAB	12.0
407341	AA918886	Hs.204918	ESTs, Weakly similar to ALU.8	SS,TM	12.0
424049	A9014524	Hs.138330	KIAA0624 protein	SS	11.9
422872	BE326786	Hs.187646	ESTs	TM	11.9
450800	BE395161	Hs.1390	proteasome (prosome, macropain	SS	11.8
428648	AF027278	Hs.188021	potassium voltage-gated channel	cNMP_binding	11.7
423232	NM_020922	Hs.2950	S100 calcium-binding protein A	S_100,ahand,SS,ahand_S_	11.6
417061	A975944	Hs.188891	Homo sapiens cDNA FLJ12033 fs	CTF_NFI	11.5
451195	U10492	Hs.438	mesenchymal homeo box 1	homeobox,SS	11.5
417955	AA424317	Hs.6229	KIAA1698 protein	SS,TM,Glyco_hydro_31,Glyc	11.5
425500	NM_014638	Hs.170156	KIAA450 gene product	SS	11.4
433124	U51712	Hs.13775	hypothetical protein SMAP31	SS	11.4
444001	A095087	Hs.152299	ESTs, Moderately similar to S6	CPase_u_chain,PYC_QADA,H	11.4
419298	A453479	Hs.85890	pyruvate carboxylase	SS	11.4
425653	AW074040	Hs.185973	degenerative spermatocyte (hom	ion_trans,SS,TM	11.2
411408	W57666	Hs.65949	calcium channel, voltage-depen	SS	11.2
404438			Target Exon	WH1,PB0,WH2,SS	11.2
427448	BE464449	Hs.2157	Wiskott-Aldrich syndrome (occe	Target Exon	11.2
405220			Homo sapiens cDNA FLJ12300 fs	Band_41,ERM	11.1
432125	AW972667	Hs.183006	ESTs, Weakly similar to Z195_H	SS,SS,Glyco_tranf_43,COLF	11.1
408832	AW056990	Hs.63428	ESTs	SS	11.0
400206			Ees Control	SS,Sema,phosase,TIG,PSI,e	11.0
455253	R35917	Hs.301338	hypothetical protein FLJ12587	SS,TM,Cys_rich_FGFR	10.9
407605	W03512	Hs.6479	hypothetical protein MGC13272	Topotin,SS,glycolytic_en	10.8
432143	AL040183	Hs.123494	Homo sapiens, clone IMAGE:4178	SS,TM,BIR,UO_con	10.8
446639	BE091926	Hs.16244	mitotic spindle coiled-coil re	SS	10.8
443539	A076765	Hs.263899	ESTs, Moderately similar to AL	SS	10.8
411298	AW33658	Hs.263899	gloFMO-LT0017-031299-001-N07 L	SS	10.8
409557	BE182955	Hs.211193	ESTs	rm,SS,rm	10.8
435158	AW63317	Hs.65598	DAZ associated protein 1	SS	10.8
444410	BE387350	Hs.33719	ESTs, Moderately similar to S6	SS	10.6

428048	BE514382		FK506-binding protein 3 (29kD)	FKBP.PIP5K	10.6
424707	BE081914	Hs.10844	Homo sapiens cDNA FLJ14476 fls	SS,SS,TM,Sema	10.6
416819	U77735	Hs.80205	plm-2 oncogene	phosphatase,SS,TM,OTU,K _{intra}	10.5
419341	N17463	Hs.118085	ESTs, Weakly similar to ALU1_H	SS,TM,UPF00916	10.5
444359	A087160	Hs.143594	ESTs, Weakly similar to HSAL_H		10.5
404333			C7001735/g17768635(hh)BAAS5	vwd	10.5
401210			C1200519.g17711004(gene)NP_05		10.5
457941	A004525	Hs.14587	ESTs, Weakly similar to AF1618	SS,TM,SS,TM	10.1
401694			NM_0248172Homo sapiens hypoth		10.3
441790	AW294802	Hs.132208	ESTs		10.3
444008	BE544855	Hs.236572	ESTs, Weakly similar to SFRA_H	SS,SS,SAC1_GANP	10.2
438185	Y19188	Hs.320461	ESTs	SS	10.2
432031	AF038196	Hs.272367	halfheart protein (putative sh	junc	10.2
416471	198872		gb-yd31a12a1 Soares fetal liv		10.1
433573	AF234887	Hs.576552	cathenin, EGF LAG seven-pass G	SS,TM,Tm_2_EGF_cathetin,	10.1
417371	N74813	Hs.289149	ESTs		10.1
428167	AA770021	Hs.16332	ESTs	SS,jug3	10.0
419563	AA526235	Hs.193162	Homo sapiens cDNA FLJ11983 fls		10.0
412674	X04106	Hs.74451	calpain 4, small subunit (30K)	ethand,SS,CAP_GLY	10.0
425863	U43604	Hs.159501	Homo unidentified mRNA, parti		9.9
442739	NM_007274	Hs.9679	cytosolic acyl coenzyme A thro	Acyl-CoA_hydro,SS,TM	9.9
429469	M64590	Hs.27	glycine dehydrogenase (decarbo	GDCP,GDC-P	9.8
420029	BE258876	Hs.94446	polyamine-modulated factor 1	aldc ₁ ,Int_Ured,SS,TM,glu	9.8
445625	BE246743		hypothetical protein FLJ22635	SS,TM	9.8
433339	AJ58300		ESTs	SS,tm	9.8
407235	C20569	Hs.169407	SAC2 (suppressor of actin muta	SS,TM,Ribosome_s13,Gatac	9.8
428758	AA433588	Hs.98502	CA125 antigen; mucin 16	SS	9.7
401349			isolectin polyphosphatase-1-phos		9.7
437915	AJ537993	Hs.202312	Homo sapiens clone N11 H1982D		9.7
424511	BE300512	Hs.193557	ESTs, Moderately similar to AL		9.7
423366	Z80345	Hs.127610	acyl-Coenzyme A dehydrogenase,	Acyl-CoA _{dh} ,Acyl-CoA _{dh} ,M	9.7
425143			NM_013432:Homo sapiens nuclea	ank,SS,TM,CPSF_A	9.6
427497	AW135476	Hs.31240	ESTs		9.6
420423	AA827718	Hs.88218	ESTs	SS	9.6
431512	BE270734	Hs.2795	lactate dehydrogenase A	klhldh ₁ ,C _{SS} ,ldh	9.6
450052	AB61298	Hs.236524	ESTs	z-C3H-C4-z ₁ -box	9.5
412738	NM04731	Hs.74502	ash binding protein 1; FBP1	homod3	9.5
444202	AL051685	Hs.12785	KIAA0939 protein	SS,TM,NH ₂ Exchanger,AB2C	9.5
451165	AJ340575	Hs.286084	MRP-1 protein		9.5
411450	H48619	Hs.127301	ESTs	SS,phnase	9.5
405371			NM_005569:Homo sapiens LIM d	phnase,LIM,PDZ	9.5
435782	N49433	Hs.285737	Homo sapiens cDNA:FLJ20895 f	SS,GPD,Glucosamine _{ase} ,Iso	9.5
416866	AA297356	Hs.80324	serine/threonine protein phosph	Metallophos,Metallophos	9.5
405474			NM_001063:Homo sapiens acylt	CPSase ₁ ,chain,biofin ₁ lp	9.4
412837	AJ922223	Hs.58389	hypothetical protein MG20690		9.3
448133	AA723157	Hs.73769	folate receptor 1 (adult)	Folate _{rec} ,SS	9.3
431081	AA491594	Hs.75813	polycystic kidney disease 1 (p	SS,TM	9.3
427640	AF958293	Hs.180015	D-dopachrome tautomerase	MIF ₁ ,lato ₁ ,protein ₁ ,L2,SS,GS	9.2
427435	AW538739	Hs.115412	hypothetical protein FLJ15881	SS	9.2
407688	W25317	Hs.37616	Human D8 splice variant B mRNA		9.2
407507	U73799		gbcHuman dyadactin mRNA, paria	SS,TM,HC03 ₁ ,cotransp,CAP_G	9.2
400833			C120050(g13746443)g1A0539	SS,TM,Tm_1	9.2
422064	AW452589	Hs.335742	ESTs	TM	9.2
452434	D30934	Hs.29549	K-type lectin-like receptor-1	lectin ₁ ,c _{SS} ,TM	9.2
451782	AB032297		KIAA1171 protein	TGC,SS,TM,phnase,Janthin	9.2
432931	AF174487	Hs.263753	Bcl-2-related ovarian killer p		9.1
407893	BE408359	Hs.43621	Homo sapiens, Similar to hypot	SS,SS,art ₁ ,ras,fn3,ras	9.1
427397	AF296055	Hs.177656	catmodulin 1 (phosphotyrosine M	ethand,RmsAD,SS,ethand	9.1
405159			ENSP00000243337:cDNA FLJ13994		9.1
422283	AW411307	Hs.114311	CCDC45 (cell division cycle 45,	CCDC45	9.1
420598	X94553		gb,H.sapiens db/actp gene exp	SS	9.0
448045	AJ297438	Hs.20166	prostate stem cell antigen	SS,TM,UPAR ₁ ,LY6,txovin,SS,T	9.0
400772	AA179549	Hs.175563	NM_003105:Homo sapiens sorb	ld ₁ recept ₁ ,h ₁ h ₁ ld ₁ reco	9.0
427315			Homo sapiens mRNA: cDNA DKFZp5	spectin,SHS,PH,CH	9.0
414391	BE408672		gb:501299559F1 NIH_MGC_21 Homo		9.0
447867	AJ525258	Hs.184203	ESTs	TM	9.0
422639	AJ529377	Hs.173724	crealine kinase, brain	ATP-gua ₁ ,Ptrans,ATP-gua ₁ Pi	8.9
454319	AW247530	Hs.101617	ESTs, Weakly similar to T32573	SS	8.9
428781	AF164795	Hs.193384	palatolase 28 kDa protein		8.9
408645	AW245738	Hs.109274	hypothetical protein MGCA365	SS,TM	8.9
429527	AA454184	Hs.289014	ESTs		8.9
406651	AJ592224		gb:h32022x1 NCJ_GCAP_U11 Hom		8.9
430893	BE502008	Hs.282057	ESTs		8.8
414413	BE294877		gb:601174162F1 NIH_MGC_17 Homo	SS	8.8
413726	AJ278465	Hs.79510	annexin A11	annexin ₁ ,SS,annexin	8.8
432211	BE274333	Hs.273333	hypothetical protein FLJ10586		8.8
421694	BE367430	Hs.106880	tyrosin-like		8.8
432683	AL078654	Hs.118598	Homo sapiens mRNA for KIAA1878	SS	8.7
456741	W07608	Hs.184492	ESTs	SS,phnase	8.7
442995	AA532511	Hs.289455	Homo sapiens cDNA: FLJ23270 f		8.7
415868	Z43379	Hs.177193	gb:HSCE1AE111 normalized infant		8.7
456977	AK000252	Hs.169758	hypothetical protein FLJ20245		8.7
439532	AW410714	Hs.334437	hypothetical protein MGCA248	SS,TM,transmembrane4	8.7
431462	AW583672	Hs.295311	granin-like neuroendocrine pep	SS	8.7

400128			Eos Control	TM, E1-E2, ATPase, HMA, Hydro	8.7
438582	A1521310	Hs.283365	ESTs, Weakly similar to ALU5_H	SS	8.7
450958	AL137669	Hs.348012	Homo sapiens mRNA; cDNA DKFZp4		8.7
410355	X37765	Hs.86718	RAD51 (S. cerevisiae) like	SNF2_N, helicase, C_SS	8.7
415126	D60945		gb:HMU1410048 Clontech human f	SS, TM	8.7
418736	T18979	Hs.87908	Snf-2-related CBP activator pr	SS, helicase, CAT_hook, SS,	8.6
431157	AR23589	Hs.132678	ESTs	SS, MAPEG, SS, MAPEG	8.6
410843	AJ251016	Hs.86320	potassium intermediate channel c	TM, CaM2D, SK_channel, TM	8.6
419167	A1589535	Hs.94875	ESTs, Weakly similar to A35383	SS	8.6
432343	NM_002960	Hs.2961	S100 calcium-binding protein A	S_100, SS, a2band, S_100, a1b	8.6
458440	A056468	Hs.135254	Homo sapiens clone 1 thrombos		8.5
420651	Y10141		gb:h.sapiens DAT1 gene, par	SNF, SS, TM	8.5
420651	AW173191	Hs.213117	ESTs	SS, Sema	8.5
422418	AK001393	Hs.116385	hypothetical protein FLJ10521	RhoGef	8.5
420836	AW558453	Hs.204959	hypothetical protein FLJ14886	SS, ras	8.5
455588	AJ129033	Hs.74689	vesicle-associated membrane pr	synaptobrevin, SS, TM	8.5
431974	AW572689	Hs.200934	ESTs	bZIP	8.5
410720	AF035154	Hs.65755	regulator of G-protein signal	RGS, G-gamma, DEP, SS, RGS, DI	8.5
449751	AW207115	Hs.26555	ESTs	SS	8.5
434330	AW162336	Hs.3709	low molecular mass ubiquinone-	SS	8.5
405557			Target Exon	Ets, SAM_PNT	8.5
443780	NM_012068	Hs.9754	activating transcription facto	bZIP, NTP_transf_2, SS, TBC	8.5
428860	U38291	Hs.194301	microtubule-associated protein	M	8.5
421901	AB014554	Hs.105299	protein tyrosine phosphatase,	SAM, SS, TM, mm, PDZ	8.4
401885			Target Exon -	kinase, SS, TM	8.4
44382	A050407	Hs.197875	ESTs	SS, mm, zif-RanBP	8.4
432962	AW004958	Hs.236720	amelinase protein	SS, MATH, zif-TRAF, zif-C3HC4	8.4
441363	AW1632211	Hs.126525	ESTs, Weakly similar to A65302	SS, TM, HSP29, Tm_1	8.4
407863	AF035332	Hs.181125	gb:Homo sapiens clone MCAIL my	SS, Ig, SS, G_alpha_transp	8.4
425380	A435639	Hs.32148	A2-O15 protein	SS, TM, LR, P_Peptidase, S8	8.4
424893	AW295112	Hs.153548	Homo sapiens cDNA FLJ13303 fts	SS, SAM, SS, TM, Tm_1	8.4
424080	AW186563	Hs.139119	Homo sapiens cDNA FLJ10987 fts		8.4
435772	AL356456	Hs.10286	Homo sapiens mRNA full length		8.3
431765	AF124249	Hs.268541	novel SH2-containing protein 1	SH2, SS, TM	8.3
404365			Target Exon	SS	8.3
424310	A4338548	Hs.50334	lesion development-related NYD	SS, TM	8.3
401935			Target Exon	PH	8.3
434796	A4812046		ESTs	SS, myb_DNA-binding, myb_ON	8.3
423098	AA321980	Hs.204682	ESTs	SS	8.3
434552	AA538818	Hs.325116	Homo sapiens, clone MGC:2962,	SS	8.2
457082	AA470587	Hs.104772	ESTs	SS	8.2
432603	AA554920	Hs.105794	UDP-glucose:glycogen glucos	SS, TM	8.2
402445			Target Exon	in3, SS, TM, BNR	8.2
422078	AW872378	Hs.120170	gb:UL-HF-BN0-slu-d-03-G-Ulr1	SS	8.2
418361	AW505268	Hs.12460	DNA (cytosine-5)-methyltransf	SS, PWWP, PHD	8.2
431354	BE046556	Hs.251673	Target Exon	TM, sulfate_transp, STAS, HM	8.2
403885	AW073390	Hs.267963	hypothetical protein FLJ10535	SS, pyridox_oxidase, zif-C2H	8.2
450229	AW363438	Hs.337835	ESTs	SS	8.2
420138	BE268854	Hs.177729	ESTs	SS	8.2
439788	NF1241	Hs.119275	ESTs	UQ_con	8.2
423682	AK001035	Hs.130881	B-cell CLL/lymphoma 11A (zinc	SS	8.2
449556	AA020028	Hs.188633	ESTs	PIPSK	8.1
452295	BE379835	Hs.28886	programmed cell death 10	SS, aaplin	8.1
448550	AW769395	Hs.204851	ESTs	SS, IL8	8.1
445035	NM_005558	Hs.13565	San68-like phosphotyrosine pr	K1-domain	8.1
444406	A1147327		Immunoglobulin heavy constant	SS	8.1
437215	AL117488		Human clone Z3564 mRNA sequenc	SS	8.1
408891	NM_005577	Hs.284284	ESTs, Highly similar to beta-1	SS, TM, DD, PDZ, DEP, Disheve	8.0
402493	AF153341	Hs.253594	Homo sapiens winged helix fork	SS	8.0
443801	AW206942	Hs.253594	litteron of trichothrophalag	GATA	8.0
452581	AA444390	Hs.155482	hydroxycarboxyl glutathione hydrol	lactamase_B, SS	8.0
458216	AW024282	Hs.104538	hypothetical protein MGC15906		8.0
401807			C15020810' gtt1113127zsp/P193		8.0
401180			eukaryotic translation elongat	SS, TM, lon_trans, IQ	8.0
454291	AW384847	Hs.213534	ESTs, Weakly similar to MUG2_H	SS, JRCO1_N, BRCT, lactamase	8.0
444014	A055718	Hs.150515	ESTs		8.0
412128	AW894709		gb:CANL-NN0033-020500-212-405 N	SCAN, zif-C2H2, XFRAB	7.9
408363	NM_003389	Hs.44336	coronin, actin-binding protein	WD40	7.9
425694	U51333	Hs.159237	hexokinase 3 (white cell)	hexokinase, hexokinase2, he	7.9
425263	NM_001197	Hs.155419	BCL2-interacting killer (apopt	SS, TM, Top1_MBR	7.9
447045	AW023294		corvair mouth 17	SS, JF-2B, PIP2C	7.9
457613	AA593869	Hs.173770	ESTs		7.9
410338	W03445	Hs.36205	gb:zsa0511.1 Soanes melanocyt	pkinae	7.9
402945			Target Exon		7.9
454246	AW245185	Hs.6996	ESTs	Glyco_transf_8	7.9
410079	U94382	Hs.58589	glycogenin 2	SS	7.9
443678	AW006065	Hs.231923	ESTs		7.9
404676			Target Exon		7.9
426649	A1569392		gb:h.sapiens c1 NCLGAP_U02 Hom	Fork_head, SS, Fork_head	7.9
402320	AL034344	Hs.284186	ferkhead box C1	SS, TM	7.9
413534	BE146361		gb:CV4-HT0222-011199-019-b12H	SS, TM	7.8
444628	U01120	Hs.242	glucose-6-phosphatase, catalyt	PAP2, SS, TM	7.8
410839	NM_005849	Hs.66581	protein disulfide isomerase	thioesterase, GDI, gnr, SS, T	7.8

5	444046	AJ308034	Hs.135094	ESTs	SS,GTP_EFTU,EFQ_C,GTP_EFT	7.8
	438501	AF065321	Hs.287452	Homo sapiens cDNA FLJ11760 fs	TM	7.8
	415441	R13977	Hs.9634	ESTs	SS,HATPase_c	7.8
	450461	BE603801	Hs.46736	hypothetical protein FLJ23476	SS	7.8
10	446933	AJ471630		KIAA0144 gene product	SS,TMLDUF289	7.8
	400923	AJ491994		Target Exon	SS,TMLDUF289	7.8
	419757	AA773260	Hs.53970	gb:td07g09.x1 NCL_GGAP_U2 Hom	SS,HATPase_c	7.8
	451721	NM_000546	Hs.26915	spectrin, beta, non-erythrocyt	SS,TM	7.8
15	458834	AJ565683	Hs.196446	ESTs	spectrin,PH,CH,SS,Peptida	7.8
	422533	X55633	Hs.118804	enolase 3, (beta, muscle)	enolase,SS,TM,kinesin,FHA	7.7
	438452	AJ202911	Hs.268969	hypothetical protein FLJ29920	SS	7.7
	421445	AJ311359	Hs.104433	Homo sapiens, clone IMAGE4054	asp,SS,TM,lon_trans,K_tel	7.7
20	437433	AJ363410		ribosomal protein S18	SS,TM	7.7
	450635	AW403954	Hs.25237	mesenchymal stem cell protein	4HT	7.7
	442394	R62928	Hs.261163	ESTs		7.7
	434333	AA116013	Hs.292154	stromal cell protein	VHL,TM	7.7
25	427221	L15409	Hs.174007	von Hippel-Lindau syndrome	phosphatase,SS,SNF2_H,Helicase	7.7
	420909	BE439552	Hs.196177	phosphorylase kinase, gamma 2	SS,zf-RanBP,MDM2	7.7
	444670	H55373	Hs.332936	hypothetical protein MGCS370	SS	7.7
	449495	AJ526333		gb:wb22c11.x1 NCL_GGAP_G06 Hom	SS,PLC-X,PH,PLC-Y,C	7.7
30	444607	AW405635	Hs.293687	ESTs	TM,Patched,TM	7.7
	449125	AJ571439	Hs.186029	Homo sapiens mRNA for KIAA1657	TM,Patched,TM	7.7
	447151	AD228113	Hs.52679	Homo sapiens clone CDABP9014 m	SS,TM,LRR,aminotran_1,2	7.6
	446926	W27670	Hs.55613	hypothetical protein FLJ22531	TM,Patched,TM	7.6
35	430432	AB037756	Hs.241419	KIAA1337 protein		7.6
	401822			C17001422.g[1]265586(emb)CAA75		7.6
	428909	AJ190714	Hs.38945	ESTs		7.6
	414334	BE257233	Hs.76359	BCL-2 antagonist of cell death	SS,homone_rec,zf-C4	7.6
40	421620	AA445183	Hs.91865	ESTs, Weakly similar to I55214		7.6
	411650	AJ261960	Hs.132545	ESTs	SS,TM,KOW	7.6
	442232	AJ537813	Hs.337450	ESTs, Weakly similar to A47562	SS,TM,TGFb_proteobde,TGF	7.6
	435339	BE345395	Hs.121589	ESTs	SS,Forkhead	7.6
45	400286			C16000922.g[7]49103(p)[1]209	TM,ABC_tran,ABC_membrane	7.5
	452833	BE559681	Hs.30736	KIAA0124 protein	WD40	7.5
	417350	AA195652	Hs.85652	hypothetical protein MGCS169		7.5
	427721	AJ522943	Hs.189455	RA-022 (S. cerevisiae) homolog	ubiquitin,UBA,Integrin_B,	7.5
50	450716	T57758	Hs.10255	ESTs		7.5
	407435	AF211876		gb:Homo sapiens LENS8 mRNA, pa		7.5
	413355	AB213351	Hs.193137	ESTs, Weakly similar to ALU7_1		7.5
	427859	AA232266	Hs.332053	serum amyloid A1	SS,SAA_protein,SS,SAA_pr	7.5
55	406485			Target Exon	SRCR,TM,Acetyltransf	7.5
	430367	AW372884	Hs.240770	nuclear cap binding protein su	rm,SS,TM,rm	7.5
	405601	U47628	Hs.56122	protein A	SS,TM,L,SS,Ig,WD40,zfUB	7.4
	424354	AW963226	Hs.15834	ESTs, Weakly similar to G01763	SS,ras	7.4
60	409832	AW963293		gb:EST375366 MAGE resequences,		7.4
	448043	AH455853	Hs.201881	ESTs	PHD	7.4
	421148	AF066236	Hs.102178	synaptin 16	Synaptin,SS,Peptidase_M17	7.4
	420570	AA350379	Hs.1342	cytochrome c oxidase subunit V	COX5B	7.4
65	419295	BE397712	Hs.144027	ESTs	myb_DNA-binding,myb_DNA-b	7.4
	448330	AL036449		ESTs		7.4
	419539	AK001502	Hs.51753	hypothetical protein		7.4
	431488	AB037785	Hs.257594	KIAA1364 protein	SS,CHLUM,SS	7.4
70	456487	AF048084		suppressor of Ty (S.cerevisiae)		7.4
	448815	AJ910658	Hs.212257	ESTs	SS	7.4
	427433	D82070	Hs.177972	chromosome 4 open reading fram	SS,phage	7.4
	441076	N49809	Hs.11197	Homo sapiens, clone IMAGE3343		7.4
75	452554	AW452434	Hs.58005	ESTs, Weakly similar to ALU5_1	SS,PAS,HLH	7.4
	411448	AA178565	Hs.271439	ESTs, Weakly similar to I38022	rm,PDZ	7.4
	442318	AJ792190		ESTs	SS,zf-C2H2	7.4
	452055	AW561959	Hs.96940	ESTs		7.4
80	412935	BE267045	Hs.75054	tubulin-specific chaperone c	SS,TM,tresmentranol	7.4
	403748			Target Exon	TM	7.4
	447282	AJ589663	Hs.197505	ESTs	TM	7.4
	422305	AJ528242	Hs.293438	ESTs, Highly similar to AF1984	SS	7.3
85	416472	AA180756	Hs.340316	ESTs, Moderately similar to AL	zf-C2H2	7.3
	427273	AW139332	Hs.107376	hypothetical protein DKFZp434N	SS,SS,TM	7.3
	412265	AA101352	Hs.86164	hypothetical protein FLJ12457	SS,PP2A,PH,SS,PHD	7.3
	447659	AK002194	Hs.19551	peroxisomal biogenesis factor	UPP_synthetase,HMG14_17	7.3
90	432747	NM_014404	Hs.278507	calcium channel, voltage-depen	PMP22, Claudin,SS,TM,PMP22	7.3
	405727	AJ219282	Hs.2186	eukaryotic translation elongat	SS,G-merin	7.3
	404199			ENSP00000211707p-Helicase 9K2	SS,RasGAP,PH,SS,PHD	7.3
	445434	BE391650	Hs.9265	hypothetical protein FLJ20917	SS,PWWP,Exonuclease,Ipo	7.2
95	428550	AW297880	Hs.89561	ESTs	SS,homobox,homobox	7.2
	454718	AW815144		gb:CV4-ST0212-120100-075-d10 S	SS,ATP-synt,gb_ATP-synt_a	7.2
	407696	AA190135	Hs.128043	chromosome 21 open reading fr	SS,TM,IKK_Channel	7.2
	418304	AA215702		gb:z97g10.1 NCL_GCAP_G031 Ho	serpin	7.2
100	424263	M77640	Hs.1757	L1 cell adhesion molecule (fyd	tn3,Ig,IRK,SS,TM,tn3,Ig,R	7.2
	407581	R48402	Hs.173508	PCGS	SS,TM,TM_1	7.2
	430746	AW977370	Hs.222812	ESTs	SS	7.2
	402651			NM_000721*Homo sapiens catclu	lon_trans	7.2
105	407323	AA181183	Hs.143504	gb:z57c02.a1 Stratiogene endot	SS,Ribosomal_S4e,ubiquiti	7.2
	407619	AL050341	Hs.37165	collagen, type IX, alpha 2	SS,Collagen,SS,Collagen	7.2
	434035	AF762074	Hs.204769	ESTs, Weakly similar to T28770	SS,TM	7.2

	400419	AF084545		Target	EGF,lg,leccln,c,sushi,Xti	7.2
	424241	AW655948			SAM_FWT	7.2
	445837	A0251700		Homo sapiens pyruvate dehydrog		7.2
	427725	U56839	Ha.180533	ESTs		7.1
5	421878	AW595807		mitogen-activated protein kina	pkinaase	7.1
	418285	H08816	Ha.293756	gb:EST371677 MAGE resequences,	SS,ENP24_GP25L	7.1
	442853	H78133		ESTs		7.1
	437829	A0358522	Ha.103834	ESTs		7.1
	450873	BE464016	Ha.239556	ESTs	SS,cf-C2H2,mm	7.1
10	433396	AF142071	Ha.133305	ESTs	SS,TM	7.1
	415555	BS4144	Ha.278107	chromosome 21 open reading fra	SS	7.1
	436629	AA861011	Ha.249795	ESTs	TM,TK	7.1
	414593	BC366764		gb:601273249F1 NIH_MGC_20 Homo		7.1
	427265	AW492534	Ha.1578	baculoviral IAP repeat-contain	BIR,TK,SS,TM	7.1
15	419823	AW277108	Ha.118918	ESTs, Weakly similar to M2OM_H	SS,TM	7.1
	405247			Target Exon	SS	7.1
	455778	BE088746		gb:CM2-BT0693-210360-123-009 B		7.1
	431005	AA405054	Ha.127269	ESTs, Weakly similar to T02245	WD40	7.1
20	435717	AF227905	Ha.105794	UDP-glucose:glycoprotein glucos	Glyco_transf_8	7.1
	405113			Target Exon	SS	7.1
	428070	TS3918	Ha.182313	retinol-binding protein 2, cel	lipocalin/lipocalin,WD40	7.1
	429029	AA443430	Ha.85524	for muscle specific ring finger	SS	7.1
	433354	AA54410	Ha.230784	human homolog of Drosophila Sc	SS,TM,Ig	7.0
	412970	AB026436	Ha.177534	dual specificity phosphatase 1	Rhodanese,DSpc,SS,DSpc	7.0
25	438701	AA307112	Ha.207788	ESTs	TM,sushi	7.0
	454756	AW819273		gb:CM2-ST0284-061299-046-a12 S		7.0
	401264			C180000207-gb122786561(NP_0	SS,Jamlnin_Nterm,Jamlnin_	7.0
	408080	AW149754	Ha.246652	ESTs, Weakly similar to T00273	SS	7.0
	418641	BE243126	Ha.85947	a disintegrin and metalloprote	disintegrin,Reprosyn,Pu	7.0
30	431402	AA743834	Ha.250861	ESTs		7.0
	422780	BE152383		gb:CM2-AT03223-171199-033-a08 H	SS	7.0
	450688	AW272352	Ha.60450	ESTs	TM	7.0
	405928			Target Exon	SS,cystatin,Copropen_oxid	7.0
35	454438	AA224053		cell division cycle 27	SS,TM,SPRY,Tnn_3,ANF_rese	7.0
	407281	A0307226	Ha.194421	ESTs	SS	6.9
	423386	AW136598	Ha.314081	ESTs	SS,WD40EPO_TPO	6.9
	453960	BE384526	Ha.25734	gb:601277913F1 NIH_MGC_20 Homo		6.9
	420187	A0301714	Ha.35744	hypothetical protein similar t	ank,TM	6.9
40	431549	AA507036	Ha.170573	ESTs		6.9
	423384	AL133632	Ha.127808	Homo sapiens mRNA; cDNA DKFZp		6.9
	454577	AW692722		gb:MR4-ST0118-040100-034-c08_1		6.9
	438118	AW753121		ESTs	SS,lipocalin	6.9
	416233	AA176633		gb:zp13g01.1 Stratagene fetal		6.9
	417012	N38970	Ha.194214	ESTs		6.9
45	452399	BE513301	Ha.29344	hypothetical protein, clone 24	SS,perlepin	6.9
	439953	AW247529	Ha.3793	platelet-activating factor ace	PAF-AH,lb,lipase_CD5L,SS,	6.9
	418416	U11700	Ha.84999	ATPase, Cu transporting, beta	E1-E2_ATPase,HMA,Hyalolase	6.9
	404956			C10032107-gb169125826(NP_03	PK3_P14_kinase,PK3_C2,P1	6.9
	451606	AA018791	Ha.7945	Alc-7S binding protein protein	SS	6.9
50	438525	AW368528	Ha.100855	ESTs	SS	6.9
	400906			C18000324-gb12229282sp(CSPPTW		6.9
	411411	AA345241	Ha.55950	ESTs, Weakly similar to K0A413	SS	6.8
	406834	A0318980		gb:ta49709.x1 NCL_GGAP_Lu25 Ho		6.8
55	414628	AA345424	Ha.76688	carboxylesterase 1 (monocystein	SS,COesterase,SS,COestera	6.8
	424198	AB029010	Ha.143026	KIAA1087 protein	SS,TM,Na_Ca_Ex,Calc-beta,	6.8
	445873	AA250970	Ha.251946	poly(A)-binding protein, cytop	SS,PABP_rrm,pklnase,14-3-	6.8
	439605	AF084541	Ha.22380	ESTs	SS,TM	6.8
	432284	AA532807	Ha.103822	ESTs	SS,TM,pklnase	6.8
	421994	BE143533	Ha.105309	hypothetical protein FLJ20035		6.8
60	443136	NM_001440	Ha.5018	exostosins (multiple)-like 3	Exostosin,SS,TM	6.8
	427158	BE397336	Ha.1422	Gardner-Rasheed feline sarcoma	SH2,SH3,phatase	6.8
	445148	NM_016578	Ha.23099	HIV pX associated protein-8	PHD,Virus_HIS,SS,Chn_chan	6.8
	400205			NM_008265:Homo sapiens RAD21	SS	6.8
	434315	AW196608		ESTs		6.8
65	418184	AA307375		Homo sapiens cDNA, FLJ14015 fis		6.8
	431808	AA000020	Ha.272018	hypothetical protein FLJ20013		6.7
	439627	A0687335	Ha.123473	ESTs	TM,Retliculin	6.7
	409649	AA159216	Ha.55505	hypothetical protein FLJ20442	Y_phosphatase,DSpc,TM	6.7
	429712	AW245625	Ha.211914	ENSP-000000233627-NAADH-ubiquino	oxidoredd,q6,SS,TM,mm	6.7
70	455866	AW089293	Ha.146296	ESTs, Weakly similar to U38022		6.7
	427461	AA531527	Ha.332040	hypothetical protein MGC13010	SS,TM,ACAT,LR	6.7
	434000	BE002846	Ha.112894	ESTs		6.7
	432530	AF131785	Ha.278033	Homo sapiens clone 25220 mRNA	SS,prolasmome	6.7
	435141	AA070201	Ha.150319	Homo sapiens, clone IMAGE3610	SS,TM	6.7
75	441794	AW197794		ESTs		6.7
	450287	AW291483	Ha.255909	ESTs		6.7
	441523	AW514263		ESTs, Weakly similar to ALUF_H	SS	6.7
	452798	AB187171	Ha.257170	ESTs	SS,TM,TNFR_c6	6.7
	451937	AF115564	Ha.27229	transcriptional regulator prot	SS,Integrin_B,hn3,Calc-be	6.7
80	421417	AA291004	Ha.262088	ESTs		6.7
	440317	BE561888		gb:601346093F1 NIH_MGC_8 Homo		6.7
	421321	NM_003009	Ha.103602	glutamic-pyruvate transaminase	aminotrans_1_2,SS,TM,LR	6.7
	444504	AW452054	Ha.161139	ESTs		6.7
	449730	R72230	Ha.117557	ESTs, Weakly similar to U38022	RasGAP,Thyroglobulin_LRI	6.7

450622	A1650285	Hs.58210	ESTs, Highly similar to ITM4_H	SS,TM,vwa	6.7
425424	NM_004954	Hs.157199	ELKL motif kinase	kinase,KAI1,UBA,SS	6.7
435864	AL035499	Hs.188491	ESTs	SS	6.7
103937	AF171917	Hs.63042	DNAZP56A/157 protein	SS,homobox,UPF0160,DUF23	6.7
454262	AW612232	Hs.254836	ESTs	SS,TM,voltage_CLC,CBS	6.7
453023	AW028733	Hs.31439	serine protease inhibitor, Kun	Kunitz_BP1T,SS,TM,lon_tra	6.6
419157	U023450	Hs.23871	ESTs	phospho	6.6
412464	T70141	Hs.22026	ESTs, Weakly similar to I55214	SS,cadherin_crystal	6.6
407332	AB01555	Hs.200113	Homo sapiens cDNA FLJ11379 fs	SS,adh_short,Transglutamin	6.6
456643	AW751497	Hs.98370	cytochrome P450, subfamily IIS	SS	6.6
111480	K39474	Hs.22026	gln:h500971 Source placenta	SS,kinase	6.6
455865	BE133524	Hs.22026	gln:PM6-HT0335-241158-002-C03 H	SS,RA,RasGEF,RasGEFN	6.6
438557	AB27912	Hs.130783	Fonsmann synthetase	SS,TM	6.6
423007	AW020869	Hs.66219	ESTs	SS,TM	6.6
453496	AA442103	Hs.33084	soluta carrier family 2 (lac)	sugar,ss,SS,TM	6.6
419182	AA234522	Hs.66147	ESTs	SS,TM,lon_tra,lon_trans	6.6
406301			Target Exon	TM	6.6
433938	AF161536	Hs.284292	ubiquitin-cytochrome c reducta	TM	6.6
445980	AL137357	Hs.289038	hypothetical protein MG3C4126	SS,TM,homobox,hsypin,PD	6.6
454265	AW178110	Hs.191705	gln:LA-HT0101-01099-013-1404 H	SS,TM,serine	6.6
45702	A120495		gln:CD33.1 Striatogen schiz	SS,TM	6.6
422201	NM_001505	Hs.113207	G protein-coupled receptor 30	7tm_1,SS,TM	6.6
406779	AA412048	Hs.279574	CG-39 protein, cell death-reg	SS,SS	6.6
404146			CG002507:gn:502186:gn:NP_00	SS,TM,serine	6.6
416576	AW568159	Hs.302740	Epithelial calcium channel 2	SS,TM	6.6
421363	NM_001381	Hs.103854	docking protein 1, 62KD (downs)	PJHRS,TM,PHIRS,krppin,	6.6
458919	AB181567	Hs.13349	KIAA0756 protein	TM	6.6
427552	AB118155	Hs.71133	Homo sapiens, clone IMAGE:3161	SS,TM,ABC_tran,Glyco_tran	6.6
412289	AW535957	Hs.170162	KIAA1357 protein	SS	6.5
447105	AW377610	Hs.111123	DKFZP564G0592 protein	SS,TM	6.5
444672	Z95536	Hs.11659	laminin, alpha 5	laminin,EGF,laminin_G,EGF	6.5
425220	AB020463	Hs.347408	hypothetical protein MG31302	SS,TM,igfa	6.5
420003	AA256906	Hs.111364	ESTs, Weakly similar to ubiqui	SS,TM	6.5
431849	AB070823	Hs.85573	hypothetical protein MG310911	SS,TM	6.5
430396	D43742	Hs.241363	hyaluronan-binding protein 2	hypan,hyal,EGF,GS	6.5
437662	AA126587		ESTs	WCHD,RC3T1,SPRY	6.5
436543	NM_002212	Hs.5215	Integrin beta 4 binding protei	eIF6	6.5
406375	AA465350	Hs.119400	CCX000741:gn:4885461:gn:NP_00	SS,TM	6.5
430116			ESTs	SS,TM,adh_short	6.5
450109			Target Exon	SS	6.5
414871	BE549179	Hs.29006	gln:G01076714F1 NH1_MGC_12 Homo	SS,acidored_nitro,SS	6.5
440696	A1979249	Hs.146221	ESTs	SS,TM	6.5
450651	US1336	Hs.6453	inositol 1,3,4-bisphosphate 5'	SS	6.5
403376			Target Exon	SS	6.5
426925	NM_001196	Hs.315069	Homo sapiens cDNA: FLJ22373 II	SS	6.5
405050	BE141732		Target Exon	Ammonium_transp	6.5
436284	AW203303		ESTs		6.4
417904	A1890347	Hs.271923	Homo sapiens cDNA: FLJ22785 II	SS	6.4
425626	NM_000020	Hs.172670	actin A receptor type II-4k	kinase,Activin_recp,SS,T	6.4
446100	AW057109	Hs.13804	hypothetical protein d4462023.	SS,TM	6.4
442146	RS259		gln:gn:0101.1 Source infant br	TM	6.4
425041	AB771150	Hs.150914	ESTs	SS	6.4
457984	AA147979	Hs.285005	mitochondrial import receptor	Josephin	6.4
435449	AA682379	Hs.303460	EST		6.4
405294			Homo sapiens mRNA full length		6.4
425944	AK000664	Hs.164256	hypothetical protein FLJ20657		6.4
453367	AW732847	Hs.70573	PKC-1-related HIT protein	SS,TM	6.4
419725	US6046	Hs.92683	Homo sapiens clone 161455 brain		6.4
412462	AJ245131	Hs.103106	suppression of tumorigenically	SS	6.4
421273	AJ245416	Hs.103106	U6 snRNA-associated Sim-like pr	Sm,SS,SRN,ymn_1,GST_C,G	6.4
432746	AA554512	Hs.24301	polymerase (RNA) II (DNA direc	SS,TM,EF1B0	6.4
429396	AA552329		KIAA0970 protein		6.4
404430			CB000069:gn:10432235:gn:hm(CAC1	SS	6.4
427339	AT134109	Hs.87984	SRF (sex determining region Y)		6.4
433689	AB11706		CHN1P.5 protein		6.4
423890	AA525226	Hs.303293	ESTs, Moderately similar to 15		6.4
445333	BE337641	Hs.44278	hypothetical protein FLJ12538	SS	6.4
414758	AW451101	Hs.150489	ESTs, Moderately similar to JC	hexokinase2,hexokinase	6.4
423847	U16937	Hs.133314	RAR-related orphan receptor C	hormone_recp,CA,SS,TM,h	6.4
406493	BE206494	Hs.49039	phosphoglycerate mutase 2 (mus	PGAM,BRCT,rvna_p0_I	6.4
435669	AW602166	Hs.222289	CEGP1 protein	CUB,EGF,SS	6.4
457274	AW674193	Hs.227152	mannan-binding lectin serine p	SS,TM,SS,TM,Clathrin,lg_c	6.4
444550	BE250716	Hs.87614	ESTs	SS	6.4
407169	HB16179		gln:040677.1 Source testis br	BIR	6.4
422262	AL137491	Hs.125511	Homo sapiens mRNA: cDNA DKFZp4	SS,TM,taush	6.4
422682	W05238	Hs.94316	ESTs, Weakly similar to T31613	SS,TM,DEAD,heflicase_C,lan	6.3
447867	AA114050	Hs.19949	casepase 8, apoptosis-related c	ICE_p20,DED,ICE_p10	6.3
400137			Eos Control		6.3
402784	AW971350	Hs.63386	ESTs	SS	6.3
435026	AW193035	Hs.187370	ESTs		6.3
438113	AA67908	Hs.8862	ESTs	SS,TM,7tm_1	6.3
417610	D28419	Hs.82609	hydroxymethylbilane synthase	Porphobil_desm	6.3
435050	AB57205	Hs.14584	ESTs		6.3

403672			C4001244.gi539933 pit A61275	tubulin, TM	6.3
448269	BE822358	Ha.61260	hypothetical protein FLJ13164		6.3
430217	N47863	Ha.180450	ribosomal protein S24	Ribosomal_S24e	6.3
426675	AW047491	Ha.133122	hypothetical protein FLJ14524	SS, TM, laminin_rn_1_2	6.3
423510	AB000924	Ha.129712	trehalase	Trehalase	6.3
428573	AA430651	Ha.209249	ESTs	SS	6.3
457052	BE167242	Ha.47099	hypothetical protein FLJ21212		6.3
44599	BE163341	Ha.47099	gb:CV3-H10458-230209-059-401 H		6.3
450334	AF035989	Ha.24879	phosphatidic acid phosphatase	PAP2, SS	6.3
416000	R82342	Ha.78956	ESTs, Weakly similar to S65557	SS, TM, sugar_jr	6.3
427860	AA436011	Ha.98187	ESTs		6.3
426722	U53623	Ha.171852	occludin	Occludin, SS, TM, BIR	6.3
420072	BE258857	Ha.27744	RAB3A, member RAS oncogene fam	ras_ar, SS, PDEase	6.2
431161	AA463591	Ha.75183	gb:bn01a12a1 NCI_CGAP_Thy1 Ho	SS	6.2
413055	AV655701	Ha.75183	cytochrome P450, subfamily IIE	p450	6.2
431250	BE264649	Ha.251377	taad resistance associated ge	SS, TM, wva-FG-GAP, Integrin	6.2
405373			Target Exon	TM	6.2
403003			NM_009444-Homo sapiens hypoph	SS	6.2
437834	AA765294		gb:ncu36g03a1 NCI_CGAP_GC81 Ho	Target Exon	6.2
406299			ESTs, Highly similar to Biml_1	SS	6.2
439327	AF086141	Ha.50760	ESTs	SS	6.2
414246	BE391090	Ha.280276	EST	SS	6.2
427812	AA770424	Ha.96162	ESTs	SS	6.2
426926	AA530402	Ha.221216	ESTs	UQ_eon	6.2
437866	N91071	Ha.105630	ESTs		6.2
431082	AA491600		gl:ncb60a1.1a1 NCI_CGAP_Ew1 Hom		6.2
420530	A1218431		coagulation factor VIII-associated	RasGAP, C2, PH, BTK	6.2
407360	X13075		gb:Human 2a12 mRNA for kappa-4	SS	6.2
439368	AW578003	Ha.22826	tropomodulin 3 (ubiquitous)	SS, tyrosin_krtglike, h2, NEG	6.2
409946	AW162263	Ha.312468	ESTs, Weakly similar to ALUC_H1	ras_ar	6.2
413272	AA127923		ESTs	SS, C2-H2	6.2
445050	AW205423	Ha.147260	ESTs		6.2
458130	AA115811	Ha.5838	ras homolog gene family, membe		6.2
449940	AW291126	Ha.187520	Homo sapiens, clone IMAGE:3834		6.2
440390	AW207365	Ha.36475	KIAA0483 protein		6.2
423106	NS2572	Ha.13702	ESTs, Moderately similar to AL		6.1
402501			sperm specific antigen 2	lg, MHC_1, SS	6.1
431470	AA832417	Ha.139650	ESTs	SS, lg, pkinase, LRRLRRCCT	6.1
416557	H68891		glcy7T103r1 Soares fetal liv		6.1
412122	AW652707		G-rich RNA sequence binding to	SS, WD40	6.1
415056	AB040652	Ha.77867	adenosine A1 receptor	7tm_1, SS, TM	6.1
400358	AF181286		Homo sapiens mutant dystrophin		6.1
405473	AW604638	Ha.155976	NM_001053-Homo sapiens acetyl	OPSase_1_chain, biotin_lip	6.1
422625	AL222315	Ha.113987	actin 4B	SS, SS, Cullin, Cullin	6.1
422262			actin, gelsolin-binding, s	Gel-bind, Jordin	6.1
401121			C12001638-gi7291960 gb:AAAF-47		6.1
452188	AK002052	Ha.155071	hypothetical protein FLJ11190	TM	6.1
457216	AA425254	Ha.263897	ESTs, Weakly similar to A41796	h2P, Mar, SS, P5CR, EF1B	6.1
456021	BE246628	Ha.250726	gb:CGAP1D5930 Pediatric pre-B	SS, TM, SS	6.1
420319	AW405289	Ha.96593	hypothetical protein	ras_ar	6.1
410082	AA081594	Ha.158311	Musashi (Drosophila) homolog 1	SS, HECT, phospho	6.1
450593	AF129005	Ha.25197	STP1 homology and U-Box contai	TPR, SS, TM, Rhomboid, lactam	6.1
437050	AA766420		ESTs	SS	6.1
458835	AB88753	Ha.76372	ESTs	SS	6.1
412777	AJ335773		ESTs		6.1
454364	BE263358	Ha.323806	gb:001191272F1 NIH_MGC_7 Homo	SS, TM	6.1
448877	AB58366	Ha.253313	ESTs		6.1
413045	X52121	Ha.75180	protein phosphatase 5, catalyt	Metallophos, TPR	6.1
406054	AW616490	Ha.8102	ESTs		6.1
417852	AJ250552	Ha.82749	transmembrane 4 superfamily me	transmembrane4.5, SS, TM	6.1
410045	AA199630		gb:gz5710r1 Stratiagene N1T a		6.1
415870	H15578	Ha.21017	ESTs		6.1
438723	M34429		gb:Human PVT-4GLC fusion prote		6.0
441307	AW071696	Ha.209355	hypothetical protein FLJ14225	SS, TM	6.0
406575			Target Exon	SS, pkinase, glnase_C, RFX_	6.0
401498			Target Exon	Glyco_hydro_1	6.0
437650	AA814338	Ha.292297	ESTs		6.0
439027	AA8485387	Ha.187386	ESTs	pkinase, DAG, PE-bind, PH	6.0
456373	BE247709	Ha.85751	membrane-spanning 4-domains, s	SS, TM	6.0
454513	BE159271	Ha.109731	gb:MR0-HT0407-180100-004-h05 H		6.0
414944	C15044		gb:C15044 Clontech human aorta	SS, TM	6.0
451277	AK001121	Ha.26176	hypothetical protein FLJ10361	TM, SS, TM, death, OED	6.0
421590	U95031	Ha.102482	muscin 5, subtype B, tracheobro	Cys_linc, wvc	6.0
401215			C12000457-gi7512178 pit T30	tyrosin, SS, TM	6.0
406117	AL138255		ESTs, Weakly similar to I38022	SS, z-CSDHC4, BIR	6.0
426357	AW759357	Ha.123396	gb:cc3-C10383-271039-021-e08 C		6.0
418530	A1351311	Ha.251946	poly(A)-binding protein, cytop	SS, pkinase	6.0
400389	AL135641		olfactory receptor, family 2,	7tm_1, SS, TM, CSD	6.0
447128	AJ271898		cyclin K		6.0
431257	AA681719	Ha.3076	ESTs		6.0
431657	W91944	Ha.271742	ADP-ribosyltransferase (NAD; p	PARP, PARP_reg, SS, TM, Pepli	6.0
430023	AA158243	Ha.227729	FK506-binding protein 2 (13kd)	SS, FKBP, SS, PDGF_C2, PI-PLC	6.0
453101	AW952716	Ha.94943	ESTs	TM	6.0
407363	AA522576		ESTs, Moderately similar to AL	SS, Palatin, ank	6.0

5	430132	AA204686	Hs.234149	hypothetical protein FLJ20647
	459111	AU077013	Hs.28757	transmembrane 9 superfamily me
	459770			NM_002622: Homo sapiens melanoma
	456611	T26376		gb:AB123C1Y1 Infant brain, LLN
	453413	AJ003294		gb:AJ003294 Selected chromosome
	424415	NM_001575	Hs.146580	enkease 2, (gamma, neuronal)
	426048	A758853	Hs.134478	ESTs
	435750	A9029012	Hs.4590	KIAA1089 protein
10	439469	W593636		gb:zd48a02.r1 Soares_fetal_hoa
	445604	AW566538	Hs.237691	ESTs, Weakly similar to KIAA06
	418630	BE513731	Hs.88959	hypothetical protein MGC4816
	452113	AJ855393		gb:wm11a02.x1 NCI_CGAP_UM Hom
	459101	AA205847	Hs.23016	G protein-coupled receptor
	437640	AA754893	Hs.272155	ESTs, Weakly similar to I58022
15	403748			NM_002122: Homo sapiens matrix
	424270	AI143593	Hs.129419	ESTs
	424149	AA749853	Hs.270532	ESTs, Weakly similar to I58022
	439986	AW730272	Hs.128608	ESTs
20	407353	Z11168		gb:HAaplans_SHT1A receptor re
	431424	AJ222859		ESTs
	442297	NM_005202	Hs.89901	phosphodiesterase 4A, cAMP-ope
	457845	H93040	Hs.257729	ESTs
	446912	A347650	Hs.129521	ESTs, Moderately similar to AL
25	451381	BE241831	Hs.172330	hypothetical protein MGC2705
	416024	AW888484	Hs.343522	ATPase, Ca transporting, plasm
	445329	NM_013272	Hs.14805	soluble carrier family 21 (orga
	431321	AW136372	Hs.1852	acid phosphatase, predile
	420039	NM_004605	Hs.94581	sulfotransferase family, cytos
30	428223	AA424313	Hs.98402	ESTs
	433333	AD16521	Hs.71816	v-akt murine thymoma viral onc
	450231	BE308438		gb:CV1-8170636-28020-086-05 B
	408511	AW206404	Hs.27268	ESTs
	414348	AF041430	Hs.79922	brain protein D3
35	459590	AF111170	Hs.306165	Homo sapiens 14q32 Jagged2 gen
	412173	T71071		glycylserine1 Stratiogene liver
	404001			Target Exon
	445263	H57646	Hs.42586	KIAA1560 protein
	441583	AT91459	Hs.205742	ESTs, Weakly similar to ALUA_H
40	430189	AW586343		DKFZ344H725 protein
	454682	AW816029		gb:MRG-ST0220-151299-027-b10 S
	453829	AL138200		gb:DKFZp547N052_r1 547 (synony
	437372	AI323568	Hs.283631	hypothetical protein DKFZp547G
	421726	AJ001337	Hs.319598	hypothetical protein FLJ16376
45	451045	AA215672		gb:zr96a09.a1 NCI_CGAP_C6B1 Ho
	439616	BE018635	Hs.56582	Homo sapiens cDNA FLJ12789 fs
	459679	BE066529		gb:RC3-BT0333-300300-017-a12 B
	457125	AW444431	Hs.134812	ESTs
	430500	AW505967	Hs.274348	HLA-B associated transcript-3
50	421707	NM_014921	Hs.107054	lectinomedin 2
	438127	W54624	Hs.11565	RIVEN cDNA 201010B012 gene
	414347	BE275835		gb:501121635F1 NH_MGC_20 Hom
	439910	H66765	Hs.335397	ESTs
	410382	AW64971	Hs.295546	ESTs
55	425391	AW161050	Hs.169611	second mitochondria-derived ac
	423588	AB15474	Hs.343856	gb:aw47710.Y1 Schneider fetal
	440146	AW014231	Hs.90790	Homo sapiens cDNA: FLJ22530 f
	402189			EHSP00000247423-D-41gic prec
	439546	AW579197	Hs.292073	ESTs, Weakly similar to ALUT_H
60	457978	AA776368		gb:aa7894.1 Stratiogene schiz
	436685	W28661	Hs.5298	Homo sapiens mRNA; cDNA DKFZp54
	411602	L01406	Hs.767	growth hormone releasing hormo
	433357	T05939		gb:EST03558 Fetal brain, Strati
	404311			Target Exon
	428092	AW879141	Hs.119286	ESTs
65	452620	AA436504	Hs.119286	ESTs
	401938			Target Exon
	407202	NS8172	Hs.109370	ESTs
	458882	R34993	Hs.226666	ESTs, Moderately similar to 15
70	453357	AI538176	Hs.283985	ESTs
	452625	AJ724707	Hs.81425	second mitochondria-derived ac
	430261	AJ878842	Hs.237524	CG4-69 protein
	430490	AW902951	Hs.301723	Homo sapiens cDNA FLJ12974 fs
	450122	BE131765	Hs.343443	ESTs, Weakly similar to I58022
75	453821	AJ739013	Hs.203348	hypothetical protein FLJ21106
	413413	BE2320	Hs.132390	zinc finger protein 36 (K0X 18
	445631	AK001822		Homo sapiens cDNA FLJ10960 fs
	419300	AJ701162	Hs.90207	hypothetical protein MGC11138
	423139	AW402725	Hs.286560	hypothetical protein FLJ21106
80	426221	AB070791		KIAA0421 protein
	443785	AW449592	Hs.190125	basic-helix-loop-helix-PAS pro
	417900	BE250127	Hs.82596	CDG20 (cell division cycle 20,
	446596	AW204515	Hs.156113	ESTs, Weakly similar to G01025
	423263	NM_015658	Hs.274411	SCAN domain-containing 1
	427625	AF082162	Hs.285013	putative human HLA class II as

	421543	AK000519	Hs.105606	hypothetical protein FLJ20512	TM	5.7
	418087	AA961613	Hs.127838	ESTs		5.7
	432751	AF152099	Hs.278911	interleukin 17C	SS	5.7
	433943	AA952605	Hs.44865	lymphoid enhancer-binding fact		5.7
5	414274	AW300691	Hs.336584	Homo sapiens, clone IMAGE:4127	SS,VapB2,Acyl-CoA_dh	5.7
	413328	AA502599	Hs.291591	ESTs		5.7
	451481	AA300228	Hs.295866	hypothetical protein DKFZp434N		5.7
	430344	AA116627	Hs.171012	hypothetical protein FLJ22349	HLH	5.7
10	419516	H62550		ATP-binding cassette, sub-famI	SS,TM,ABC_tran,ABC_membr	5.6
	413564	BE260120		gb:601146990F1 NIH_MGC_19 Homo		5.6
	418588	HI0942		gbym06c1.1r1 Soares Infant br	SS,TM	5.6
	401402	BE299427	Hs.21446	Target Exon KIAA1716 protein		5.6
15	451545	AL133056	Hs.341906	ESTs	SS,DX,PDZ,DEP,Dnaheise	5.6
	452626	L25973	Hs.198726	old shock domain protein A	TM,SAM_decarbox,SS,plinas	5.6
	435500	AA24285	Hs.116348	ESTs	CSO,jomeobox,SS,TM,Ten_2	5.6
	449285	AA912702	Hs.139135	ESTs	TM,ECH,chromo	5.6
	418255	AW845318	Hs.12271	Ebox and leucine-rich repeat		5.6
	417442	AA199940	Hs.124039	ESTs	SS,SS,TM,HSF_DNA-bind	5.6
20	405931			Target Exon		5.6
	455285	BE144384		gbyb09-HIT0166-191199-004-c11 H	SS	5.6
	446931	AA348856	Hs.21627	gb:b05a05.x2 NCL_CGAP_Lu26 Ho		5.6
	446548	AT879352	Hs.200215	C17000146.gij2143629[gij]A57	SS,TM,Ribosomal,S25,sugar	5.6
25	401594			Target Exon		5.6
	404095			ESTs	SS,RNA-synt_2a,NGTP_anti	5.6
	418363	AA218628	Hs.202977	ESTs		5.6
	458198	AA286100		ESTs		5.6
	432278	AL137606	Hs.274256	hypothetical protein FLJ22563	SS,TM,GNS1,SUR4,SS,TM,Rho	5.6
	432285	AA572239	Hs.195471	6-phosphofructo-2-kinase/fruct	PGAM,PF7K2	5.6
30	421671	AA001416	Hs.306122	glycoprotein, synaptic 2	TM,Steroid_dh,SS	5.6
	415514	F11301	Hs.138329	ESTs	SS,TM	5.6
	426208	AA370379	Hs.132216	ESTs	SS,TM	5.6
	425367	AB007867	Hs.278311	plend B1	Sema,PSI,TIG,SS,TM,TIG,Se	5.6
35	405939			Target Exon		5.6
	457331	AV547405	Hs.18443	alkyldehydrogenase 6 famII	GTP_EFTU	5.6
	438705	AA249624	Hs.283330	ESTs, Weakly similar to 210825	SS,E2F_TOP,E2F_TDP	5.6
	428524	AI125272	Hs.98712	hypothetical protein DKFZp434H1	SS,TM,MSP_domain	5.6
	419389	AA074951	Hs.319055	ESTs	SS,DPPV,Nf_kam	5.6
	447595	AW379130	Hs.18953	phosphodiesterase 9A	PDEase	5.6
40	408015	AW136771	Hs.244349	epitomal differentiation comp		5.6
	413241	BE951580	Hs.61622	gb:AF010049-091299-201-c07 B	SS	5.5
	425849	AF044924	Hs.30792	hook2 protein	SS	5.5
	434357	AW132284	Hs.3828	merlonia (di-phospho) decarbo	SS	5.5
45	455274	BE151022		gb:PA0-HIT0303-271059-001-c08 H	GIMP_kinases,SS,TM	5.5
	453904	AW033281		ESTs	SS,TM,RNA_pol_L	5.5
	424624	AB032947	Hs.151301	Ca2+-dependent activator protei	Fork_head	5.5
	425576	AA381720	Hs.27181	gb:EST394853 Activated T-cells	wva,Integrin_AFG-GAP	5.5
	440682	AA932152	Hs.27181	nuclear receptor binding facto		5.5
50	419125	AA542452	Hs.130881	B-cell CLL/lymphoma 11A (zinc	SS	5.5
	450207	T87615	Hs.14716	ESTs		5.5
	405211			C70005000.gj4508027[ref]NP_003	SS	5.5
	413537	H55775	Hs.207915	ESTs		5.5
	426793	X95887	Hs.172360	HIR (histone cell cycle regula	WD40,Cathrin,Cathrin_fr	5.5
55	412091	R06185		gb:ye94003.r1 Soares fetal liv	SS,TM,IBR,IBR	5.5
	446536	W74413	Hs.16251	ESTs	SS	5.5
	451117	AA015752	Hs.205173	ESTs		5.5
	405647	AA040985	Hs.335877	Homo sapiens, clone MGC:4659,	TM	5.5
	412673	AL042957	Hs.31845	ESTs		5.5
60	428440	BE382756	Hs.169902	solute carrier family 2 (facil	sugar_fr,SS,TM,sugar_fr	5.5
	449225	R39109	Hs.6777	ESTs	SS,TM,Nu_suph_symp	5.5
	403938			Target Exon	Ephrin	5.5
	441197	BE244638	Hs.166	sterol regulatory element bind	HLH	5.5
	455904	BE011183		gb:PA3-BN0316-10550-003-009 B		5.5
	457468	AW071345	Hs.292715	ESTs		5.5
65	447677	AA119235	Hs.344456	gb:lf2p402.x1 NCL_CGAP_Bm23 H	SS,gf-C2H2,SCAN,SCAN_d-C	5.5
	415473	R35986	Hs.12778	ESTs	TM,Ion_trans	5.5
	408422	AW971031	Hs.143554	ESTs, Highly similar to B45036		5.5
	447860	AW17621		ESTs	SS,TM,Tm_1	5.5
	451568	NM_001089	Hs.26630	ATP-binding cassette, sub-famI	ABC_tran,SRP54,SS,TM,ECH	5.5
70	439422	AA452791	Hs.249625	ESTs	SS,TM	5.5
	423479	NM_014328	Hs.129208	death-associated protein kinase	phlase	5.5
	429568	AUS78951	Hs.289709	ESTs, Weakly similar to 210256	SS	5.5
	441187	AW195237	Hs.7734	hypothetical protein FLJ22174	SS,TM,tubulin	5.5
75	420894	AA744597	Hs.88854	ESTs	SS,ank	5.5
	404710			C8001584.gj7499203[gij]T2099		5.5
	447827	U73727	Hs.19718	protein tyrosine phosphatase,	Y_phosphatase,hs,Ig,MAM	5.5
	445387	AB874402	Hs.292690	ESTs		5.5
	419541	AW749617	Hs.280776	lantryase, TRF1-interacting an		5.5
80	443686	AA027213	Hs.270868	ESTs, Moderately similar to AL		5.5
	425315	AA545422	Hs.348137	Homo sapiens, clone IMAGE:3542	SS,cyristall	5.5
	451312	AT709831	Hs.337054	ESTs	SS	5.5
	432538	BE258332	Hs.278382	male-enhanced antigen	SS,TM,AAA,Ribosomal_L2	5.5
	446790	AAW452105		ESTs	SS,gf-C2H2	5.5
	446562	T09471	Hs.250820	hypothetical protein FLJ14827		5.5

425234	AW152225	Hs.165909	ESTs, Weakly similar to I38022	SS	5.5
411219	AW532917		gb:QV2-TT0003-161159-013-h06 T	SS	5.5
438142	A8277721	Hs.284298	Homo sapiens mRNA full length	PDGF,SS	5.5
432004	BE018302	Hs.2894	placental growth factor, vascu	HCO3 ₂ ,cotransp,SS	5.5
402916			EHSP00002025877-Bicarbonate t	RCO1	5.5
405346			Rag C protein	TM	5.4
415976	R43144	Hs.21919	ESTs	SS,MDM2	5.4
435964	T70740	Hs.31433	ESTs		5.4
440024	AA969333	Hs.160068	ESTs		5.4
431525	AA606656	Hs.6185	KIAA1557 protein		5.4
458644	AW270149		ESTs, Moderately similar to GG		5.4
410895	AW680676	Hs.26333	gb:U4A-510124-261099-015-065 S		5.4
441350	AB020690	Hs.7782	paraneoplastic antigen MA2		5.4
413034	BE392895	Hs.129126	Homo sapiens, clone MGC:109592,	SS	5.4
444654	N26362	Hs.11815	map kinase phosphatase-like pr	DSPC,Rhodanese,SS,TM	5.4
445987	NM_004729	Hs.26532	As-flike transposable element	2-FED	5.4
445871	AU702901	Hs.145582	ESTs, Weakly similar to FQR4 M	SS,TM,ethand,ethand	5.4
411992	AW616214	Hs.143055	ESTs	SS,TM	5.4
458341	AWQ73593	Hs.221894	gb:QV4-ET0534-281299-053-a08 B		5.4
451677	AAG26222	Hs.33338	Homo sapiens similar to oxygen	LRR	5.4
432656	NM_000246	Hs.3076	NHC class II transactivator		5.4
417739	Z43995		gb:HSC1QB121 normalized infant	SS,Ari(Gap,wwa,TSPM,13,Co	5.4
424618	L29472	Hs.1802	major histocompatibility compl	TM,lg,KHC,II_beta,SS,TMA	5.4
445847	T51454	Hs.82945	Homo sapiens cDNA: FLJ21330 liv	SS,TM,BNIF,h3J3J_recept	5.4
436094	AU798701		ESTs		5.4
433168	AU054536		glucow4g06.21 Soares_fetal_jiv	SS,TMPID	5.4
417359	T99264	Hs.191117	ESTs		5.4
436014	AF281134	Hs.263741	oncosome component Rsp46	RNase_PH,RNase_PH_C,SS,TG	5.4
435154	AA686764	Hs.301637	ESTs	SS,TM	5.4
431630	NM_002204	Hs.265829	Integrin, alpha 7 (antigen CD4	Integrin_A,FG-GAP,Rhbd,lg	5.4
444064	W85970	Hs.16222	ESTs	SS,TM,Dihydroorotase	5.4
415970	H23233	Hs.26022	KIAA1706 protein		5.4
445303	AW582198	Hs.12503	Interleukin 15 receptor, alpha	SS,sushi,SS	5.4
421542	AA411607	Hs.118654	ESTs, Weakly similar to KIAA11	SS,SS	5.4
459704	AA719572	Hs.274441	Homo sapiens mRNA; cDNA DKFZp4		5.4
402265			adenylate cyclase 1 (brain)	SS,TM	5.4
431543	AW69619	Hs.259758	Homo sapiens mRNA; cDNA DKFZp4	TM	5.4
431534	AL137531	Hs.258890	ESTs	SS,TM,ras	5.4
417516	AA20473	Hs.81529	ESTs	TM	5.4
423233	BE048021	Hs.11067	ESTs, Highly similar to T46395	SS,phlamin,lg	5.4
420733	AW291446	Hs.88651	ESTs	SS	5.4
404807			Target Exon	UPF0027	5.4
436483	AJ272063	Hs.263010	vanilloid receptor subtype 1	SS,TM,ank,ion_trans,SS,TM	5.4
425316	AA354077	Hs.29010	ESTs, Moderately similar to T1	SS,phlamin,lg	5.4
425565	AA359485	Hs.173084	gb:EST68511 Fetal lung II Homo		5.4
413341	H78472	Hs.191325	ESTs, Weakly similar to T18967	filament	5.4
401203			Target Exon	SS,ss,PGAM	5.4
423462	AL110255	Hs.116808	Homo sapiens mRNA; cDNA DKFZp5	SS,TM	5.4
436718	AW015227	Hs.289053	hypothetical protein FLJ14733	TM	5.4
428501	AL041162	Hs.58587	ESTs	TM	5.4
435959	W28548	Hs.285050	ESTs	TM,ion_trans,K_tetra,Kv2c	5.3
417514	AA203445	Hs.325819	ESTs		5.3
441358	AW173212		ESTs		5.3
401722			Target Exon	TM,PLAT,SS	5.3
408905	AW655763	Hs.861	Target CAT		5.3
454453	AW752781		hypothetical protein FLJ12614		5.3
410312	AW680953	Hs.75350	gb:U3-C10220-150200-068-A11 C	Vinculin	5.3
437926	BE383605	Hs.300816	small GTP-binding protein	SS,TM,TPR	5.3
458662	AW639151	Hs.262961	ESTs		5.3
411605	AW008931		ESTs	TM,myotub,treblev	5.3
405164	AA706639		gb:gc90c069.91 Stratagene hNT n	SS,TM,hnt,Ht-Lglnat,bubu	5.3
438868	AW246243	Hs.334800	hypothetical protein FLJ20974		5.3
435034	AF075993		gb:Homo sapiens full length in	filament,filament	5.3
411425	BE141714		gb:QV4-ET0101-021095-032-c04 H	SS	5.3
428186	AW504300	Hs.296605	mannosidase, alpha, class 2A,	Glyco_hydro_38,SS,TM,Pept	5.3
438470	AW936329	Hs.227823	p16 protein	SS,TM	5.3
427789	AA412428	Hs.48642	hypothetical protein FLJ23093		5.3
432020	BE267724	Hs.236551	ssbD	rm,SS,2-Hacid_DH,WD40	5.3
434314	BE392921	Hs.3797	RAB26, member RAS oncogene fam	ras,ar,SS	5.3
428539	AW410063	Hs.184877	solute carrier family 25 (ntro	mito_car,SS,TM,profilin,	5.3
414927	T83587	Hs.186476	ESTs	SS,Sulfase	5.3
404596			Target Exon		5.3
454151	AA047169	Hs.154088	hypothetical protein FLJ22756	SS,TM,Glycos_transf_4	5.3
431627	AW659720		HSPCD42 protein		5.3
422379	AA302660	Hs.133864	ESTs		5.3
426765	AA743803	Hs.172108	nucleoside 65kD	MAM33	5.3
433325	AW205986	Hs.143905	ESTs	SS	5.3
403128			KIAA1033 protein	SS,TM,tubulin,EGF,F5_F8_I	5.3
447730	AJ421251	Hs.114085	Homo sapiens mRNA for KIAA1755	SS,SS,SNF2_N_helicase_C	5.3
405085			Target Exon		5.3
438090	AA777381	Hs.291530	ESTs, Weakly similar to ALUC_H		5.3
435091	AA830144	Hs.135613	ESTs, Moderately similar to i3	KH-domain	5.3
427226	AD287878		gb:qv2306.61 NC1_CGAP_Lym6 Ho	SS,TM,Tm,1,SS,TM	5.3
427659	AA416559	Hs.36170	ESTs	SS,TM,UPF01,hyppin,CUB,0	5.3

5	421779	A879159	Hs.108219	wingless-type MMTV integration	SS,wnt,SS	5.3
	408270	AW17805	Hs.348000	gb:L3-HT0059-10089-007-806 H		5.3
	418437	AJ71738	Hs.348000	ESTs, Moderately similar to AL	SS, TM	5.3
	409879	BE03422	Hs.56851	hypothetical protein MGC2658	SS, TM	5.3
10	428304	A743177	Hs.167379	ESTs	SS, TM, cf-C2H2	5.3
	418678	NM_001327	Hs.167379	cancer/testis antigen (NY-ESO-	SS, TM	5.3
	436540	BE397032	Hs.14468	hypothetical protein MGC14226	SS, TM	5.2
	437161	AJ654477	Hs.25391	ESTs	SS, TM	5.2
15	400171	BE299671	Hs.256310	ENSP0000021197:Helicase SKZW	SS, proteasome	5.2
	431461	BE299671	Hs.256310	likely ortholog of mouse ZFP28		5.2
	402197			Target Exon	SS, TM, ATP1G1, PLM, MAT8Jg,	5.2
	445514	AW970440	Hs.23642	protein predicted by clone 236	SS, PK- α , tyrosine, PH.D.,	5.2
20	442472	AW950559	Hs.194519	gb:MRO-ST0020-081199-004-c03 S	SS, TM, Unc-1-P, synth, Ocul	5.2
	409679	BE250521	Hs.76394	ras homolog gene family, membe	SS, homeobox, CUT	5.2
	439150	AF066005	Hs.279623	gb:Homo sapiens full length in		5.2
	412334	BS011437	Hs.19447	gb:CM4-BN3220-080500-170-03 B		5.2
25	435185	AL119470	Hs.205984	ESTs	SS	5.2
	400668			Target Exon	CARD, ICE, p20, SS, ICE, p20,	5.2
	409125	R17269	Hs.343567	axonal transport of synaptic v	SS, kinesin, PH, FHA, kinesin	5.2
	445304	AW449320	Hs.248655	ESTs	SS, homeobox	5.2
30	414557	BE281057	Hs.194519	hypothetical protein FLJ12949	SS, TM, ank, Adap, comp, sub	5.2
	414551	AJ815639	Hs.76394	enoyl Coenzyme A hydratase, sh	ECH, PepLidase, U7, SS, TM	5.2
	432872	A906894	Hs.279623	seleuinoprotein X, 1	DUF25, SS, Ribosomal, L3, PDZ	5.2
	419492	AJ235347	Hs.19447	PDZ LIM protein myotube	LIM, SS, SH3, Sorb, Metalloph	5.2
35	407479	L73559	Hs.205984	gb:Homo sapiens DCS-B partial		5.2
	457892	AA744369	Hs.10041	ghmy61e10.t NCL_GCAP_Py18 Ho		5.2
	457228	U19177	Hs.10041	Human cosmid CRJ-CJ2015 at D10	6PF2C, PGAM	5.2
	437536	XH1221	Hs.144665	ESTs	SS, TM, Na, Ca, Ex	5.2
40	420285	AJ238124	Hs.293378	ESTs, Moderately similar to ZN		5.2
	431275	T56571	Hs.10041	ESTs	SS, HLH	5.2
	428021	AJ022287	Hs.111991	ESTs, Weakly similar to T33903	SS	5.2
	422400	AJ874434	Hs.126333	ESTs		5.2
45	446442	BE221533	Hs.257858	ESTs		5.2
	415585	R59946	Hs.184852	KIAA1553 protein	SS	5.2
	438429	D16918	Hs.12547	Homo sapiens cDNA: FLJ23388 i	TM	5.2
	401077			Bai1-associated protein 3	SS, TM, cf-C2H2, kinesin, sh	5.2
50	405537			Target Exon		5.2
	450437	X13956	Hs.24998	hypothetical protein MGC10471	SS	5.2
	408216	BE514290	Hs.13219	synactin 10	SS, SS, TM, HLH, TRAM, cf-CCCH	5.2
	452686	AW194601	Hs.13219	Target Exon	PI-PLC- γ , PLC- γ , C2, PH	5.2
55	401553			Target Exon		5.2
	447541	AJ000288	Hs.18800	hypothetical protein FLJ20281	cf-CCCH	5.2
	453434	AJ771378	Hs.333243	ESTs		5.2
	450351	BE547257	Hs.59791	hypothetical protein MGC13183	SS, TM	5.2
60	411456	AW847538	Hs.333243	gb:L3-CT0213-15129-038-G09 C	SS, TM	5.2
	445634	AJ624849	Hs.344612	ESTs, Weakly similar to NEL1_H	vwd	5.2
	453740	AL120295	Hs.311809	ESTs, Moderately similar to PC		5.2
	425318	AJ371525	Hs.17112	Homo sapiens cDNA: FLJ22322 i	SS, TM, EPH, lmb, kinase, fn3	5.1
65	416470	N90644	Hs.303023	beta tubulin 1, class VI	SS, tubulin, SS	5.1
	432022	AL162042	Hs.272348	Homo sapiens mRNA: cDNA DKF2p7		5.1
	457579	AB308916	Hs.36761	HRA5-like suppressor	TM	5.1
	439484	AW021071	Hs.253330	ESTs, Weakly similar to p40 H		5.1
70	422802	NM_004278	Hs.27008	phosphatidylcholine glycerol	DUF158, ank	5.1
	401724			C16001374.gi67550309:ratNIP_G3	TM, PLAT, SS	5.1
	438670	AJ75803	Hs.123428	ESTs		5.1
	414757	U48922	Hs.77252	fragile histidine triad gene	HECT, cf-UBR1, PABP	5.1
75	425098	AW295349	Hs.8538	ESTs	SS, TM	5.1
	431896	AW297844	Hs.101428	ESTs	SS	5.1
	416732	H81066	Hs.285017	hypothetical protein FLJ21799	SS	5.1
	404571			NM_015902:Homo sapiens prog	HECT, cf-UBR1, PABP	5.1
80	433675	AW977853	Hs.75319	ribonucleotide reductase M2 po	SS	5.1
	426358	AA376438	Hs.123428	gb:EST88856 HSC172 cells II Ho	TM	5.1
	456767	AJ064412	Hs.123054	Homo sapiens chromosome 19, co	SS, TM, tyrosine, kringlike, UPA	5.1
	412915	AW087727	Hs.74823	NM_004541:Homo sapiens NADH de		5.1
85	443553	AL040535	Hs.9573	ATP-binding cassette, sub-fam	ABC, tran, SS	5.1
	415886	Z42737	Hs.105986	gb:HSC05E081 normalized infant	SS	5.1
	401674			C16001417.gi7500345:ph1T21	FAD-oxidase, C, FAD_binding	5.1
	424266	AA337810	Hs.149152	ESTs, Weakly similar to PHCP M		5.1
90	450335	AW851734	Hs.149152	gb:MR2-CT0222-011199-007-e10 C		5.1
	408567	ST7321	Hs.226755	ciliary neurotrophic factor	CNTE	5.1
	438616	AW799109	Hs.226755	ESTs	14-3-3	5.1
	429078	AW822315	Hs.186776	ESTs		5.1
95	447976	AW972653	Hs.283681	ESTs, Highly similar to CR2_HU		5.1
	457720	AA592835	Hs.186776	ESTs		5.1
	402528			NM_020875:Homo sapiens rel pr	catharin, kinase, SS	5.1
	407757	BE048414	Hs.165215	hypothetical protein MGC53955	SS, EFG, domain, GST_C, GST,	5.1
100	452446	AA061123	Hs.297856	ESTs	rm, NTF2	5.1
	450807	AJ739282	Hs.105986	gb:w17b08.x1 NCL_GCAP_Co16 Ho	SS, TM	5.1
	432540	AJ821517	Hs.105986	ESTs		5.1
	443324	AJ838706	Hs.2041	ESTs, Weakly similar to A47582		5.1
105	426434	M17755	Hs.292911	thyroid peroxidase	EGF, aushi, An_peroxidase, p	5.1
	407652	WZ7953	Hs.292911	ESTs, Highly similar to S60712	Tropomn	5.1
	443952	A149106	Hs.12496	ESTs	SS, kinase	5.1
	448689	AJ792798	Hs.12496	ESTs, Weakly similar to ALU4_H	SS, TM	5.1

422837	U25441	Hs.121478	dopamine receptor D3	7mL1,SS,TM,7mL1	5.1
407143	C14078	Hs.332229	EST	SS,TM	5.1
442296	NM_007278	Hs.8186	lung cancer candidate	SS,TM,Glyco_hydro_56,Glyc	5.1
407722	BE2522	Hs.38041	prolactin (prolactin, vitamin	ph6,SS	5.1
427335	NM_005659	Hs.2134	TNF receptor-associated factor	MATH,SS,MATHA2M_NA2M,NT	5.1
447960	AW53477	Hs.26412	ring finger protein 26	SS,TM,CdL_N,CdL_N2,CdL_N3	5.1
408663			C11002296g11892557ghAAG39	SS,TM	5.1
420034	A164149	Hs.172035	hypothetical protein similar t	SS	5.1
421696	AF033306	Hs.106890	Homo sapiens clone Z3771 mRNA	SS	5.1
427587	BE348244	Hs.284239	ESTs, Weakly similar to 178885	SS,UOPGT	5.1
407204	R41533	Hs.140237	ESTs, Weakly similar to ALU1_H	SS,histone,Nistone	5.1
454219	X75242	Hs.44313	v-vet avian reticulodendroto	R10,TIG	5.1
430513	AJ112008	Hs.21586	G6C protein	SS,TM,GST_C,abhydrolase	5.1
435902	AA71857	Hs.297726	ESTs	SS, fibrinogen_C, Rhodanese	5.1
442743	AJ801351	Hs.302110	ESTs, Weakly similar to MUC2_H	SS,Caldesmon	5.1
454923	AW897238		gb:CAO-IN0057-150400-335-c06 N	SS,TM	5.1
440518	A488946	Hs.233325	ESTs	TM,Ribosomal_S7	5.1
448237	A1471790	Hs.305386	ESTs	SS,TM,Inclin_e	5.1
428924	A016405	Hs.98959	ESTs, Weakly similar to JC3314	SS,TM,SS_PSV_GATA	5.1
413281	ZX4655	Hs.233018	gb:HS657122 STRATAGENE Human	SS,TM,Glycos_intron_4	5.1
437141	BE324017	Hs.311057	hypothetical protein FLJ21478	efluid	5.1
421658	X04048	Hs.301760	frequent (Drosophila) homolog	SS,TM,GDPD,SS,TM,SH3,PDZ,	5.1
423467	AK002014	Hs.125014	hypothetical protein FLJ20207	PH	5.0
417151	AA194055	Hs.263858	ESTs	Armadillo_sug	5.0
403307	AT61706	Hs.304614	ESTs		5.0
404752			NM_024778:homo sapiens hypoth		5.0
453126	AA032155	Hs.61622	ESTs		5.0
413983	BE348384	Hs.279194	ESTs	SS	5.0
405366			NM_003371:Homo sapiens vav 2		5.0
412425	AW949158		gb:QV4-FT0005-110500-205-b06 F		5.0
437036	A1571514	Hs.133022	ESTs	SS,TM,Glycos_intron_2	5.0
448455	AJ252625	Hs.269560	ESTs, Moderately similar to S6	SS,TM	5.0
411413	BE379436	Hs.211572	haptan effluin proteoglycan 2	ss,laminin_B,laminin_EGF,	5.0
432579	AF043244	Hs.278439	nuclear protein 3 (apoptosis	CARD,SS,Hsf_HA-bind,E2F_	5.0
424874	AA347561	Hs.279688	Homo sapiens cDNA FLJ20812 fs	SS	5.0
408023	BE016069		ESTs	homeobox,homeobox	5.0
411758	AW656867		gb:QVQ-CT0363-210400-304-d03 C		5.0
410660	A061118	Hs.65328	Fanconi anemia, complementatio		5.0
427411	AA402242		ESTs	SS,TM,ERG4_ERG34	5.0
437018	AA898378		ESTs	SS,ras	5.0
427029	AA387096		ESTs	SS	5.0
452047	N33953	Hs.43510	ESTs, Weakly similar to BOX B	SS	5.0
432093	H26383		gb:y52zd03.1 Soares breast 3N	Band_41,ERM	5.0
453059	H52087	Hs.31659	thyroid hormone receptor-associ	SS	5.0
441456	A459811	Hs.127765	ESTs	SS	5.0
414356	AW505085	Hs.335147	gb:U1-FH-BN0-abs-a-10-d-ULr1	SS,TM	5.0
434067	H16913	Hs.124023	Homo sapiens cDNA FLJ14219 fs	Galactosyl_T_2	5.0
436383	AW022213		ESTs		5.0
402227	AA806185	Hs.130323	Homo sapiens, clone IMAGE:3950	WD4QS,SS,TM,KOW,HLH	5.0
448680	AW245890	Hs.21753	JM5 protein		5.0
435343	AF086161	Hs.114611	hypothetical protein FLJ11808	SS,TM,lypsin	5.0
428079	AA421020	Hs.20919	ESTs		5.0
421951	BE327432	Hs.109804	H1 histone family, member X	SS,SS	5.0
427204	AA405044	Hs.216725	ESTs		5.0
406950	W45393	Hs.55888	activating transcription facto		5.0
436574	AW233277	Hs.156465	ESTs		5.0
457751	AW401809	Hs.4779	KIAA1150 protein	SS,LIM,SS	5.0
435294	T84084	Hs.195008	Homo sapiens cDNA FLJ11723 fs	HMG_box	5.0
445372	N36417	Hs.144928	ESTs	SS,PI0,PDZ	5.0
440511	AF132659	Hs.7235	cHOS Interacting protein	SS,TM,AGE_Ribosomal_S17,	5.0
424437	BE244700	Hs.147049	cut (Drosophila)-like 1 (CCAAT	OUT,homeobox,beta-lactame	5.0
401639			NM_002675:Homo sapiens promyel	zf-B_box,zf-C1HC4,SS	5.0
417903	NM_002342	Hs.11116	lymphotxin beta receptor (TNF	TNFR_c6,SS	5.0
442451	AJ498080	Hs.129916	ESTs	SS	5.0
450536	A189529		gb:U17w02.x1 NCL_GCAP_GC6 Hom	SS,G-alpha,arf	5.0
425169	AW292500	Hs.128514	ESTs	SS	5.0
432582	AA677088		ESTs		5.0
444855	BE402070	Hs.12084	TU translation elongation fact	GTP_EFTU,GTP_EFTU_D3,GTP_	5.0
433507	A1817306	Hs.191791	ESTs	pinase	5.0
432396	AW299595	Hs.11900	hypothetical protein FLJ14972	SS	5.0
438395	AA017514	Hs.6211	methyl-CpG binding domain prot	MBO,zf-CXCC,SS,zf-CXCC	5.0
446803	NM_014835	Hs.15519	crystallin-binding protein-rela	Oxytelol_BP,SS	5.0
400782			Target Exon		5.0
440133	A1056255	Hs.133349	ESTs	SS,TMEF1B0	5.0
444903	AJ374787	Hs.132781	class I cytokine receptor	homeobox,SS,homeobox,home	5.0
412540	BE295770	Hs.819	homeobox b7	TM	5.0
419269	A235538		gb:z41b04.s1 Soares_NhlhMPu_S1		5.0

TABLE 20B:

Phy: Unique Eas probe/seq identifier number
 CAT number: Gene cluster number
 Accession: Genbank accession numbers

Play	CAT Number	Accession
408117	104000_1	AL138255 BE380045 AAD47314 D82381 T18585 H64978 T10798
408215	104078_1	BE614230 AA307674 N35529 AA338538 AL193603 AA781096 A1800061 A1813258 AW276647 BE221263 A1348910 A1805031 A1090798 A1359617 AA665931 AL160210 AA464651 A1353545 A1343638 A1343640 A1275091 M78146 AW262795 AW250002 AA503756 A1934519 AW127208 N26520 AA526638
5	408270	1040990_1 AW177805 AW177895 AW177816 AW177901 BE141597 BE141584 AW177822 AW177818 AW177899
	408294	BE141732 U75823 BE141331 AW178416 AW178430 BE141343 BE141298 BE141702 BE141285
	408567	106831_1 S72921 MAL00314 X58865 X20542 X50477
10	409070	1099768_1 AW527615 A1932774 A1932751
	409164	110421_1 AA70659 AA067407 AL038520 A1651598
	409679	BE205021 AA70637 BE249870 AA584291 AW502442 AW501551 A1221491 AA194239 D63046 AA153426 AA732343 AA193293
	409822	115554_1 AW953293 A0865310 AW107791 AA362540
	410445	120374_2 AA119933 AL113885 AW951629 AA322482
	410471	1204721_1 T68872 AW749857
15	410895	1220501_1 AW809679 AW809678 AW810113 AW810182 AW809900 AW809851 AW810110 AW810228 AW810342 AW810181 AW809532 AW805745
	411219	1235055_1 AW810372 AW809861 AW809752 AW809806 AW810452 AW809875 AW809964 AW810033 AW810111 AW809846 AW809847 AW809717
	411298	1237959_1 AW8252917 AW8252913 AW8252905 AW823788 AW8252915 AW823776
	411426	1245515_1 AW835848 AW835834 AW835823 AW835831 AW835832 AW835833 AW835834 AW835835 AW835836 AW835837
20	411456	1245515_1 BE141714 AW845993 AW845999
	411480	1246706_1 AW847698 AW847716 AW847694 AW847592
	411490	1247426_1 R39474 AW548420 R76343
	411605	125123_2 AW008331 AA678258 R12579 W66152 AL123683 A6699780 A672156 BE052587 AA094200 A1633815 AA526153 W66151
	411758	1256751_1 AW860687 AW860665
25	412091	1276504_1 AW848155 AW848203 AW848008
	412122	127836_2 AW852707 N57282 AA725075 A1703492 AW5612137 AL1096372 A879394 A1653605 W26914
	412128	1278726_1 AW894709 N78140
	412173	1280876_1 T71071 AW1902279 AW897808
	412425	128278_1 AW848155 AW848203 AW848008
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35	413272	1337518_1 AA127924 AA127846 AA534131 N53566 AA533669 AW511251 A174441 AA127875 A1652393 AA127913 N75225 AW70336 N69010 AW070312
	413534	133730_1 BE140881 BE140876 BE145788 BE140897 BE140774 BE140863 BE1446907
	413564	1376722_1 BE260120 BE148538
	413447	1374008_1 BE275835 BE390063 BE388764 BE409101
40	413371	143988_8 A1059685 BE294601 BE562308 BE236767 AW167051 A1819883 AW162529 BE439610 AW157225 AW162675 AW161998 A1816168 AW162599 AW161816 AW161520 AW162518 AW162539 M17733 AW157639 A1879416 BE258811 AW157436 AW162433 AW161533 AW162155 AW157104 AW157269 AW1612
	413391	1441921_1 BE409872 BE281460
	414413	1443696_1 BE294877 BE294759
45	414593	1444900_1 BE386764 BE387660
	414944	1509480_1 C15004 D08043 C15696
	415126	1523506_1 D06945 D61346 D81968 D80539
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	415866	1560411_1 Z42737 T08938 N07956
	415958	1563222_1 H10942 Z42911 R60453
50	416233	158010_1 AA178633 AW981842 AA309418
	416597	160308L_1 H66891 R38149 R38467
	417739	1698183_1 Z43805 T12527 R34740
	418184	172744_1 AA367375 AA485701 BE152479 BE152800 AW161691 AA214097
55	418304	173558_2 AA215702 AA368006 AA215703 BE060555 BE060876
	419269	183444_1 AA235838 BE180775
	419516	185333_1 H62589 H43802 AA43820 AL040762 N24315 U66692
	420530	19446_1 A1218431 AA42322 AW183040 X86012 AA868831 A191789 AA912999 A0204291 A205744 A218259 AA426396 AA933742 AA030660 A1018669 AW879431
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	423790	23031_1 BE152933 AA330994 BE379904
	424874	244523_1 AA347951 A698463 AA83123
	426221	26281_1 AB07881 U32581 AW131202 AW955994 W31364 N24261 A1033045 H66994 AA364848 A1222031 AA907216 A1215730 AA776581 AW473826 W01373
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	426578	265378_1 AA381720 AA382040 AW963564
	427029	274544_1 AA397596 A119827 AA453832
	427326	277223_1 A287878 A1804160 AA400787
	427411	278474_1 AA42242 AA813659 A1153116 AA412054
70	428092	286920_1 AW879141 AA421182 A1734104 A1733923 AA430600
	428304	289503_1 A1743177 AA425743 A1804283 A1743189
	428948	2937_1 BE514322 AA673343 BE272670 BE616350 AW163444 AW161588 AW378754 AW228082 BE267205 BE047746 BE207113 BE312782 BE266301 BE265413 BE273846 BE280665 BE278633 BE281417 BE407796 BE387176 BE392818 AW377597 BE365651 BE363978 AW327483 BE3294175 BE358795 BE275683 BE3
75	429328	303954_1 AA452229 A1262172 A1825886 A1690941 H66626 A768463 A1871422 A1915824 AA746891 AA521087 AA814103 AW953151 AW059977
	430168	313927_1 AW855343 AA466807 A1740223 AW513008 A176212 A1554512 AA85642 AA68976
	431082	327712_1 AA416160 AA416145 A102098
	431161	328713_1 AA433891 AA429120 AA533782
	431424	333110_1 A222259 AA806550 AA504839 AA805261
80	431627	AW805720 AW809735 AA8082767 N08531 R23418 N55937 BE549484 AW161584 AW1615947 AW161697
	432093	341283_1 A262383 AW87570 H05859 AA455808
	432943	356589_1 AL043883 AA570638 AA907456 AL043882 AW362288
	433168	360235_1 A1085436 AA579438 AA579002
	433587	36402_1 T06639 AF024702

5	434315	383402_1	AW196608 AAB84617 AW758108 AI126321 AA629291 AW196549 AI208031
	434743	3825_1	AI336410 AI356019 H00141 T78748 ALD49365 AL079911 AI750972 Z42602 AI452523 AI232826 AA215407 AI633829 AA292122 H42783
			AW595653 AF06596 N63040 N63271 AA131836 AW607273 AA527132 Z32315 AA421961 T34951 AW596680 H78807 N31947 AA521151
10	434766		AI278686 AW44764 A4700
	435186	383400_1	AA81006 AW574514 AA76499 AA64302
	435262	402143_1	AL119470 AA659492 AI628351 AI263835 AL119498
15	435339	403605_1	AA677088 AI022246 AA671107
	435394	404485_1	AI338300 AI762881 AA678073 AA988621
	436389	414444_1	AI787001 AW700526 AW704731
20	436389	41894_1	AI811706 AW297340 AI227887 AA879580 AA228003 AI610234 AI921618 AI756806 N37039 AA061104 BE172693 D06503 Z28595 Y99651
	436393	41893_1	AA282389 AA283505 N28751
	437018	413333_1	AW022213 AI274032 AI227898 AI653412 AB08451
25	437050	432210_1	AA980978 AI4907263 AI424199
	437215	43473_1	AA766420 AA743319 AW975442
	437662	440374_1	AL117488 ALD44479
30	437834	443574_1	AW653807 AA032241 AI222134 AI216405 AI655943
			AW749296 AW749289 AW749287 BE535498
			AW753311 AW663081 AA778411
35	438118	450293_1	M04429 M34431 M34432 M25802 AW538720
	438723	46392_1	AF07503 H52291 H62828
	439034	46802_1	W69836 AF088287 BE56567
40	439150	46919_1	BE561888 AF360616 BE362102
	439469	47274_1	AI481594 AW138040 AA889255 AI700895
	440117	49187_1	AW173212 AA983948 AI080705 AA331334
45	440546	499676_2	AW514263 AI587908 AL229628 AI299043 N51706 AA36483
	441358	515468_1	AW197794 AW195867 AW197787 AA686403
	441523	519049_1	BE5289 T65201 F11984 F13188 AA577679 T77028 H12167
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	442146	533072_1	AW806889 AW068852 AF049582
	442318	538564_1	AD17521 AI017613 AW511133
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	442780	551403_1	AI149106 AI500318 AI334156 AW803028 AI765678 AI769652 AI167308 AI128865
	442933	553987_1	AI147237 AI805017
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70	445837	652068_1	HI9058 H11124 T1
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	446790	693032_1	R31107 AI341136 AI653196 HI9553
75	447045	70510_1	AA452165 A341280 AB17445
			AW262394 AA579531 AW282131 AA103161 BE146145 AW595562 AW595777 BE146152 BE146040 BE145972 BE145099 AW003280 AA869470
			BE146306 T85009 AI087294 BE146299 BE146319 BE146307 W44912 AI703134 AW026017 BE382873 AA903733 AI655933 BE551223 AA847694
80	447128	70934_1	AW173582 AW587240
	447904	714913_1	AW21889 BE485052 AI452509 AI244810 XH4721 AI858001 AI553937 AI419853 H00719 AI765259 AW973696 F25787 F32749 AI568815
	448330	758690_1	AW015380 AA554539 C00201 AA61610 AW059537 R71727
85	448393	79225_1	AW206303 AW267644 A785705
			AI035449 AW016705 AI492482
			AW171639 BE026541 AW407710 BE513882 BE546739 AA053597 BE140603 BE218514 AW966702 AI656234 AI636283 AI567265
90	449324	804808_1	AW340858 BE207794 AA053385 BE9173 AI292343 AI454908 AA233504 AI659741 AB2478 AI339460 AI760441 AA346416 BE047245
	449495	803345_1	AA703080 AA394063 AA454
	450251	822987_1	AI638706 BE502922 R11026
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	450807	847591_1	BE060453 BE080416 AI658238
	451045	85673_1	AI695829 BE161564 BE077251
100	451752	8835_1	AI728623 R26418
			AI215672 AW656828 AA013335 H86334 AA017006
			AB032997 T74050 BE467119 AW237035 AI141678 AA934774 AW978722 AI61408 H09487 AI934521 AA716567 H62600 AW9668 Z40632
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	453413	966269_1	AJ003294 AJ005315 AJ003293
	453829	982731_1	AI138200 T71830 T71828
110	453904	986581_1	AW003821 AW247475 AW025661
	454038	120132_1	AJ224053 AA114150 AI143175 AA224027 T58431 AA211908 AA659657 AA109744 AA330511 AA164864 T58463 AA214394 AA161378
			AA161386 AA206211 AA167824 AA084940 AA223825 AA191190 AA309486 AW961804
115	454543	1206827_1	AW752781 BE143749 AW752727 AW752559 AW752578 AW752584 RA5742
	454577	122567_1	AW809272 AW809169 AW809179 AW809192 AW809166 AW809372 AW809191 AW809168 AW809197 AW809181 AW809237 AW809226
			AW809259 AW809259 AW809259 AW809259 AW809273 AW809270 AW809147 AW809168 AW809245
120	454682	1228976_1	AW816029 AW813292 AW816156 AW813333 AW816159 AW813302 AW813344 AW813172
	454718	1230532_1	AW815144 AW815150 AW861007
	454756	1233646_1	AW819273 AW819283 AW819287 AW819281 AW819274 AW819282 AW819277 AW819286
125	454923	1243024_1	AW857236 AW804506
	455035	1249672_1	AW851734 AW851676 AW851693 AW851713 AW851722 AW851616 AW851731 AW851618 AW851646 AW852215
	455274	1272212_1	BE151622 BE151636 AW885648
130	455286	1273576_1	BE144384 AW8587474 AW887403 BE144386
	455557	132597_1	AW059830 AW059807
	455604	1337197_1	BE011183 BE011170 BE011333 BE011188 BE011181 BE011324 BE011161 BE011169
135	455679	1349914_1	BE066529 BE066274 BE066390 BE066356 BE066419 BE066345 BE066298 BE066292 BE066359
	455778	1364506_1	BE086746 BE086802 BE086758 BE086876 BE086947 BE086881 BE086952
	455865	1380385_1	BE153524 BE153576 BE153563

456487 19270_1 AF064804 AA320303 N83343 AA564588 AF059734 AA343248 AW5964366 T85411 AW511100 T85442 AW070452 AA013172 AT67005 T32140
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 457892 432926_1 AA744389 AA744270 AA744284 AA744299 AA745380 AA744337 AA846905 AA847686
 457878 448300_1 AA776638 DE495640
 458198 594334_1 AC28100 AA652934 AA918305
 458644 670856_1 AW270149 AW564628 AT285912

TABLE 20C:

Phy: Unique number corresponding to an Eos probe set

Ref: Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham 1 et al." refers to the publication entitled "The DNA sequence of

human chromosome 22" Dunham, et. al. (1999) *Nature* 402:489-495

Strand: Indicates DNA strand from which exons were predicted

NI_positon: Indicates nucleotide positions of predicted exons

Phy	Ref	Strand	NI_positon
400460	8389428	Plus	35599-36205
400500	6785136	Minus	120239-120495
400528	6981824	Plus	472381-472528,474170-474277,475328-475542,475878-476000
400668	8118719	Plus	121756-122043
400748	8115063	Plus	84237-84398
400762	8131616	Plus	7235-7605
400772	8131629	Minus	34896-35021,41078-41197
400833	8705148	Minus	187599-188138
400863	9796116	Plus	21675-22330
400906	9566280	Plus	112863-112983,120162-120286
400923	7637839	Minus	94518-94659
401121	8570296	Plus	57211-57525
401180	9438648	Minus	15098-152128
401203	9745387	Minus	17261-17308,173086-173028
401210	7712287	Plus	166569-167133,169780-169877,171563-171733
401215	9850408	Plus	103739-103919
401264	9797154	Plus	133810-133927,133367-133504
401278	9799536	Plus	98428-98573
401349	9930791	Plus	72440-73030
401402	7710964	Plus	76730-76877
401488	7341775	Plus	54523-54686,55364-55451,55737-55846,58047-58175,58261-58356
401507	7534110	Plus	71058-71259
401539	8072433	Minus	62028-62608
401553	8099284	Minus	83950-84161
401594	7220963	Plus	7997-7997
401674	7689803	Plus	138785-138927,139157-139298,139440-139599,139990-140159
401877	9965537	Minus	62856-63066,63063-63084
401722	7656694	Plus	143851-144064
401724	7656694	Plus	150055-150241
401822	6730824	Plus	88400-88559
401885	8140731	Plus	148324-148321,150365-150559
401936	3828091	Plus	48329-48473
401938	6182666	Plus	151891-152032
401984	4454511	Plus	103825-104024
402189	8576043	Minus	128316-129601
402197	8576113	Plus	19846-199585
402286	2865079	Minus	92386-92534
402365	9454515	Minus	70828-71185
402445	9796614	Plus	80925-91054,91172-91331
402501	8797862	Plus	8801-8876
402545	9038114	Minus	48547-48578,50604-50737,51384-51467
402651	7960381	Plus	174215-174380
402916	7406502	Minus	361474,541-687
403003	5441423	Minus	79403-79560,79712-80021
403128	7331426	Plus	127884-123018,123134-123283,123372-123695,123779-123940,124069-124256
403672	7283286	Minus	96560-96881,97551-97620,97933-97994
403748	7658423	Minus	128503-130344
403865	7710403	Minus	53259-53324
403938	7711795	Plus	48536-48822
404001	8555948	Minus	137995-138317
404066	3367505	Minus	71040-71288
404149	7534008	Plus	121831-121851,124044-124150
404189	6010176	Plus	1659-2740
404311	8570412	Minus	149189-149303
404333	5802821	Minus	137948-138024,138111-138300
404365	9584977	Plus	50151-50319,50853-51098
404430	7407979	Plus	42321-43109
404438	6984205	Plus	63413-63553
404571	7249189	Minus	112450-112648
404596	9595282	Minus	104807-105043
404676	8777204	Minus	51167-51242,48906-58189,58891-59048,60452-60628
404710	8801097	Minus	45190-45339,47509-47622,48137-48264,48805-48946,50073-50345,51467-51688
404752	7109522	Minus	120168-120328
404807	4185210	Minus	124246-124422
404956	7307343	Plus	55883-56033
405085	8072509	Minus	44045-44230
405113	8086927	Plus	170073-170894
405143	9438278	Plus	5894-5983,7355-7427
405159	9965252	Plus	79659-79804

5	405211	6652345	Minus	31340-32609
	405247	7249301	Minus	65578-65776,68038-68234
	405345	2991263	Plus	101982-102171
	405366	2182280	Plus	22478-22632
	405371	2078469	Minus	47657-47766,48461-48596
10	405375	1552539	Plus	11646-12050,12207-12485
	405378	1552533	Plus	28576-29099
	405473	8433781	Plus	153074-153343,154501-154598,156879-156999,159883-159905,159910-160053,161109-161228,163305-163131,165163-165258,165858-166003,167375-167552,169252-169304,171127-171281
	405474	8433781	Plus	172005-172175
	405557	1621108	Plus	36383-40047
15	405637	6289229	Plus	189592-189598
	405770	2735037	Plus	61057-62075
	405928	7717155	Minus	2923-3209
	405931	6758795	Minus	146233-146705
	405939	6758795	Plus	170503-170554
20	406109	9127147	Minus	68328-56485
	406230	4760409	Plus	71716-72515
	406284	7549620	Plus	74002-74159
	406289	6862078	Minus	35565-36119
	406301	8575858	Plus	57291-57494
25	406373	9256130	Plus	188922-189162
	406495	7711328	Minus	174661-174978
	406575	7715779	Plus	142034-142473

Table 21A lists about 333 genes up-regulated in ovarian cancer compared to normal adult tissues that are likely to encode intracellular or cell-surface proteins. These were selected as for Table 20A, except that the ratio of "average" ovarian cancer to "average" normal adult tissues was greater than or equal to 3.0, the "average" ovarian cancer level was set to the 90th percentile value amongst various ovarian cancer specimens, the "average" normal adult tissue level was set to the 75th percentile value amongst various non-malignant tissues, the "average" ovarian cancer value was greater than or equal to 400 units (this selects for the most abundant of the up-regulated genes), and the predicted protein contained a structural domain that is indicative of extracellular localization (e.g., Ig, fn3, etc, 7tm domains, signal sequences, transmembrane domains). The predicted protein domains are noted.

TABLE 21A:

Play: Unique Eex probe/identifer number
ExAccn: Exon/Accession number, Genbank accession number
UG ID: Unigene number
Title: UniGene gene title
Pred. Protein Dom.: Predicted protein domain
R1: Ratio of tumor to normal body tissue

Play	ExAccn	UG ID	Title	Pred. Protein Dom.	R1
45	407223	H98593	gpcr/glyc12.s1 Soares melanoyt	SS,TM,SS,TM,DDOST_48KO	59.8
	421256	NM_002666	perlepin	perlepin,SS	47.6
	430281	A078942	CQI-69 protein	nmb_carr,SS,TM	46.7
	410418	D31362	transmembrane protease, serine	SS,TM,ML_recep_t_a,bypsi	41.0
	431773	BE49442	pleckstrin homology-like domain	PH,SS,TM,Tropoin	37.1
50	428738	AA43398	CL25 mitogen: muscle 16	SS	35.6
	438424	A912498	hypothetical protein FLJ14995	SS,TM	35.3
	450461	BE40981	hypothetical protein FLJ23476	SS	34.4
	437887	AA770561	hypothetical protein FLJ22959	SS,TM,2x-DHHC	33.9
	452554	AAW62434	ESTs, Weakly similar to ALUS_H	SS,PAS,HLH	32.5
55	422310	AA316622	cytochrome P450, subfamily IIS	SS,TM,pkinase,fn3,Ig	30.5
	452849	AF044924	hok2 protein	bZIP,SS,Ahpc-TSA	29.6
	407722	BE252241	pyridoxal pyridoxine, vitamin	p60,SS	29.2
	116819	U77735	p16-2 oncogene	pkinase,SS,TM,OTU,K_tetra	27.9
	430357	A924533	bicarbonate transporter relate	HCO3_cotransp,SS,TM	27.7
60	477225	U65839	mitogen-activated protein kina	pkinase	27.5
	454917	AW322517	prostaglandin G synthase	SS,TM,myosin_head,R4,DAQ	27.2
	445434	BE391690	hypothetical protein FLJ20917	SS,PWWP,Exonucleas,ipoc	26.8
	452389	BE513301	hypothetical protein, clone 24	SS,perlepin	26.5
	119451	A907117	synthase binding protein 2	Sec1,SS,TM	25.1
65	434420	BE114743	Homo sapiens, Similar to hypot	MAPEG,SS,TM,MAPEG	25.1
	412674	X04106	catpain 4, small subunit (50K)	SS,SS,ar,ras,fn3,ras	25.0
	428023	AA158243	FK506-binding protein 2 (13kD)	ethand,SS,CAP_GLY	24.4
	444672	Z96538	laminin, alpha 5	SS,PGRP,SS,PDGF,C2,PL-PLC	24.3
	113726	AJ278455	anexin A11	laminin_EGF_jamminin_G_EGF	24.0
70	438951	U51336	inositol 1,4,5-triphosphate 5'	anexinD,SS,anexinD	23.1
	423099	BE439582	phosphorylase kinase, gamma 2	SS,addored_nitro,SS	23.0
	423645	L49227	glycogen synthase kinase 3 alp	pkinase,SS,SANF2_N,helicas	23.0
	427659	AA825286	serum amyloid A1	pkinase,SS,Cu	22.4
	407117	AA146625	gpcr/glyc12.s1 Stratogene pancr	SS,SAA_proteins,SS,SAA_pr	22.2
75	42916	U16623	gpcr/glyc12.s1 Stratogene pancr	HCO3_cotransp,SS	21.3
	425769	D17629	galactose oxidase (N-acetyl)-6-ox	addored,SS,TM	20.8
	422058	H03117	similar to mouse neuronal prot	TM	20.6
	442332	A357813	ESTs, Weakly similar to A47582	SS,TM,TGFB_propeptide,TGFB	20.1
	431517	AF077036	DKFZP586G1722 protein	SS,Tropomyosin	20.0
80	422178	AF091619	dyad, axonemal, intermediate	WD40,SS	20.0
	419444	NM_002495	Target CAT	trr4,SS,TM,V_ATPase_sub_a	19.5
	116893	AA455588	hypothetical protein FLJ22573	SS,rm,SS	19.2
	434030	AW162336	low molecular mass ubiquitinone	SS	19.1
	411813	NM_014931	KUAI115 protein	SS,TM,V_phosphatase	18.9
	422305	A928242	ESTs, Highly similar to AF1984	SS	18.8

419167	AU589535	Hs.94875	ESTs, Weakly similar to A35363	SS	18.6
406663	U24683		immunoglobulin heavy constant	SS	18.5
429712	AW248285	Hs.211914	ENSP00000233627-NAID-Hubiquitin	ordered_g5,SS,TM,rm	18.5
425846	BE242709	Hs.159537	retY-RNA synthetase 2	GST_C, GST_I, N, Troponomyosin, S	18.4
447151	AJ228113	Hs.92579	Homo sapiens clone CDAP0014.0 m	SS,TM,IR,amino,trans_1,2	18.4
413343	BE392026	Hs.334546	hypothetical protein MGC13045	SS,DnaJ	18.2
450209	AW073380	Hs.267563	SS,Pyridox_oxidase,cf-C2H	SS,Pyridox_oxidase,cf-C2H	17.7
427721	AJ582643	Hs.108455	ubiquitin,UBA,Integrin_3	ubiquitin,UBA,Integrin_3	17.6
443780	NM_012088	Hs.97354	RAD23 (S. cerevisiae) homolog	l2p,NTP_trans_2,SS,TBC	17.2
421612	AF161254	Hs.106196	activating transcription factor 806 antigen	l2p,NTP_trans_2,SS,TBC	17.1
444620	AW405533	Hs.251367	ESTs	SS,PLC-X,PH,PLC-Y,C	16.7
406621	X57605	Hs.181125	immunoglobulin lambda locus	SS	16.6
443456	AJ026973	Hs.96402	target of myb1 (chicken) homol	VHS,GAT,TM,Heme_oxycanase	16.6
440104	AA132638	Hs.239894	hypothetical protein MGC2803	SS,DS	16.3
427640	AF582923	Hs.180015	D-dopachrome tautomerase	MF,late_protein_1,2,SS,GS	16.2
445625	BE240743		hypothetical protein FLJ22535	SS,TM	16.1
427461	AA331527	Hs.132040	hypothetical protein MGC13010	SS,TM,ACAT,LR	15.9
423356	ZB3045	Hs.127610	acyl-Coenzyme A dehydrogenase	Acyl-CoA_dh,Acyl-CoA_dh,M	15.7
409017	TB9397	Hs.272299	hypothetical protein RP4-622L5	SS,TM	15.6
428157	AA770021	Hs.16332	ESTs	SS,g,h3	15.5
420229	BE258676	Hs.94446	polyamine-modulated factor 1	site,Jet_red,SS,TM,g,h	15.5
404650			C11022523-g112099 [p]P23267	SS,TM,SCAN,cf-C2H2,KRAB	15.4
407767	W15338		hypothetical protein	SS,CF	15.4
409918	M86357		g,h-Homo sapiens DNA-binding pr	zr-C2H2,SS	15.4
435158	AW063017	Hs.65588	GA2 associated protein 1	rm,SS,CH	15.3
407641	AL050341	Hs.37165	collagen, type IX, alpha 2	SS,Collagen,SS,Collagen	15.3
421273	AJ245416	Hs.103106	U6 snRNA-associated Sm-like pr	Sim,SS,RNA-eynL1,GST_C,G	15.1
402365			Target Exon	SS,SS,TM,g,h	14.9
420503	R35917	Hs.301338	hypothetical protein FLJ12587	SS	14.8
427502	A811865	Hs.71133	Homo sapiens, clone IMAGE3161	SS,TM,ABC_tran,Glyco_tran	14.8
423872	A908984	Hs.279523	selenoprotein X, 1	DUF25,SS,Ribosomal_L3,PDZ	14.5
439233	AA631893	Hs.232167	hypothetical protein FLJ23109	zr-C2HC4,TM,Sulfate_trans	14.5
116897	MT8146	Hs.324700	hypothetical protein MGC25953	SS	14.4
447304	Z58883	Hs.180719	phosphatidylinositol glycan, c	SS,Phosphatidylinositol_glycan,c	14.2
431543	AW595919	Hs.255976	adenylate cyclase 1 (brain)	TM	14.0
447944	AA401573	Hs.288284	hypothetical protein FLJ23778	SS,TM	14.0
117595	AA242117	Hs.145981	KIA11098 protein	SS,TM,Glyco_Hydro_31,Glyc	13.9
435127	W54824	Hs.11565	RIKEN cDNA 201010012 gene	Corona_7,SS,TM	13.8
112623	R28898	Hs.74170	metallothionein 1f (functional	SS,TM,metallothio,DEAD,meta	13.7
446133	AA723157	Hs.70769	folate receptor 1 (adult)	Folate_rec,SS	13.5
435387	AW322847	Hs.70573	PKC-1-related HIT protein	SS	13.5
431462	AW583672	Hs.256311	granin-like neuropeptide pep	SS	13.2
408724	A6585842	Hs.264143	ESTs, Weakly similar to T22914	SS,phkinese,bubulin	13.2
423464	NM_016240	Hs.128856	CSF1 protein	Collagen,SS	13.1
429539	AW410053	Hs.154877	soluble carrier family 28 (mto	mto_car,SS,TM,profilin,	13.0
435014	AF281134	Hs.283741	oxosome component Rrp46	RNase_PH,RNase_PH,C,SS,TG	12.9
438857	A627912	Hs.130783	Forsman synthetase	SS,RA,RasGEF,RasGEF	12.8
444410	BE307369	Hs.33719	ESTs, Moderately similar to S6	SS	12.8
427527	A690397	Hs.153261	immunoglobulin heavy constant	SS,TM,g,h	12.6
430169	AW963343		DKFZ4641735 protein	SS,TM,ethand,ethand	12.5
437543	H16443	Hs.7117	glutamate receptor, ionotropic	SS,TM,g,h,chan,ANF_recept	12.4
413711	AW291765	Hs.75469	heat shock transcription factor	MA,SS,CFP_TDP	12.3
429255	AW046898	Hs.155976	cutl1a.49	SS,SS,Cullin,Cullin	12.2
441336	NM_001440	Hs.9018	exocytosis (multiple)-like 3	Exocytosis,SS,TM	12.1
407143	C14076	Hs.332329	EST	SS,TM	12.1
421707	BE051914	Hs.10844	Homo sapiens cDNA FLJ114476 fs	SS,SS,TM,Sema	12.0
425251	Z22521	Hs.155342	protein kinase C, delta	phkinese,DAG_PE-bind,phkine	12.0
421574	NM_005658	Hs.2134	TNF receptor-associated factor	MATH,SS,MATH_A2M_NAZM,NT	12.0
421572	AAS31607		hypothetical protein FLJ22878	SS,TM,TGF-beta,ASC	12.0
447946	AJ561664	Hs.156827	ESTs	SS,PTM,HK7m_1,DAGK2,DAG	11.9
429554	A0000633	Hs.164476	hypothetical protein FLJ20626	SCAN,zf-C2H2,KRAB,SS,KRAB	11.7
427273	AW139032	Hs.107376	hypothetical protein DKFZ434N	SS,SS,TM	11.7
427387	A529685	Hs.177656	calmodulin 1 (phosphorylate h	ss,ethand,PmaD,SS,ethand	11.7
424415	NM_00104575	Hs.145580	enolase 2 (gamma, neuron)	enolase,SS,Arginase_1,AP	11.7
417852	AJ250582	Hs.82749	transmembrane 4 superfamily me	transmembrane4,SS,TM	11.6
447451	AJ379925	Hs.270525	ESTs	SS,phkinese,PH,phkinese,C	11.5
410397	AF217517	Hs.83042	DKFZ5564157 protein	SS,homobox,UPP0160,DUF23	11.4
433554	AA364810	Hs.23574	human homolog of Drosophila Sc	SS,TM,g,h	11.3
419390	AD01162	Hs.50207	hypothetical protein MGC11138	SS,TM,PMP22_C,SS,TM,PMP22	11.3
422682	W05238	Hs.94316	ESTs, Weakly similar to T31613	SS,TM,DEAD,relclease,C,1,am	11.3
421278	AL122093	Hs.122093	Homo sapiens mRNA: cDNA DKFZ4	SS,TM	11.2
450122	BE231678	Hs.134549	ESTs, Weakly similar to 130022	SS,TM,TY_phosphatase,LOHA	11.1
435958	AA847843	Hs.62711	High mobility group (nucleolin	SS,HMG_box	11.1
444744	BE384732	Hs.147582	ESTs	SS	10.9
422270	BE384920	Hs.125252	aldol	WD40,TM,Activin_recop,phn	10.9
417116	Z43516	Hs.73574	hypothetical protein FLJ12287	SS,TM,Semaphorin_F,Jul	10.9
436729	AA412048	Hs.279574	CS9-39 protein; oct desah-rep	SS,SS	10.8
450593	AF129085	Hs.25197	STIM1 homology and U-box conta	TPR,SS,TM,Rhomboid,Jadcam	10.7
406837	RF0292	Hs.156110	immunoglobulin kappa constant	SS	10.7
434234	C32634	Hs.156110	C-type lectin-like receptor-1	lectin_c,SS,TM	10.7
440150	AW975738	Hs.7001	Homo sapiens, clone IMAGE3940	SS,TM,SS,TM,Popliteal_M22	10.6
418641	BE243136	Hs.86947	a disintegrin and metalloprote	disintegrin,Repolyrin,Po	10.6
414313	NM_004371	Hs.75887	coatomer protein complex, subu	WD40,SS,WD40,Ribosomal_S2	10.6
420307	AW502899	Hs.86219	ESTs	SS,TM	10.6

414918	AI219207	Ha.72222	hypothetical protein FLJ13459
445652	BE272686	Ha.15356	hypothetical protein FLJ20254
418846	NM_015977	Ha.285681	Williams-Beuren syndrome chrom
455023	AD289333	Ha.31439	serine protease inhibitor, Kun
435900	AB371108	Ha.4518	seven transmembrane domain orp
431275	T56571	Ha.10041	ESTs
407241	M34516	Ha.322456	gcbHuman omega light chain pr
441238	A1372555	Ha.108324	hypothetical protein DNF276710
433325	AL350098	Ha.4973	hypothetical protein from EMBL
435605	AF151815	Ha.12785	hypothetical protein
444202	AL031885	Ha.158324	KIA0539 protein
455597	U28694	Ha.158324	chemokine (C-C motif) receptor
415200	AL040328	Ha.158324	SHSNF-related, nucleic acid
445528	AUX76540	Ha.15243	nuclear protein 1 (120kD)
414874	D26351	Ha.77515	Incal-2, 4,5-bisphosphate re
423524	AF059989	Ha.125938	potassium voltage-gated channel
434552	AA359818	Ha.325116	Homo sapiens, clone MGC-229
406836	AW514501	Ha.159110	immunoglobulin kappa constant
420233	AA258714	Ha.194864	hypothetical protein FLJ22578
421452	BE208364	Ha.25283	ESTs, Weakly similar to LKHU p
427672	AJ355815	Ha.336916	cell-associated protein 6
423218	NM_015896	Ha.167380	BLU protein
403028			Target Exon
412790	NM_014767	Ha.74583	KIA0475 gene product
418923	AW217108	Ha.118918	ESTs, Weakly similar to M20M_H
433866	AA613536	Ha.28412	ESTs
428092	AW879141	Ha.165373	ESTs
450483	M33718	Ha.98219	nitric oxide synthase 3 (endoth
420423	AA827718	Ha.28906	ESTs
452302	AF173867	Ha.28906	glucocorticoid modulatory elem
444681	AJ243337	Ha.288316	chromosome 6 open reading fram
414248	AJ797984	Ha.279929	gp25L2 protein
424283	M77848	Ha.123473	L1 cell adhesion molecule (hyid
438627	AJ067335	Ha.123473	ESTs
407065	Y10141	Ha.209065	gcbH.sapiens DAT1 gene, partia
441307	AW017696	Ha.209065	hypothetical protein FLJ14225
402549	AA119216	Ha.6259	hypothetical protein FLJ20442
424487	T08754	Ha.6259	KIA1698 protein
444633	AF111713	Ha.286218	junctional adhesion molecule 1
427747	AAW11425	Ha.180555	serine/threonine kinase 12
450437	X13958	Ha.180555	hypothetical protein MGC10471
415619	W42913	Ha.78039	ATPase, vacuolar, 14 kD
400021			NM_006150-Homo sapiens neural
454319	AW247736	Ha.101817	ESTs, Weakly similar to T25257
421680	AL031166	Ha.289106	Human DNA sequence from clone
445143	U28171	Ha.75852	casein kinase 1, delta
407507	U73799		gcbHuman dyxactin mRNA, partia
450883	NM_001348	Ha.25619	death-associated protein kinase
411874	AW581123	Ha.76686	gcbRCS-CT1027-12020-414-a05 c
414625	AA333738	Ha.76686	glutathione peroxidase 1
455950	AF111170	Ha.306165	Homo sapiens 14q32 Jagged2 gen
445333	BE537641	Ha.44279	hypothetical protein FLJ12538
407204	R41833	Ha.140237	ESTs, Weakly similar to ALU1_H
412338	AA151527	Ha.69485	hypothetical protein FLJ12436
439963	AW247529	Ha.6793	platelet-activating factor ac
412104	AW205197	Ha.240851	Homo sapiens, Similar to RIKEN
443553	AL049635	Ha.9923	ATP-binding cassette, sub-fam
448994	AW751555	Ha.22753	hypothetical protein FLJ22318
418776	AA041004	Ha.88411	lymphocyte antigen 117
418843	AJ251016	Ha.89230	potassium intermediate/alkali c
415244	AA335587	Ha.89781	ATP synthase, H transporting,
451855	RF4913	Ha.175804	ESTs
420489	AF209085	Ha.153357	procollagen-lysine, 2-oxogluta
447374	AF263462	Ha.18376	KIAA1919 protein
430167	Y08976	Ha.234799	FEV protein
409936	AK001691	Ha.57655	hypothetical protein FLJ10829
437926	BE383605	Ha.300816	small GTP-binding protein
430237	BE049849	Ha.227769	mitogen-activated protein kin
424919	BE314461	Ha.57058	U3 snRNP-associated 55-kDa pr
414534	BE257293	Ha.76366	BCL2-antagonist of cell death
433333	AJ016521	Ha.17816	v-akt murine thymoma viral onc
423228	AL137491	Ha.125511	Homo sapiens mRNA, cDNA DNF24
419493	AF001212	Ha.59744	proteinase (protease, macrophag
420160	AA92840		ESTs
421871	AK001416	Ha.306122	glycoprotein, synaptic 2
447827	U73727	Ha.18716	protein tyrosine phosphatase
417193	AB922189	Ha.18716	hypothetical protein FLJ2795
419678	NM_001327	Ha.187379	carcinoembryonic antigen (NY-ESO
458963	AJ701353	Ha.278728	Rad and Gem-related 2 (rat hom
406868	AA505445	Ha.330657	immunoglobulin heavy constant
431405	AA065214	Ha.13094	proteinase associated thrombol
421726	AK001237	Ha.331968	hypothetical protein FLJ10375
421707	NM_014921	Ha.107054	lectonectin-2
453998	AW003512	Ha.232770	arachidonate lipoxygenase 3

SS, TM, Methand	10.6
hormone, SS, p68	10.5
SS, JH, SS, TM, WD40	10.4
Kaniz_BPTLSS, TM, Ion, tra	10.4
SS, TM	10.3
SS, JH	10.3
SS, JH, PH, PH	10.3
homobox, SS, TM, Rho, GDI, h	10.3
SS, JH, SS, C, S9	10.3
SS, TM, SS, TM, ABC, Iran, ABC	10.3
SS, TM, JH, H, Exchanger, ABC2	10.3
7tm, 1	10.3
SNF2, H, Helicase, C, bromodo	10.3
Ncl1_Nep2_Sun, SS, SNF2, N	10.2
TM, RYDR, ITPR, Ion, Trans, M	10.2
Ion, Trans, K, Tetra, thumal	10.2
SS, TM	10.2
SS	10.1
SS, F3, F8, Iype, C, EGF, TGT	10.1
SS, ITB, JH, hydroxase, 2, RasG	10.0
z-MYND, SS, TM, Glyco, hydro	10.0
SS, Irefol	10.0
kazal, thyroglobulin, 1, z	10.0
SS, TM	10.0
SS	9.9
SS, TM	9.8
flavodoxin, FAD, binding, NO	9.7
SS, TM	9.7
SAND, SS	9.7
notch, EGF, ank, Loco, SS, TM	9.7
SS, TM, EMP24, GP25L, SS, TM	9.6
SS, JH, PK, SS, TM, JH, R	9.6
TM, Refactor	9.6
SNF, SS, TM	9.6
SS, TM	9.6
SS, phosphatase, DSP, TM	9.6
SS, SS, TM, Glyco, hydro, 31, G	9.5
lg, SS, TM, JH	9.4
phosphatase, SS, TM, synaptobrev	9.4
ATPase, F, SS, TM, Cyt, F	9.4
ubiquitin, SS, TM, Transglut	9.4
SS	9.4
SS, SS, rm, z, RanBP, rm, GA	9.4
phkase, SS	9.4
SS, TM, HCO3, cotransp, CAP, G	9.4
phkase, GTP, E_TU, EFG, C, GT	9.4
SS	9.3
GSH, PK, SS, rm, JH	9.3
SS, TM, DSL	9.3
SS	9.2
SS, Histone, Histone	9.1
SS, TM, JH, Sema, PSI	9.1
PAF, AH, JH, Lipase, GDGL, SS	9.1
SS, TM	9.1
ABC, Iran, SS	9.1
SS	9.0
SS, TNF, TNF	9.0
TM, CaMBD, BK, channel, TM	9.0
ATP, eyn1, DE, SS, rm, Ephrin	8.9
SS, TM, vwa	8.9
ZOG-Fat_Oxy, Glycos, Iran	8.9
SS, Myosin, JH, M	8.9
SS, Cys, zytall	8.9
SS, TM	8.7
SS, TM, TPR	8.7
phkase	8.7
WD40, SS, JH, domain	8.7
SS, hormone, rec, z, C	8.7
homobox, phkase, P, Phkine	8.7
SS, TM, JH	8.7
PC1, SS, COX5, activator	8.7
SS, TM	8.6
TM, Steroid, d, SS	8.6
V, phosphatase, JH, JH, MAM	8.6
SS, TM, z, C2H2	8.5
ras, SS, Peptidase, M10, homo	8.5
SS, TM, JH	8.3
TM, Rho, Bcl2, SS, TM	8.3
TM	8.3
Letrophilin, OLF, 7tm, 2, Gal	8.2
SS, TM, lipoygenase, PLAT, a	8.2

456672	AK002016	Ha.114727	Homo sapiens, clone MGC:16327,	SS,PK,PK_C,myosin_head,Rh	8.2
421592	AF009801	Ha.105941	bagpipe homeobox (Drosophila)	homeobox,SS	8.2
409829	M33522	Ha.56729	lymphocyte-specific protein 1	Cedersom,SS,Ribosomal_M2	8.1
444341	K14257	Ha.146550	EST	SS,TM,Repophysin_Put_S2	8.0
417382	NW11479	Ha.846	FKBP-binding protein 4 (56kD)	FKBP,TPR,SS	8.0
436695	W28661	Ha.5288	Homo sapiens mRNA; cDNA DKFZp2	SS,TM,phospho_AcylCoA_rec	8.0
420932	AW374605	Ha.11607	ESTs, Weakly similar to T21697	SS,B2P_Maf	8.0
431493	AF71493	Ha.128873	ESTs, novel cytochrome P450	SS,B2P50,SS	7.9
447598	AF70968	Ha.129530	EST	SS,TM	7.8
415758	BE270465	Ha.78793	protein kinase C, zeta	phkase,DAG_PE-bind,phkase	7.8
457022	AW37258	Ha.169902	gbr1472-CT0222-26109-003-a10 C	SS,Ribosomal_L17Ae	7.8
426440	BE382756	Ha.169902	sulfate carrier family 2 (acid	esugr_v,SS,TM,sugar_v	7.8
432747	NM_014404	Ha.78907	calcium channel, voltage-dependent	PMP22_Claudin,SS,TM,PMP22	7.4
441084	W25453	Ha.5911	hypothetical protein FLJ11773	SS,TM,hormone_rec,zf-C4	7.8
424443	AF751281	Ha.284161	hypothetical protein from EUKO	SS,TM,SS,TM	7.7
424198	A8029010	Ha.143026	KIAA1087 protein	SS,TM,Ha_Ca_Est,Catc-beta,	7.6
430513	AJ012068	Ha.241586	G6P protein	SS,TM,SGT_C,phospholase	7.8
417900	BE590127	Ha.82306	CDC20 (cell division cycle 20,	WD40,SS,TM,hn3,EGF,hn3,g	7.6
432891	AF161483	Ha.279781	HSPC134 protein	SS,TM,ubiquitin,Transglut	7.5
432234	AA531128	Ha.115803	ESTs	SS	7.5
433485	BE520712	Ha.33025	hypothetical protein PP247	SS,TM	7.5
441327	AK001705	Ha.7778	hypothetical protein FLJ10751	SS,TM,Tm_1	7.5
436540	BE397032	Ha.14468	hypothetical protein MGCI4226	SS,TM	7.5
418256	AW543518	Ha.12271	F-box and leucine-rich repeat	SS,SS,TM,HSF_DNA-bind	7.5
457274	AW574193	Ha.227152	proteinase binding lectin varieg	SS,TM,SS,TM,Cadherin,lg_c	7.5
437141	BE304917	Ha.31097	hypothetical protein FLJ21478	SS,TM,glycos_transf_4	7.5
425428	AL110261	Ha.157211	DKFZ598602 protein	C1q,Collagen,SS	7.4
431934	A8031481	Ha.272214	STG protein	SS	7.4
418349	NM_001353	Ha.84183	diphtheria toxin resistance pro	Diphtheria_toxin,SS	7.4
430000	AW550567	Ha.274348	HLA-B associated transcrip-3	ubiquitin,SS,TM,g-patch,	7.3
421768	BE397336	Ha.1422	Gardner-Rasheed feline sarcoma	SH2,SH3,phkase	7.3
412841	AF751157	Ha.101395	hypothetical protein MGCI1352	SS,TM	7.3
418313	BE442621	Ha.8422	CCR-08 protein	SS,snap	7.3
420867	AK007836	Ha.278311	placsin B1	Sema,PSI,TIG,SS,TM,TIG,Se	7.3
418837	UA8263	Ha.89040	preproenkephalin	Opoids_neuropep,SS	7.2
423015	U18548	Ha.123034	G protein-coupled receptor 12	TM	7.2
440188	AK001812	Ha.7036	N-acetylglucosaminase kinase	CKK,SS,TM	7.2
421975	AW591017	Ha.6459	hypothetical protein FLJ11855	SS,TM,CAT	7.2
423858	AL137326	Ha.133483	Homo sapiens mRNA; cDNA DKFZp2	SS,TM	7.2
440143	BE454342	Ha.306079	sec61 homolog	sec7,SS,TM	7.2
417704	NM_001747	Ha.84242	coiled-coil protein (actin filament	Cadherin,SS,Gelsolin	7.2
440969	NM_014297	Ha.7485	protein expressed in thyroid	Cadherin,BSS,XPRC1_N,JB	7.1
435059	AK004770	Ha.4755	flag structure-specific endonu	XPG_N,XPC_L1_3_exonuclease	7.1
438556	N40327	Ha.7473	ESTs	SS,TM,cinnexin	7.1
425268	AF034240	Ha.160913	acetylcholinesterase kinase 24 (S	phkase,phkase	7.1
418373	AW750770	Ha.84344	CQI-135 protein	SS,TM,PMP22_Claudin,ZOG-F	7.1
445087	AW893449	Ha.12303	suppressor of Ty (Scer[trachea	ST,SH2,Ribosomal_L23,phk	7.1
427448	NM_014718	Ha.107809	KIAU0726 gene product	cadherin,TM,TPR	7.1
413837	AW163325	Ha.171834	Usp-cup (ubiquitin)	SS,Methyltransf_3	7.0
421691	NM_006201	Ha.171834	PTAUPE protein kinase 1	phkase,SS,PCTA-1,UQH-1,rr	7.0
409125	R17265	Ha.343567	axonal transport of synaptic v	SS,kinesin,PH,PHA,kinesin	7.0
424251	AA677466	Ha.143096	coactivator-associated antigen	SS,SNF2_U,Helicase_C,chrom	7.0
431530	NM_002204	Ha.263929	Integrin, alpha 3 (enigen C24	Integrin_AFG-GAP,Rhbd_g	7.0
428156	BE269388	Ha.182698	mitochondrial ribosomal prot	SS	7.0
469255	AA93244	Ha.239500	hypothetical protein MGCI3114	SS	7.0
441323	AA528413	Ha.150089	ESTs, Weakly similar to ALU7_3	SS,Peptidase_C1,zf-C2H2	6.9
455928	BE170913	Ha.205736	G3C4V-H703C-040503-153-002	kazal,SS,TM,lg,phkase	6.9
420856	BE513294	Ha.205736	HLA class II region expressed	TM	6.9
421543	AK000519	Ha.105050	hypothetical protein FLJ20512	SS,TM,glyco_hydro_56_Glyc	6.9
422296	NM_007275	Ha.81185	lung cancer candidate	Galectin,LT_2,SS,TM,TPR	6.9
440937	AK52943	Ha.312131	UDP-Galactose-4-epiase beta 1-4-g	SS,SNF2_U,Helicase_C,chrom	6.8
439732	AW529004	Ha.187641	hypothetical protein from EUKO	SS,TM,TM,AM2M,A2M,NTR	6.8
429542	AF038660	Ha.206713	UDP-Galactose-4-epiase beta 1-4-g	Galectin,LT_2,lg,SS,TM,A	6.8
420190	AB16029	Ha.95867	hypothetical protein EST00095	SS,dynamin_2,dynamin,PH,G	6.7
402151	BE514230	Ha.26249	synthase 19	SS,SS,TM,H14,TPR,zf-COOH	6.7
410277	R88621	Ha.26249	ESTs, Weakly similar to T203_H	SS,TM,SS	6.7
415667	AU077005	Ha.92208	e disintegrin and metalloprote	disintegrin,Repophysin,Pe	6.7
425228	AF067067	Ha.100523	FGS-like antigen 2	SS,TM	6.7
425238	NM_005263	Ha.301612	FGS-like antigen 2	SS,BP,SS	6.6
425238	BE258332	Ha.278362	male-enhanced antigen	SS,TM,AAA,Ribosomal_L2	6.6
421864	BE387198	Ha.108973	dolichyl-phosphate mannosyltra	SS,TM,SS,TM	6.6
425982	M89113	Ha.226755	glutathione S-transferase pi	GST_C,GST_N,SS,ethand	6.6
426867	AA157057	Ha.172295	keratin 19	filament,UPF,SS,Ramnel	6.6
429558	AF029778	Ha.165154	jagged 2	SS,EGF_vwc,granulin,SS,T	6.5
429344	UA5905	Ha.277445	diacylglycerol kinase, zeta (1)	enik,DAGKa,DAGK,DAG_PE-bl	6.5
414981	AA054408	Ha.151706	KIAA0134 gene product	Helicase_C,PRK,SS,TM,Tm	6.5
417933	NM_002342	Ha.1116	lymphokine beta receptor (TNF	TM,TNFR,SS,SS	6.5
423876	BE502635	Ha.15453	Homo sapiens, clone IMAGE:2959	SS,ethand	6.4
434349	AA431176	Ha.133230	ribosomal protein S15	SS,SS,TM,TPR,RS	6.4
441379	AW175787	Ha.334641	zelenin binding protein	SS,RFX_DNA_binding	6.4
423968	BE514162	Ha.778869	melanoma-associated antigen re	SS,TM,PRK,DIK	6.4
456863	T16837	Ha.4241	ESTs	fusion_gly,homeobox,TM	6.4
432269	NM_002447	Ha.2942	macrophage stimulating 1 recep	phkase,Sema,PSI,TIG,AA_E	6.4
426676	AW140656	Ha.159161	Rho GDP dissociation inhibitor	Rho_GDP,homeobox,SS,Cytd	6.4

443420	RO6846	Ha.191208	ESTs	SS	6.4
436322	AL355092	Ha.120243	parvin, gamma	CLSS, TM, CTCT_NFI	6.4
440088	BE553977	Ha.183232	hypothetical protein FLJ22638	SS, zf-CHCA, SPFY, zf-B_box	6.4
447855	BE204245	Ha.20071	hypothetical protein MG2293	SS, TM	6.4
431785	AA282385	Ha.258273	Breakpoint cluster region prot	BAF, Kazal, TM	6.3
422714	AB018335	Ha.119387	KIAA0792 gene product	DUF21.1, SS, TM, TGFb_propept	6.3
434915	AF161833	Ha.284207	Homo sapiens, Similar to RIKEN	TM	6.3
414511	AB155293	Ha.76354	enoyl Coenzyme A hydratase, sh	ECCH, PGadhesin_LUT, SS, TM	6.3
413254	U40272	Ha.75253	isocitrate dehydrogenase 3 (NA)	isodh, SS	6.3
458367	AA088470	Ha.83135	Homo sapiens, Similar to RIKEN	SS, IRNA-cytl_2d	6.3
415010	NM_094203	Ha.77783	membrane-associated tyrosine-	phkase, SS, PMF22_Claudin	6.3
410878	T05387	Ha.76591	ESTs	SS	6.2
412940	BE250701	Ha.819	homoio box B7	SS, TM, Wd40, vwd, MAM, EPO_TP	6.2
440042	AB073387	Ha.133898	ESTs	SS	6.2
414023	BE243628	Ha.284207	glt TC8AP1D10553 Pediatric pra-B	SS	6.2
415133	AK228400	Ha.76297	G protein-coupled receptor kin	phkase, RGS, phkase, C, SS,	6.2
446692	NM_013223	Ha.15827	scoring nexin 11	PX, SS	6.2
409882	J243191	Ha.56874	heat shock ZNF protein family	HSP20, SS, TM, zf-C2H2, BTB_E	6.2
414576	AK000405	Ha.76480	ubiquitin-like 4	ubiquitin, SS, TM, GPRD, GPRD	6.2
447507	H05956	Ha.18147	POPT (processing of precursor,	SS, TM, Wd40, vwd, MAM, EPO_TP	6.2
453447	AW771318	Ha.325586	hypothetical protein MG61134	SS, TPR	6.1
429668	AW151451	Ha.111577	integral membrane protein 3	Nm	6.1
424441	X14850	Ha.147097	H2A histone family, member X	Histone, CBFD, NFYB, HMF, SS,	6.1
434558	AK264102	Ha.29158	ESTs	SS, TM, LRCT, LRR	6.1
434202	BE362411	Ha.37654	guanylate kinase 1	Guanylate_kin, CoA5, Viral_d	6.1
432183	AW151552	Ha.46679	hypothetical protein FLJ20739	SS	6.0
444416	AA288085	Ha.111558	ESTs	zf-CHCA, Spoa_P, PHD, TM, yna	6.0
447205	BEA17015	Ha.11006	HSA, Moderately similar to T1	SS, TM, LRCT, Sema	6.0
407704	BE119172	Ha.78768	malignant cell expression-anha	TM, MBOAT, SS, TM	6.0
453190	AB002354	Ha.32312	KIAA0356 gene product	PLP, PLD, RUN, SS	6.0
433975	AA328081	Ha.6817	inosine triphosphatase (nucleos	Hmtp, Ika, SS	6.0
443514	AW870440	Ha.23542	protein produced by clone Z36	SS, P, xzf, Ipoctate, PHD_x	6.0
432955	X94330	Ha.3107	C597 antigen	SS, TM, TN, zf_2, GFS, EGF, SS, TM	6.0
414362	AA347934	Ha.75932	N-ethylmaleimide-sensitive fac	NSF, SS, TM	6.0
417483	BE549343	Ha.82203	acyl-Coenzyme A dehydrogenase,	Acyl-CoA_dh, Acyl-CoA_dh_M	6.0
427988	AF185333	Ha.181349	hypothetical protein 628	SS, SS	6.0
423473	H01014	Ha.129858	hypothetical protein FLJ14768	zf-C2H2, GST, nm, RENTH	6.0
408773	AA812424	Ha.750267	heat shock ZNF protein 1	HSP20, SS	5.9
409938	AW974648	Ha.153937	gbc:ST386752 MAGE resequenes,	SS, Adap, comp, sub, GYF	5.9
424953	NM_025781	Ha.31608	activated p21cdc42-like kinase	phkase, SH3	5.9
453082	H19835	Ha.27910	hypothetical protein FLJ20041	SS, TM, Ion_trans	5.9
452094	AF049105	Ha.25516	centrosomal protein 2	bZIP_3_3_exonuclease, M, SS	5.9
451524	AK001466	Ha.170011	hypothetical protein FLJ10604	SS, SS, TM, phkase, phkase	5.9
427439	AW328215	Ha.7236	hypothetical protein FLJ20257	SS, TM	5.9
439865	AW956781	Ha.293537	ESTs, Weakly similar to FXD2_H	SS, PWWP, TSC22	5.9
440511	AF132959	Ha.157240	eNOS interacting protein	SS, TM, MAGE, Ribosomal_S17,	5.9
417334	AA337572	Ha.334514	hypothetical protein MGCA737	SS, TM, Ion_trans	5.9
425976	C75994	Ha.3196	WGD2 protein	SS, TM, phkase, SH2, SH3, BMR	5.8
433173	Z35093	Ha.6311	surfact 1	SURF1, SS, TM, SURF1, SURF4	5.8
437851	AW006593	Ha.61273	hypothetical protein FLJ20859	TM, SET	5.8
410239	AF069350	Ha.296259	hypothetical protein MG22650	SS, AKT, TM	5.8
450660	RS2650	Ha.9100	hypothetical protein MG23121	SS	5.8
409591	AA532063	Ha.55879	Homo sapiens cDNA FLJ13100 fs	SS, TM, LM, homobox	5.8
409868	AK000002	Ha.25450	Homo sapiens mRNA: cDNA DKFZp4	SS, ABC, tran, SS, TM	5.8
450778	U81375	Ha.1986	schke carter family 29 (nuc)	Nucleoside_tran, SS, TM, HSP	5.8
423612	NM_002057	Ha.119273	guanine nucleotide binding pro	C-alpha, zrf, SS, C-alpha	5.8
422701	NM_014699	Ha.75087	KIAA0295 gene product	zf-C2H2, GST_C, PHD, SS, TM, H	5.8
412958	BE391579	Ha.122962	Fas-activated serine/threonine	SS, phkase	5.8
436957	AA024888	Ha.157982	ESTs	SS, DAGK2, DAGK4, RAA, DAG_P,	5.8
423158	H07591	Ha.98428	cyclin-dependent kinase (CDC2-	Mook, NTR, Pqet, SS, TM	5.8
414788	H76342	Ha.77313	Target CAT	phkase	5.8
420504	AL035964	Ha.100221	neuronal receptor subfamily 1,	phkase, rec, zf-C4, SS, DNA,	5.7
410431	BE261220	Ha.158196	transcriptional activator 1 (ADA	homobox, SS, homobox, home	5.7
420508	AJ270893	Ha.4964	homoio box B6	Herpes_HEPAS, SS	5.7
435593	R88972	Ha.30002	DKFZ595J1624 protein	TM	5.7
433064	D79991	Ha.27239	SH3-containing protein SHOGLB2	SS, TM, SS, TM	5.7
415120	AA224453	Ha.31547	DKFZ596C0524 protein	Target CAT	5.7
453054	AB189098	Ha.78016	polymyocytin kinase 3'-phosp	Viral, TM, TM, SS, TM	5.7
415977	Y00815	Ha.75216	protein tyrosine phosphatase,	SS, zf-C2H2, DNase_I	5.7
425246	AB05561	Ha.155321	serum response factor (p-fos s	IRF3, IF, flavonidin, SS, TM, p	5.7
432321	BE521697	Ha.1086	nuclear protein family A, me	TM, SS, TM, Kunitz_BPTI	5.7
448484	BE513340	Ha.334725	Homo sapiens, Similar to RIKEN	nmr, SS, zf-C2H2, DNase_I	5.7
449139	BE268315	Ha.23111	phenylalanine-ARNA synthetase-	C2, SS, TM, Y_phosphatase, Tr	5.6
449181	X95783	Ha.23179	synaptobrevin V	ATP-ent, C-SS, TM, phkase	5.6
414457	AW514320	Ha.15169	ATPase, H transpoting, lysoso	SS	5.6
424954	AW161271	Ha.153961	ARPI (actin-related protein 1,	SS, TM, Wd40, phkase	5.6
415193	AL048881	Ha.12185	hypothetical protein MGCI4333	SS, TM, aminotran_1_2, LRR	5.6
407754	AA527348	Ha.288987	Homo sapiens cDNA FLJ14105 fs	SS, TM, SS, TM, TSP, Nbs_3, SE	5.6
413049	NM_021511	Ha.823	heparin (transmembrane protease	SS	5.6
454222	H50256	Ha.63236	ribosomal protein S15a	SS	5.6
431787	AW972024	Ha.343661	ret finger protein	SS, Wd40, phkase	5.6
431607	AB033037	Ha.183699	KIAA1271 protein	SS, TM	5.6
405762	AA403373	gbc:zw1.01.1	Source: ovary tum	SS	5.6

5	444364	AL137294	Ha.10954	hypothetical protein FLJ22351	SS, TM, kinase	5.6
	427834	AA506101	Ha.58513	hypothetical protein FLJ11807	SS, TM	5.5
	443789	BE390832	Ha.134729	FXD domain-containing kn tra	SS, TM, ATP1G1_PUM, MATS, ATP	5.6
	415322	BE019494	Ha.738217	pyridine-C-oxalylate oxidase	PCSD, Oxidation, DH, N, SS, TM	5.5
	406673	MA4596	Ha.198253	major histocompatibility compl	SS, TM, MHC, Ii, alpha, Ii, SS, S	5.5
10	415351	U44755	Ha.78403	small nuclear RNA activating c	SS, TM, kinase	5.5
	411030	BE387193	Ha.678956	7-60 protein	SS, Collagen, Collagen	5.5
	416553	BE353768	Ha.583338	5S rRNA pseudocaps protein	I-CCHC4, SS, SH2, Nucleic	5.5
	433012	NM_004045	Ha.279910	ATX1 (antioxidant protein 1, y	HMA, SS, TM	5.5
	437741	BE561610	Ha.5809	putative transmembrane protein	SS, TM, SS, TM, RAVP59, SH2	5.5
15	421863	XS5079	Ha.1437	glucosylase, alpha, acid (Pump	trefoil, Glyco, hydro, 31, SS	5.4
	427361	AW732480	Ha.73798	cellular retinoic acid-binding	SS, TM, Membrane, 1, 2, LRR	5.5
	411574	BE42842	Ha.6780	protein tyrosine kinase 9-Da	collin, ADF, SS, TM	5.4
	457313	AF047002	Ha.241520	transcriptional coactivator	SS, rm, SS, Cytidylyltransf	5.4
	426345	A1242431	Ha.118282	PAP-1 binding protein	SS, TM	5.4
20	434845	BE676757	Ha.325321	hypothetical protein R32184_1	SS, TM, CH, cadonin, ARD	5.4
	427162	AB011153	Ha.173664	KIA0061 protein FLJ20452	SS, kinase, PDZ, SS, SH2, Rho	5.4
	447402	HS4520	Ha.18490	hypothetical protein FLJ20452	SS, TM	5.4
	433676	AW371389	Ha.250173	hypothetical protein FLJ13158	SS, SS	5.4
	424373	AJ133798	Ha.146219	caspase VII	C2, SS	5.4
25	423402	BE167615	Ha.141556	Homo sapiens cDNA FLJ12976 fs	SS	5.4
	409983	DS0922	Ha.57729	Kelch-like ECH-associated prol	BTB, Kelch, SS, TM	5.4
	450184	W31096	Ha.237617	Homo sapiens, clone IMAGE:3447	phkase, SH2, SH3	5.3
	431629	AW077025	Ha.265927	Interferon, alpha-inducible pr	I, A, SS	5.3
	430413	AW942182	Ha.241352	small inducible cytokine A5 (R	SS, TM, IP, trans, kinase, pk	5.3
30	440333	AJ378424	Ha.288761	hypothetical protein FLJ21749	SS, TM	5.3
	424927	AW973658	Ha.153850	hypothetical protein C32102.4	MP, SS, TM, MF, super, 3	5.3
	412276	BE262621	Ha.73798	macropage migration inhibitor	SS, TM, GalP, UDP, trans, Gal	5.3
	416181	AA174126	Ha.329263	ESTs	SS, Acyl-CoA, dh, Acyl-CoA, d	5.2
	440609	AD287585	Ha.7301	G protein pathway suppressor 2	SS, H, Myc, N, term, Myc, L, Z	5.2
35	435327	BE301871	Ha.4067	mannosyl (alpha-1,3)-glycopr	SS, TM	5.2
	421138	AW953533	Ha.303172	KIA1552 protein	SS, TM, alpha, 1,3-glycopr	5.2
	453446	W16752	Ha.32981	serum domain, immunoglobulin do	SS, TM, alpha, 1,3-glycopr	5.2
	414411	XS4079	Ha.240170	shee shock 2HD protein 1	HSP20, SS	5.2
	420996	AW161556	Ha.109281	hypothetical protein MG2731	SS, TM, uric-like, kinase, SS	5.2
40	440869	AJ011895	Ha.109281	Net-associated factor 1	Virus, HS, ZIP, G-gamma, Myo	5.2
	435473	AJ715529	Ha.147787	ESTs	SS	5.2
	451585	AK001171	Ha.326422	hypothetical protein MG04549	SS, Metallophos	5.2
	407191	AA609751	Ha.179516	glae56H07.s1 Stratiogene lung	SS, Peptidase, C1	5.2
	427515	T79526	Ha.179516	integral type I protein	ENF2H, GP26, SS	5.2
45	455235		Ha.253560	C1400788.gj7002514j6j3BA9	SS	5.2
	434119	AF193844	Ha.3758	COP9 complex subunit 7a	SS	5.1
	413052	BE249841	Ha.3758	glae60042857F2 Nrl, LMG, C, 15 Homo	SS, TM, SS, TM	5.1
	445109	AF039916	Ha.12230	adenonucleoside triphosphate d	SS, TM, GDI, C, D39, SS, TM, pho	5.1
	403323	HB2855	Ha.53447	Homo sapiens mRNA; cDNA DKFZp7	TPR, SS, TM, kinase, Ii	5.1
50	438707	L08239	Ha.324051	amino acid system N transporte	SS, TM, ACAT, MBOAT, SS, TM, TB	5.1
	442599	AF078037	Ha.324051	RelA-associated inhibitor	SH3, ank, SS, TM, HHV, Ii	5.1
	423372	AW960498	Ha.253560	ESTs	SS	5.1
	436576	AA58213	Ha.77542	ESTs	SS, TM, tm, 1, Dnal	5.1
	439012	BE383814	Ha.6455	RuvB (E coli homolog)-like 2	AAA, DnaB, UPF0079, SS, Cys, L	5.1
55	418910	Z23821	Ha.89498	Homo sapiens, Similar to dodec	ECH, SS, TM, aminotran, 3, ABC	5.1
	414849	AW572721	Ha.252723	ESTs, Weakly similar to xenob	TM, kinase	5.1
	425743	BE396496	Ha.159428	BCL2-associated X protein	Bcl-2, SS, fertin, Bcl-2	5.1
	418231	AA326895	Ha.83848	tricarboxylate kinase	TM, SS, TM, zf-UBP, UCH-2, UB	5.0
	419328	AW959538	Ha.321214	hypothetical protein DKFZp564D	SS, TM, WH2	5.0
60	441917	AB089225	Ha.24891	ESTs, Highly similar to xenob	SS, TM, aminotran, transp	5.0
	437617	AD25701	Ha.5716	KIA00310 gene product	SS, zf-CCHC4, Peptidase, M16	5.0
	412867	AU076861	Ha.74637	testis enhanced gene transcript	UPF0005, SS, TM	5.0
	419579	WA9529	Ha.286200	hypothetical protein AF035356	MSP, domain, SS, TM, CUB, NTR	5.0
	425824	AJ059663	Ha.155608	ESTs	SS, PHD	5.0
65	439414	NM_001183	Ha.6551	ATPase, H transporting, lysoso	SS, SS, TM, GDI, Sema7, TIG, PSI	5.0
	430442	AF284422	Ha.119178	carbon-chloride cotransporter [SS, SS, am, permeases, SS, TM	5.0
	410775	AB014460	Ha.58196	hypothetical protein FLJ23538	HH-CFD, SS, TM, REJ, PLAT, PK	5.0
	433360	AB177711	Ha.51730	HER2 receptor tyrosine kinase	SS, SS, TM, EMP70, PA29, alpha	4.9
	403030	X03363	Ha.172609	nucleobind, 1	kinase	4.9
70	428811	BE259228	Ha.148495	proteasome (prosome, macropain	ehand, SS, TM, GFO, IDH, MoA	4.9
	421179	U72654	Ha.148495	finger protein 5	UM, SS, TM, PMP27, Oxidat, P	4.9
	429762	AJ246255	Ha.216354	5S rRNA-specific protein, 116	SS, zf-CCHC4, P, dm, P, dm	4.9
	426031	BE258216	Ha.172673	S-adenosylhomocysteine hydrola	SS, TM, tm, 1, BAU, zf-COCC, D	4.9
	442103	AA333367	Ha.8098	similar to 3. cerevisiae Sec3p	Ado, byase, SS	4.9
75	414820	AA371931	Ha.7422	gatedfold protein 2 (antibio	SS, SS	4.9
	426347	AA454912	Ha.169407	SAC2 (suppressor of actin mta	SS, TM, HCO3, cotransp	4.8
	423880	BE278111	Ha.134200	DKFZP564C186 protein	SS, TM, ACAT, LRR	4.8
	423545	AJ624164	Ha.8535	lymphocyte antigen 6 complex,	VnuP, SS, TM, kinase, zf-C2	4.8
	443044	BE25327	Ha.1063	quintessence phosphonotriphos	zAMP, binding, SS, TM, zAMP, b	4.8
80	417080	BE392846	Ha.7854	small nuclear ribonucleoprotei		
	441455	AJ271671	Ha.39544	zincfin regulated transporta		
	410182	NM_001983	Ha.11862	excision repair cross-compleme		
	455052	AB056986	Ha.28393	ESTs, Weakly similar to xenob		
	439270	BE268278	Ha.332040	hypothetical protein MG213010		

5	433251	AB040555	Ha.322735	KOA1522 protein	SS,SS,zf-C3HC4,SPRY	4.3
	420531	A062069	Ha.98614	ribosome binding protein 1 (do	bZIP,SS	4.3
	432179	H75208	Ha.2913	EphB3	EPH,Id,fn3,kinase,SAM	4.3
	448398	Y09763	Ha.22785	gamma-aminobutyric acid (GABA)	Neur_chan_LBD,Neur_chan_m	4.3
	425526	A115472	Ha.323879	inhibitor of kappa light poly	zf-C2H2,SS	4.3
10	432966	ALD37895	Ha.279861	CGI-31 protein	thioredo,SS,TM	4.3
	428870	BE276891	Ha.194691	refinolic acid induced 3	7m_3,SS,TM	4.3
	428953	AA306610	Ha.348183	tumor necrosis factor receptor	TNFR,c6,SS	4.3
	401128			C1200544g4g5727683refNP_00	SS,SS,TM	4.2
	446899	NM_005397	Ha.16426	podocalyctin-like	SS,TM,SS,TM	4.2
15	426153	H25836	Ha.301527	ESTs, Moderately similar to un	SS,TNF	4.2
	429613	U96132	Ha.171280	hydroxyacyl-Coenzyme A dehydro	adh_phoat,SS	4.2
	428516	RS14204	Ha.1608	KAA1608 protein	SS,CDEN,DCAN	4.2
	446516	R65964	Ha.334873	ESTs, Weakly similar to ALLU_H	SS,2n_carbOpap	4.2
	414467	AW903820	Ha.85752	copine II	SS	4.2
20	458587	T70192		glycyl-1803.1.1 Stragene lung	SS,TM,both	4.2
	401757			RAR binding protein 3	SS,Onch,SH2,STAT	4.2
	400563			Target Exon	SS,Pap_1M2B_prosep	4.2
	430237	A127214	Ha.236522	DKFZP434P106 protein	abhyrloase,TM	4.2
	406101			C11000273"q11.2656107lgbAAK0	SS,TM,7m_1	4.2
25	412061	BE281303	Ha.299148	hypothetical protein FLJ21001	SS,WP	4.2
	444590	AA45456		hypothetical protein FLJ20435	SS	4.2
	408187	AF034373	Ha.43509	ataxin 2 related protein	SS	4.2
	437696	Z8384	Ha.5790	hypothetical protein dJSTE16.5	SS,Hydrolase,SS,Gal-bind	4.2
	402278			JENP00000243264-dialcyl-diphe	SS,TM	4.2
30	407354	AF005081	Ha.18528	gb-Homo sapiens skin-specific	SS	4.2
	474707	BE387301	Ha.18528	Sjogren's syndrome nuclear aut	SS,HLH,ras,GSHp	4.2
	410237	A770509	Ha.61238	arginine nucleoside lyase	lyase_1,SS	4.2
	415410	AF037332	Ha.273559	sorting nexin 17	FX,zf3,kinase,SAM,EPH,lb	4.2
	457757	AA434109	Ha.12721	floor and kuzniec-rich repeat	SS,F-box,SS,TM,HGF_DNA-bl	4.1
35	446388	AA292979	Ha.7788	NPO007 protein	SS,TM	4.1
	412825	AW167439	Ha.190551	Homo sapiens cDNA FLJ13826 fs	SS	4.1
	439737	A751438	Ha.41271	Homo sapiens mRNA full length	SS,Collagen	4.1
	422256	M64673	Ha.1459	heat shock transcription factor 3	NA,SS,TM,F-box	4.1
	441164	AB023180	Ha.7724	KAA0953 protein	helicase_C,SS,RNA_pol_H	4.1
40	401727			Target Exon	A_dexam,SS	4.1
	411142	NM_014258	Ha.69509	transmembrane protein 3	Galactosyl_T,SS,Ribosomal	4.1
	458176	A1951519	Ha.140309	Homo sapiens, clone IMAGE3677	SS,kinase,kinase_C	4.1
	432178	BE265369	Ha.272814	hypothetical protein DKFZP434E	SS,amine_carbop	4.1
	421337	BE383488	Ha.105547	neural proliferation, differen	SS,TM,Glyco_hydro_47	4.1
45	412380	D31631	Ha.1372	angiotensin vasopressin receptor	7m_1	4.1
	422702	AJ011373	Ha.115285	chromosome 9 open reading fram	SS,TM,SS,TM	4.1
	434142	U47927	Ha.3759	ubiquitin specific protease 5	zf-UBP,Uch-2,UBA,Uch-1,SS	4.1
	423696	Z92546		Sushi domain (SCR repeat) cont	SS,TPP,vwd,sushi,Somatone	4.1
	427407	BE368549	Ha.177766	ADP-ribosyltransferase (NAD; p	BROT,PAP,zf-PARP,PARP_n	4.1
50	413749	A1929320	Ha.75516	tyrosine kinase 2	SS,TM,SS,TM,jg	4.1
	411927	BE274009	Ha.772	glycogen synthase 1 (muscle)	Glycos_transf_1,SS	4.1
	433320	D06047	Ha.250679	ESTs, Highly similar to CTXN R	SS,TM,mm	4.1
	433980	AF103601	Ha.10351	hypothetical protein	DAO,SS	4.1
	452903	AW410601	Ha.30226	HSPC182 protein	SS	4.1
55	444496	BE302472	Ha.11314	DKFZP564N1363 protein	SS,GKAP,Band_41	4.1
	422558	NM_006545	Ha.118244	protein phosphatase 2, regulat	856,SS,TM,Atrophin-1,Exo_	4.1
	447347	AA870055	Ha.122730	ESTs, Moderately similar to KJ	TM,SS	4.1
	428284	AA535762	Ha.183435	NM_004545:Homo sapiens NADH de	SS,TM,Josephin,UIM,Joseph	4.1
	426551	AA381258	Ha.323947	ESTs	SS,sushi	4.0
60	417782	T10149	Ha.4243	hypothetical protein FLJ12650	SS,TM	4.0
	443539	BE269042	Ha.8951	prolactinase (prosome, macroph	prolactinase,SS,TM,LACT,try	4.0
	410039	AF267999	Ha.58014	Homo sapiens, Similar to G pro	SS,TM,7m_3,SS,TM	4.0
	452715	Z21093	Ha.30352	ribosomal protein S6 kinase, 5	phatase	4.0
	442549	AJ751601	Ha.8375	TNF receptor-associated factor	zf-C3HC4,MATH,zf-TRAF,SS,	4.0
65	430503	AA148164	Ha.247280	HIV associated factor	zf-C3HC4,zf-RanBP,p16in	4.0
	427239	BE270447		ubiquitin carrier protein	UQ,con,SS,TM	4.0
	402665			Target Exon	SS,TM,jg,DSpC	4.0
	413818	BE161405	Ha.79	hypothetical protein MGCI5429	SS,KH-domain,W40,Ribosom	4.0
	409119	BE6539		gb-Homo sapiens DNA-binding p	SS,mm	4.0
70	412556	AF005011	Ha.74375	diseasewell1 (1 homologous to D	SS,PZM,DEP,DIX,Diseasewell	4.0
	437546	AW074836	Ha.173984	T-box 1	SS,TM,T-box,GTP_CDC,LRRC7	4.0
	419489	AW411280	Ha.930633	replication initiation region	zf-C2H2,UIM,TM	4.0
	410043	C38612	Ha.2055	zinc finger protein 282	zf-C2H2,RAB,SS,zf-C2H2,k	4.0
	430057	U79458	Ha.231840	VW domain binding protein 2	GRAM,SS	4.0
75	408449	NM_004408	Ha.168611	dynamitin 1	PH,GED,dynamitin,dynamitin_2,	4.0
	448059	BE21433	Ha.61976	Homo sapiens cDNA FLJ12947 fs	SS,TM,sugar_tr_PID	4.0
	435556	K35568	Ha.59167	hypothetical protein FLJ20543	Integrin_B,EGF,SS,TM	4.0
	424512	SS3002	Ha.149846	Integrin, beta 5	SS,TM,kinase	3.9
	440346	A192385	Ha.59821	ESTs, Weakly similar to A40815	SS,TM	3.9
80	420065	AW140093	Ha.125926	ubiquitin-activating enzyme E1	zf-TUBACT,SS,kinase,Uch	3.9
	426516	BE248234	Ha.2055	stem cell growth factor; lymph	lectin_c,SS,TM	3.9
	421579	NM_002975	Ha.105927	methyl-CpG binding domain prot	SS,HLH	3.9
	427438	NM_003926	Ha.178728	RAR (RAS like GTPase)	SS,TM,Rhomboid	3.9
	457820	AA341497	Ha.31408	hypothetical protein FLJ23338	SS,SS,TM,EXP70,P28_alpha	3.9
	429918	BE558534	Ha.81790	cleavage and polyadenylation	zf-CCHC,zf-CCHC,Ubaamin	3.9
	438552	AA223599	Ha.6351	early development regulator 2	SAM,SS	3.9
	414303	NM_004427	Ha.165263	calcium/calmodulin-dependent p	kinase,SS,hexokinase,hex	3.9
	434506	Z69693	Ha.4884			

	414168	AW732396	Hs.103845	ESTs, Moderately similar to I5	SS	3.9
	451982	F13036	Hs.27373	Homo sapiens mRNA; cDNA DKFZp5	SS	3.9
	418181	U37012	Hs.83727	cleavage and polyadenylation a	CPSP_A,SS,TM	3.9
5	402733			Target Ecton	SS,TM,cyidin,cyidin_C	3.9
	416581	AA267786	Hs.23449	Insulin receptor tyrosine kina	SS,SSS	3.9
	412521	L40397	Hs.74137	transmembrane trafficking prot	EMP24,GP26L,SS,TM	3.9
	420531	AW976530	Hs.28355	hypothetical protein FLJ22402	SS,TM	3.9
	438483	AW566735	Hs.321635	ESTs, Weakly similar to A43032	SS,TM,IP,trans	3.9
10	431472	A3561023	Hs.258545	nucleic acid binding protein 2 (forL,NH,PA,AP,kinase	3.8
	447800	AL060092	Hs.19810	DKFZP644N1362 protein	SS,TM,SS,TM	3.8
	436668	AW450205	Hs.305890	BCL2-like 1	TM,BC2-BH4	3.8
	408815	AW567514	Hs.25485	hypothetical protein FLJ22341	SS,TM	3.8
	441195	BC387802	Hs.7744	NM_007103 Homo sapiens NADH	Complex1,5,1K,SNF2,N_halic	3.8
	433030	AW068657	Hs.279929	gp32L2 protein	SS,TM,EMP24,GP26L,SS,TM,G	3.8
15	408721	BE515274	Hs.47062	polymerase (RNA) II (DNA direc	RNA_POL_III,SS,COX7A	3.8
	430439	AL122087	Hs.4746	hypothetical protein FLJ21324	SS,pk8	3.8
	431347	A133461	Hs.251864	Insulin-like growth factor 2 (SS,Insulin,Insulin	3.8
	450585	BE267733	Hs.25584	hypothetical protein FLJ10767	ArtCap,SS,wva,TSPN,hd,Co	3.8
20	414134	X50188	Hs.861	mitogen-activated protein kina	pk,kinase,SS,kinase,T-box	3.8
	418090	UT5059	Hs.83429	tumor necrosis factor (ligand)	TNF,SS	3.8
	446832	AW243312	Hs.22199	ECOT	SS,mm	3.8
	447256	AW593008	Hs.6126	hypothetical protein DJ11141E15	SS,TM,SS,TM	3.8
	448107	D45853	Hs.20313	protein tyrosine kinase 2 beta	Focal_AT,kinase,SS,Pepti	3.8
25	426433	L38569	Hs.168675	thrombospondin 3	TSPN,Top_3,SS,TM,SEA,TSPN	3.8
	431626	AL035561	Hs.26327	-hypothetical protein DKFZp751	SS	3.8
	430956	AI183529	Hs.2706	glutathione peroxidase 4 (phos	GSHPx,SS,TM,ABC,tran	3.8
	450998	BC387814	Hs.25797	splicing factor 3b, subunit 4,	SS,TM,sugar_tr,halone	3.8
	434899	BE813631	Hs.283365	FOX-4-like antigen-1	b2P,SS,b2P,cofilin,ADF,	3.8
	444734	NM_0011360	Hs.11805	7-dehydroxycholesterol reductase	ERG4,ERG4A,SS,TM	3.8
30	411090	BE165550	Hs.339697	VP52B protein	SS,TM,CPSP_A	3.8
	452135	AA92175	Hs.21446	KAA1715 protein	SS,DX,POZ,DEP,Diobello	3.8
	421339	AA070224	Hs.103581	SRp25 nuclear protein	SS	3.7
	405535			Target Ecton	SS,TM,Ribosomal_S19u,gl	3.7
35	447281	AA017018	Hs.18021	hypothetical protein FLJ20446	SS,SS,Tekin,Pw,PAZ	3.7
	433216	AB021262	Hs.99816	beta-catenin-interacting prote	SS,TM	3.7
	425215	AC030291	Hs.155165	zinc finger protein-like 1	PHD,SS,TM,DnaJ,ERG4,ERG2	3.7
	420536	AL117455	Hs.275458	Nucleic deacetylase 7A	SS,deacetyl,SS,Nst,dna	3.7
	417958	AW567420		gb:EST379495 MAGE resequencs,	SS,TM	3.7
40	430890	X54232	Hs.2699	glypican 1	Glypican,SS	3.7
	427863	AF189712	Hs.181002	MLL septin-like fusion	SS,GP,CTD,SS,TM	3.7
	446506	BE113362	Hs.13662	Homo sapiens ubiquitin conjuga	SS,TM	3.7
	421961	AB032993	Hs.109929	linely homolog of rat GRIP-ase	TM,AK,Leu,trans,H,H,	3.7
	410283	AK000047	Hs.61950	E1B-55kDa-associated protein 5	K,Leu,SS	3.7
	425233	T19891	Hs.155218	hypothetical protein MCC01812	SPRY,SAP,SS,TM,SPRY,SAP,p	3.7
	425983	BC388899	Hs.4188	hypothetical protein FLJ20391	SS,Peptidase_C15,TGF-beta	3.7
	415997	AC056003	Hs.78505	DKFZP5681024 protein	SS,qm60,TCPI	3.7
	415825	Y18024	Hs.76877	Inositol 1,4,5-trisphosphate 3	SS	3.7
50	418052	AA350559	Hs.83347	amgo-associated, migratory cy	WD40,Bacterial_PQO,TM,UPP	3.7
	444706	A0900308	Hs.11747	hypothetical protein FLJ20391	SS,SS,TM	3.7
	407381	AA420659	Hs.183110	ESTs, Weakly similar to ALUC_H	SS,TM	3.7
	423432	BE252996	Hs.44067	ESTs	TM	3.7
	444982	AK032182	Hs.12211	GDP-fucose transporter 1	SS,TM,DUF5,SS,TM	3.7
	407777	AA161071	Hs.71405	equilium epoxidase	SS,TM,Monooxygenase	3.7
55	422715	AA332178	Hs.119403	hexosaminidase A (alpha polype	Glyco_hydro_20_Glyco_hydr	3.7
	422809	Z46023	Hs.118721	sialidase 1 (lysosomal sialida	SS,TM,BNR,SS,TM,SET,HP870	3.7
	414732	AAW12676	Hs.77152	mitochondrion maintenance def	MCM,RIP,SS,of-C2H2,KRAB	3.7
	452579	AA131637	Hs.29830	ESTs	SS,COI,hydrolase	3.7
	419332	W81330	Hs.58643	ESTs, Highly similar to JAK3B	SS,SH2,Insulin,PK	3.6
60	411165	NM_000169	Hs.69069	galactosidase, alpha	Meillass,Ribosomal_L44,z	3.6
	444000	AD095024	Hs.135528	ESTs	SS,HLH	3.6
	441174	BE312776	Hs.264005	Homo sapiens, clone IMAGE:3050	SS,TM	3.6
	429491	NM_012111	Hs.264041	chromosome 14 open reading fra	SS	3.6
	438433	AB018274	Hs.6214	KIA0731 protein	SS	3.6
65	425162	BE514651	Hs.154666	crutinin kinase-like	Cam,acyltrans,Choline_k	3.6
	425671	BE379336	Hs.15594	proliferone (prosome, macropain	AAA,NB,ARC,TM	3.6
	421018	AI586028	Hs.123888	hypothetical protein FLJ14768	zf-C2H2,SS,mm,ENTH	3.6
	433604	NM_013442	Hs.3439	stomatin-like 2	Band_7,SS,TM,AAA,cof48,N	3.6
	451644	AD090429	Hs.26570	hypothetical protein FLJ20422	SS,TM,COX3,SS,TM,SPF-TF	3.6
	444389	AW456286	Hs.26793	ESTs	SS	3.6
70	406660	X55371	Hs.172550	poly(2'-5')uridylic tract binding p	mm,beta-lactamase,SS,by	3.6
	456503	AW977779	Hs.194613	ESTs	SS,TM,bromodomain,ahydro	3.6
	451711	AD000461	Hs.26680	cat eye syndrome chromosome re	SS,SS,TM,deaminase	3.6
	423594	AA356730	Hs.323949	harsyl 1 (suppression of tumor	SS,TM,transmembrane4	3.6
75	428011	BE387514	Hs.161418	KIA0152 gene product	Acyl-CoA_dh,SS,ahand	3.6
	407627	AA190020	Hs.62620	chromosome 6 open reading fra	SS	3.6
	436437	F12200	Hs.5811	chromosome 21 open reading fra	SS,Syts,N_Ext,endo_phos	3.6
	419418	X70521	Hs.90303	tuberosc sclerosi 2	Rap,CAPI,Tuberin,Peptidase	3.6
	440300	N39760	Hs.8859	Homo sapiens, Similar to FKBP	kinase,PBD	3.6
80	448136	AA036680	Hs.20447	protein kinase related to S.c	SS,TM,SS,TM,ubiquitin,Rib	3.6
	435977	AL138079	Hs.5012	brain-specific membrane-anchor	kinase,PK,kinase_C	3.6
	419305	AA234009	Hs.189715	ESTs	SS	3.6
	447267	AL360143	Hs.17936	DKFZP444132 protein	SPRC1,lysoyl_oxidase,SS,TM,	3.6
	418054	NM_002318	Hs.83354	lysyl oxidase-like 2	SS	3.6
	444394	AA947582	Hs.10927	hypothetical protein R33729.1		3.6

42098	AF030249	Ha.196176	enoyl Coenzyme A hydratase 1,	ECU/Herpes_V23.S5,Gal-bin	3.6
430622	BE616971	Ha.247478	Homo sapiens, Similar to DNA s	G-patch,SS,TM,Ubiquitin,a	3.6
440675	AW050504	Ha.47883	ESTs, Weakly similar to KCC1,H	phnase	3.6
440676	NM_005632	Ha.100362	small cytosolic (Drosophila)	TM,Peptidase_C2	3.6
441307	BE363876	Ha.75196	actin repeat-containing prot	ank,SET,SS,TM,phnase,SH2	3.6
442579	AA366143	Ha.179669	hypothetical protein FLJ20637	HECT,SS,HECT	3.6
442914	UJ2882	Ha.50642	interferon-induced protein 35	SS,ribosomal_L27e,KOW	3.5
445528	BE513248	Ha.172684	Homo sapiens, clone HA656227	SS,PHD,SH2	3.5
444426	AL121105	Ha.11170	RNA binding motif protein 14	rm,SS,spectrin,PH,arm,ss	3.5
440297	R34662	Ha.53066	hap70-interacting protein	SS	3.5
441138	TS6785	Ha.10101	hypothetical protein FLJ12675	SS	3.5
435163	AF148509	Ha.279981	manadase, alpha, class II, R	TM,Myo,hydra_47	3.5
422575	AK000546	Ha.118552	Homo sapiens mRNA for FLJ00016	TM,SS,TM,SCR,Myo,trans	3.5
430326			C200042-g17705383[refNP_05	SS	3.5
437895	AB014568	Ha.5898	KIA0668 protein	TM,UL21,LIpprotein,6_GBP	3.5
449030	AI365552	Ha.57100	Homo sapiens mRNA for FLJ00016	SS,Synaptin	3.5
425542	AF180746	Ha.170310	cat eye syndrome chromosome re	A,desmin,SS,TM,Hydro	3.5
439873	BE159253	Ha.300638	ESTs	SS	3.5
428950	BE311879	Ha.194673	phosphoprotein enriched in ste	DED,SS,TM,Calsequestrin	3.5
421564	AB078864	Ha.105850	KIA0404 protein	SS	3.5
441094	U33819	Ha.7647	MYC-associated zinc finger pro	SS,zf-C2H2,LM,PHD,TFIS,	3.5
450007	BE270693	Ha.24301	polymerase (RNA) II (DNA dec	N,AS,SS	3.5
422888	AL043101	Ha.127401	DKFZ434A163 protein; selectv	SS,TM	3.5
444914	AA049847	Ha.12142	WD repeat domain 13	SS,SS,TM,TBC,rm	3.5
420178	D05550	Ha.96559	luteal gland lavene (Drosophi	WD40,SS,TM	3.5
418984	AA421401		ribosomal protein L16	SS,TM	3.5
414166	AW888941	Ha.75789	N-eryc downstream regulated	Ndr,ubiquitin,SS	3.5
405944	BE297325	Ha.37687	four and a half LIM domains 3	LM,SS	3.5
421468	NM_003654	Ha.104576	carboxylate, fraction sulfate	SS	3.5
423599	AB05664	Ha.31731	peroxiredoxin 5	Ahp,C-TSA,SS,hormone_rec,z	3.5
427715	BE245274	Ha.180428	KIA1151 protein	SS,SS,TM,KOVI	3.5
425496			Target Exon	SS,ubiquitin,SS	3.5
417911	AA333387	Ha.82916	chaperonin containing TCP1, su	cpn60,TCP1,SS,pp60,TCP1	3.5
433520	AA604520	Ha.269468	ESTs, Moderately similar to AL	SS,UCH-2,UCH-1	3.5
430053	AF052155	Ha.227949	SEC13 (S. cerevisiae)-like 1	WD40,SS,TM,EL-EX-ATPase,C	3.5
458687	AW024615	Ha.170088	GLUT4 enhancer factor	SS	3.5
424679	AL117477	Ha.12960	DKFZ727G21 protein	chromo,SS	3.5
417360	AW651703	Ha.82023	hypothetical protein similar t	SS,TM,GDA1_C39,GDA1_C039	3.5
439841	AZ51317	Ha.33184	ESTs	SS,TM,GYP,actin,PA	3.5
425437	BE076837	Ha.163988	ubiquitin-conjugating enzyme E	U2,conn,SS,TM,Adm,ss,ss	3.5
427117	BE26846	Ha.73611	Target CAT	complex_1,49k,SS,TM,ATAM,	3.4
422051	AW327546	Ha.111024	solute carrier family 25 (into	SS,NTA,car,SS,milo,car	3.4
422729	AA316682	Ha.224571	ESTs	SS	3.4
417230	U40598	Ha.81728	enol13 (C.elegans) homolog	SS,glycolytic_enzy	3.4
439158	AK001999	Ha.24545	hypothetical protein FLJ11137	SS,zf-C2H2,SCAN,TFIS,SS	3.4
425421	L11669	Ha.167145	tetracycline transporter-like	SS,SS,TM,SS,TM	3.4
415515	F11327	Ha.167408	gH-SC2VD101 normalized infant	SS	3.4
427868	AI360119.comp	Ha.161013	phosphoglucomutase 1 (bra	PGAM,SS,TM,LM,sh	3.4
415503	BE410228	Ha.75410	heat shock 70kD protein 5 (gu	SS,HSP70,homobox,Hydranto	3.4
413014	AW250533	Ha.75139	partner of RAC1 (parafin 2)	SS,Jamospain,Flamin,H,L	3.4
457655	AA322968	Ha.71574	hypothetical protein FLJ14926	SS,PGCF,EF1B0	3.4
418432	AK021459	Ha.30375	hypothetical protein FLJ10597	PEP-ubiquitin,PEP-ubiquit	3.4
421086	AL076725	Ha.101408	branched chain aminotransfer	emoltrin,ATM	3.4
428038	AW134756	Ha.192477	ESTs	SS,Exonuclease,f-C2H2	3.4
433352	AW750535	Ha.50742	Homo sapiens cDNA: FLJ23331.1	TM	3.4
425247	AB07481	Ha.278581	fibroblast growth factor recep	U,phnase,SS,TM,LM,phnase	3.4
421310	AW630087	Ha.103315	tinuacido repeat containin	TM,zf-C2H2,SS,PHD	3.4
420999	AA338903	Ha.100915	peroxisomal biogenesis factor	SS	3.4
420561	U50408	Ha.181338	procollagen (type III) N-endop	SS,TM	3.4
419727	AW160796	Ha.30700	DKFZ564A0243 protein	Herpes_suv,SS,TM,Peptidase	3.4
429657	BE314724	Ha.103081	ribosomal protein S6 kinase, 7	SS,phnase,phnase_C,SS	3.4
411501	AB002389	Ha.70500	KIA0370 protein	SS,TM,SS,TM	3.4
448741	BE614657	Ha.19574	hypothetical protein MGC5469	SS	3.4
427103	AA244861	Ha.26522	hypothetical protein MGC15170	SS,TM,tyrosin	3.4
422808	AA49014	Ha.121025	chromosome 11 open reading fr	SS,TM,tyrosin,CUB,ubiquit	3.4
448173	H95657	Ha.68820	ESTs, Moderately similar to YO	SS	3.4
456335	H81851		gry80E10.1 Soares fetal liv	SS,TM,homobox,LM	3.4
405856	MI16714	Ha.181392	major histocompatibility compl	SS,HC_Lig,SS,TM	3.4
416599	AB867781	Ha.31619	HTD14	SS,ubiquitinase_2	3.4
411077	AW977263	Ha.58257	general transcription factor I	SS,TM,TGF-beta	3.4
427062	AW637785	Ha.173421	KIA1564 protein	SS,Peptidase_XM4	3.4
421890	AW955428	Ha.21622	ESTs	SS,zf-C2H2,AFRY	3.4
412568	AW050508	Ha.75102	alanine-tRNA synthetase	DHWA1,SS,RNA-actin_2c,DH	3.4
439496	BE516501	Ha.32343	Homo sapiens, Similar to RIKEN	SS	3.4
433659	AK001301	Ha.34887	hypothetical protein FLJ10439	WD40,SS,TM,Synaptin,Syn	3.3
447578	AA191247	Ha.156385	ESTs, Weakly similar to JC3514	SS	3.3
441722	AW960504	Ha.371033	FESS-LIKE 2	SS,TM	3.3
452345	AA293279	Ha.29173	hypothetical protein FLJ20515	DSPC,SS,ImC-F-box	3.3
451714	AK000344	Ha.26589	hypothetical protein FLJ20337	SS,TBC,FHA,zf-C2H4	3.3
410633	BE346742	Ha.26749	hypothetical protein MGC5260	SS,TM	3.3
410609	BE298441	Ha.287361	ADP-ubiquitylation factor relat	ar,RAS,SS,ar,Stathmin	3.3
414775	AA992036	Ha.177202	ESTs, Weakly similar to (defi	SS,PCI	3.3
428495	NM_013279	Ha.184640	hypothetical protein MGC10781	SS,TM,XPG_N,XPG_L,S_3_oxo	3.3
429215	NM_005341	Ha.3364	GL-Kruppel family member HWR3	zf-C2H2,STB,TP2,K,Ietna,S	3.3

445618	AL110307	Hs.15591	COP9 subunit 1 (MOV34 homolog,	Mov34,SS,zf-C2H2,SCAN	3.3
444688	BE560471	Hs.12101	hypothetical protein	SS,PCI	3.3
430041	AW247237	Hs.227835	KIAA1049 protein	SS,TM,Tm,1,Iubulin	3.3
116950	AL949798	Hs.80552	demaupolisin	SS	3.3
431203	AW248421	Hs.250758	proteasome (prosome, macropain	AAA,Sigma54,actin,SS,TP	3.3
432714	Y12055	Hs.278675	bromodomain-containing 4	bromodomain,SS,TM,SNF2_N,	3.3
145674	BE394784	Hs.78596	proteasome (prosome, macropain	SS,proteasome,SS,TM,Cathe	3.3
426152	BE269190	Hs.167246	P450 (cytochrome) oxidase	SS,carboxyl,F4D_biding,SS	3.3
118440	NM_006636	Hs.85119	SMTS (suppressor of mitf 2, 3,	ubiquitin,SS,UQ,con	3.3
1010545	U32324	Hs.64310	Interleukin 11 receptor, alpha	lig,fn3,SS,TM,GaP_JUDP_tra	3.3
409428	M33580	Hs.54457	CD81 antigen (target of anlip	transmembrane,cydotin,SS,	3.3
443121	VAMP	Hs.90457	VAMP (vesicle-associated membr	TM,ASP_domain	3.3
453856	AA050479	Hs.15647	POZ-LIM protein myslque	LM,SS,SH3,Sorb	3.3
430137	NM_005456	Hs.234249	miogen-associated protein kina	SS,SH3,PID,SS,PID	3.3
446427	AW255863	Hs.119632	ESTs	SS,SH3	3.3
40747			Target Exon	SH3	3.3
445580	AF167572	Hs.12912	est1 (S. pombe) homolog	SS,SS	3.3
452568	AA050534	Hs.300870	Homo sapiens mRNA; cDNA DKFZp	SS,SM,Egfrin,phkine,ATP	3.3
148558	AW032266	Hs.86131	Fas (TNFRSF6)-associated via d	death,DEO,SS,TM	3.3
401655			Target Exon	SS	3.3
429460	D56263	Hs.203238	phosphodiesterase 1B, catinoid	PDCase,SS,PDCase	3.3
146448	L13210	Hs.78339	lectin, galactoside-binding, s	SRCS,SS,TM	3.3
433038	AF192559	Hs.279939	mitochondrial carrier homolog	TM,mito_car,TM	3.3
440251	AW798016	Hs.332012	Homo sapiens, clone IMAGE3687	SS,TM,SS,TMRK	3.3
412822	M60721	Hs.74870	H2 Q (Chromatin)-like homeo 1	SS,homocore,SS	3.3
432941	WD4083	Hs.279651	hypothetical protein FLJ10241	SS,RNase_PH,N2ase_PH,C	3.3
141244	BE612535	Hs.164052	PP1201 protein	SS,TM,WD40	3.3
438175	AJ376727	Hs.122110	ESTs	SS,TM,myosin,fringe,fn2	3.3
433024	AA053731	Hs.325853	ESTs, Moderately similar to AL	SS,TM,C2H2,C2H3	3.3
430120	AW675238	Hs.233694	hypothetical protein FLJ11350	phkine	3.3
115571	AW674362	Hs.91146	protein kinase D2	SS,SS,DAG_PE-bind,PHDC	3.3
143019	BE281604	Hs.75140	low density lipoprotein-relatio	SS	3.3
405296	X07729	Hs.171995	kallistatin 3, (cretale spec)	tyrosin,SS,tyrosin,tyrosin	3.3
433519	BE263901	Hs.4099	ESTs, Weakly similar to S37431	SS,TM	3.2
434702	AL039734	Hs.273385	nardilysin (N-arginine diabolic	Peptidase_M16,H600,cooran	3.2
422442	AJ251760	Hs.273385	garnine nucleotide binding pro	G-alpha,ar,SS,G-alpha	3.2
433480	AL070399	Hs.241435	DKFZ1001c124 protein	SS,TM,homocore,Somatomad	3.2
452438	BE514230	Hs.25955	JM4 protein	SS,TM,KOW,HLH	3.2
456939	AA416333	Hs.163867	NM_002458-Homo sapiens NADH d	SS,RNase_synt_2x,WHEP-TRIS,	3.2
421009	AL045709	Hs.343357	Human DNA sequence from clone	TM	3.2
141969	Y12459	Hs.72390	Protein P3	SBF,SS,TM,G6PD,G6PD_Chex	3.2
405197	NS4706	Hs.330325	chromosome 11 open reading fra	SS	3.2
147896	AA379770	Hs.82590	defender against cell death 1	DAD,SS,TM	3.2
146026	BE379727	Hs.83213	fatty acid binding protein 4	Ippocin,SS,Ippocin	3.2
405617	AA102336	Hs.180600	ESTs	SS,TGFr,propeptide,TGF-be	3.2
437859	W91976	Hs.250834	ESTs	SS,TM,SH3,zf-CHC4	3.2
413211	AW967107	Hs.109274	hypothetical protein MGCA365	SS,TM	3.2
425080	A333496	Hs.12570	lecitol 1,4,5-triphosphatase	SS,CITF_NFI	3.2
445533	NM_005993	Hs.12570	tubulin-specific chaperone d	ATP-synt,B_HEAT_PBS,SS,TM	3.2
421943	BE615520	Hs.343912	Homo sapiens, Similar to RIKEN	SS,SS,SS,TM	3.2
443337	Y07604	Hs.9235	non-metastatic cells 4, protel	NDK,SS,adh_short,NDK	3.2
141885	DY1530	Hs.85454	drubins 1	cofin_AJF,SS,cofin_AJF	3.2
141817	BE302900	Hs.72241	miogen-activated protein kina	phkine,SS	3.2
413891	BE271020	Hs.278408	tumor suppressor deleted in cr	SS,TM	3.2
445455	T60748	Hs.34783	hypothetical protein	TM	3.2
1419153	D25643	Hs.62554	dichoty-diphosphoglycerate	SS,TM,DDOT_48Q,VPT,SS,T	3.2
406701	AA780613	Hs.91681	feritin, heavy polypeptide 1	SS,TM,UDPTG	3.2
435467	AW450278	Hs.14839	ESTs, Weakly similar to DCHUO	SS,RNase_synt_H,IRNA_bind	3.2
446534	U52427	Hs.14839	polymerase (RNA) II (DNA direc	S1,S5	3.2
101220	AF27142	Hs.12646	tumor endothelial marker 1 pr	SS,TM,EGF,Jactin_synth,	3.2
445411	AL137295	Hs.12646	hypothetical protein FLJ25953	SS,homocore_reczf-COCH	3.2
458018	A1195575	Hs.37716	ESTs	SS,TM,Oxytelol_BP	3.2
426530	U24578	Hs.278825	complement component 4A	SS,AJNTR,AJN,N_prenyltr	3.2
445804	T68556	Hs.12956	Tax interaction protein 1	POZ,SS,TM,P2X_receptor,FG	3.2
443402	U77846	Hs.2985	elastin (supravascular aortic	SS,POZ,LIM,phkine	3.2
432416	BE410337	Hs.2985	emerin (Emery-Dreifuss muscula	LEM,SS,Ribosomal_L10a,AY	3.2
429662	AJ929701	Hs.211586	phosphoinositide-3-kinase, reg	SH2,SH3,RhoGAP,SS,GLT,SH	3.2
429150	AF126103	Hs.303646	protein (Chromatin) bound	SS,TM,Fz,Fz-related,Tm_2,S	3.2
427729	BE4033100	Hs.83583	KIAA1274 protein (placenta) in	RhoGAP,REV,PH,SS,TM,Ribos	3.2
1418151	AA864238.comp	Hs.20776	actin related protein 2/3 comp	Ribosomal_S2,SS,Ippocin	3.2
442550	NM_016934	Hs.136290	Homo sapiens cDNA: FLJ22288.6	SS,Exonuclease	3.2
431158	AW65129	Hs.75875	ubiquitin-conjugating enzyme E	UQ,con,SS,TM,SAM_PNT	3.2
414292	BE384027	Hs.347286	Target Exon	SS,TM,Tm_2,SS,TM,Tm_2,G	3.2
406307			hypothetical protein FLJ22427	SS,TM,Surp,ubiquitin,TBC	3.2
423225	R55565	Hs.179718	v-erbA avian myeloblastosis 4	SS,SS	3.1
427534	AA233601	Hs.6945	ESTs, Weakly similar to CA13_H	NA,SS	3.1
431717	BE395150	Hs.21036	mitochondrial ribosomal protel	SS,TM	3.1
443881	D51580	Hs.50322	Homo sapiens mRNA; cDNA DKFZp	RhoGAP,SS,TM,SET,zf-CXCK,	3.1
413394	AD011124	Hs.5036	KIAA5551 gene product	SS,ly	3.1
436240	BE386573	Hs.75612	hypothetical protein MGIC10433	SS,TM,Ets,COXKB,transmemb	3.1
143900	AW409747	Hs.82327	stress-induced-phosphoprotein	TPR,SS,TM,DnaJ	3.1
147920	S47833	Hs.108595	adenosine monophosphate deamin	A_deaminase,SS,G-alpha,GS	3.1
421819	NM_013403		zadine	WD40,phkine,phkine	3.1

426362	BE257158	Hs.169474	DKFZ5966.0119 protein	IF-2B,SS,PP2C	3,1
408917	AW249025	Hs.7768	fibroblast growth factor (acid	SS,B2IP,cofilin,ADF,EGF	3,1
443099	AI372836	Hs.9003	hypothetical protein FLJ13668	TM	3,1
427022	AW245839	Hs.173255	small nuclear ribonucleoprotein	rm,SS,rm,SH3,ras,ZOG-Fe	3,1
452711	AW957047	Hs.293274	ESTs, Weakly similar to U0375	SS	3,1
407236	W79485	Hs.173980	nuclear matrix protein NMP200	WD40,SS,TM,PTPRZ,7m_1	3,1
452537	AW247390	Hs.77735	hypothetical protein FLJ11618	SS,SNF2,Nhalasease_C	3,1
452139	AA099559	Hs.16331	Homo sapiens cDNA: FLJ21482.1	SS	3,1
447620	AF034750	Hs.19105	translocase of inner mitochond	Tm17,SS,TM,actin,OTU	3,1
401097			C1200658-gene7363437[refNP_0	SS,TM,7m_1,SS	3,1
452736	C01164	Hs.4232	Homo sapiens PAC clone RPI-130	SS,SS,TM,TBC,Surp,ubiquit	3,1
435507	AI13579	Hs.26510	vacuolar protein sorting 33B 1	SS,Scet1,Scet1	3,1
424934	U75370	Hs.15380	polyoma virus PTA01A12 mitochondrial	PPV,SS,TM,actin,ubiquitin,RN	3,1
413245	BE244334	Hs.75249	ADP-ribosylation factor-like 6	SS,TM,karA,ribosomal_SS	3,1
400858	NM_006586	Hs.56828	trideutide repeat containin	SS,SS,TM,B56	3,1
424582	AF026849	Hs.150922	BOS1 (yeast homolog)4aa	AAA,SS,PI-PLC-X,PH,PI-PLC	3,1
431677	AK000466	Hs.30696	hypothetical protein FLJ20488	SS	3,1
417947	AA323563	Hs.325309	hypothetical protein FLJ14595	SS,TM,PTPA	3,1
409283	NM_004890	Hs.52788	fragile X mental retardation,	IGH-domain,SS,TM,HMG_box	3,1
412813	AF069947	Hs.74817	dyncactin 1 (p150, Glued (Dros	CAP, GLY,SS	3,1
456535	AA350979	Hs.1342	cytochrome c oxidase subunit V	COX5B,SS,SS,ASQ,actin	3,1
432462	L19367	Hs.275924	dystrophia myotonia congenita	WD40,SS,plasmae kinase	3,1
437255	AI137404	Hs.97871	Homo sapiens, clone IMAGE:3545	TM,SS	3,1
440191	AJ990417		tubulin, beta 5	SS,formin/ntr,premytran	3,1
407972	AA427039	Hs.16587	JDA1568 protein	SS,TM	3,0
420890	AA434058	Hs.160071	6-phosphogluconolactonase	Glucosamine_1aa,SS	3,0
440060	AI696387	Hs.126451	ESTs, Weakly similar to A46302	SS	3,0
452222	AW906287	Hs.21432	SEX gene	SS,TM,Sema,TIG,PSI,GOI	3,0
401772			NM_014520:Homo sapiens MYB 1in	SS	3,0
453754	AW972580	Hs.172763	ESTs	SS,TM,ras,Ribosomal_S16,T	3,0
423865	H05202	Hs.133968	FGF receptor activating protei	SS,TM	3,0
450982	BE353647	Hs.25723	Spargan's syndrome/hidradenoma	SS,TM	3,0
441954	AI740335	Hs.04747	Fancp1-related, complemented	TPR,SS,TM,AAA,cof,UB,ban	3,0
412787	BD7452	Hs.74579	AKO2053 gene product	TC-COCH,SS,TM,NTP_transf	3,0
422034	AC056486	Hs.333069	Ets2 repressor factor	Ets,SS,phnase,PAF-AH,ub	3,0
450788	AI739410		ESTs	SS,TM	3,0
452511	BE408178	Hs.265165	Homo sapiens cDNA FLJ20845 fs	SS,Internal,PCR	3,0
414380	BE391815	Hs.76981	ubiquitin specific protease 14	UCH-2,UCH-1,ubiquitin,SS	3,0
407587	AA043925	Hs.339352	Homo sapiens brother of CDO (B	SS,TM,SS,TM	3,0
434955	BE276128	Hs.284286	mitochondrial ribosomal protel	SS	3,0
456532	AF420049	Hs.45549	uncharacterized hemaphysalid	SS,SULQ,co	3,0
432465	DS5165	Hs.275163	non-metastatic cells 2, protei	NDK,SS,NDK	3,0
430526	AF181862	Hs.242407	G protein-coupled receptor, fa	7m_3,homobox,SS,TM	3,0
453412	AJ003290		gtaA003290 Selected chromosom	phnase	3,0
446456	BE513033	Hs.15105	chromosome 14 open reading fra	UPP19143,SS	3,0
433180	AB038651	Hs.31854	K562 cell-derived leucine-zipp	TM,Acetyltransf,TM,Acetyl	3,0
447322	BE617649	Hs.77890	RAB5B, member RAS oncogene fam	SS,ordered_mylb,haeme_1,	3,0
422468	N25485	Hs.330310	maternal G10 transcript	G10,SS,WD40	3,0
410578	AF044053	Hs.91229	guanine nucleotide binding pro	WD40,SS,EPO_TPO	3,0
446929	AA076132	Hs.9460	Homo sapiens mRNA: cDNA DKFZp5	SS,TM,WD40	3,0

TABLE 21b:

Play: Unique Eos probe/ Identifier number

CAT number: Gene cluster number

Accession: Genbank accession numbers

55	Play	CAT Number	Accession
408215	10478_1	BE614290 AA307674 K35629 AA338538 AI193603 AA781096 AB068001 AB613256 AW277647 BE212623 AI348910 AI985031 AI009078 AI359517	
		AA656391 AI160210 AA464641 AI355345 AI343638 AI343640 AI275091 M78746 AW262795 AW250002 AA035076 AI934519 AW272086 N26520	
		AA626939	
409938	116091_1	AW074648 AA652154 AA649571 AW078592	
411674	123747_1	AW861123 AW861125 AW858717 AW861116 AW856706 AW856788 AW856774 AW856787 AW856780 AW856782 AW856783 AW856784 AW856786 AW856778 AW856776 AW856635 AW856757	
413052	1741714_1	BE249841 BE262687 BE352771 BE626236 BE626231 BE626296 BE62695 BE626747 BE626719 BE293541	
413937	133663_1	AW163626 AW163265 AW163386 AI029359 BE279279 AI313290 AW157323 AA584408 AW157252 AI692198 AW003514 T244362 AI765658	
		AW157458 AI10740 AI695382 AI695924 AI829284 AI340993 AI349493 AW299522 AW664650 AW295153 AA132529 AI340591 AI912836	
		A341293 AI650609 AA278	
413951	139759_1	BE271020 AI763358 AI925430 AI805151 AW003726 T15690 AA648945 AW128911 AI570746 T57462 AI826202 AW237602 AW003539 AI139045	
		AI502698 BE343625 AW778973 AI287658 AI953351 AW515101 AW150029 AI358496 AI621173 AA846105 AI470521 AW160748 AI951020	
		AW513748 AI84058	
414023	1410860_1	BE243628 BE246081 BE247016 BE241534 BE246091 BE245679 BE243620 BE243698 BE243239 BE241147 BE241457 BE242452	
		BE241989 BE241464	
		AW974420 AA210915 AA236991 AA210915	
416535	1599332_1	AA421401 T43526 AA330666 AA328941 W53573 AA758023 AA576306 H52254 AA877107 BE207784 AW664584 AI924890 AA458586 AI422142	
4171375_1	171375_1	AI951087 AI611174 BR9866 T43327 AA233722 AH51136 AA910314 AI379416 AI129321 AA851574 AA635649 AI939443 AW009533 AA577038	
418984	181094_1	AK48287 AA62	
419069	181650_3	AA233801 BE383487 AA913939 AI623861 AI813277 AI373652 AW136402 AI863574 AW1306364 AI858557 AI670746 AI015036 AI935384 AI93537	
419250	183829_2	AI138658 AW024971 AI765223 AA2894145 AA973341 AA234082	
		AW770185 AW262771 H11254 AW405510 AI032766 AA767046 AW376115 AI582209 AA465955 AI886633 AI016900 R05715 AI127382 AI660953	
		AI029644 I04045 AW658578 AA415039 AW029223 R05714 AA515462 AA235654 AA461274 W24033 AA530091 H00515	
420160	191054_1	AW157458 AI287657 AA255898 AI698206 AA468558	
421572	204022_1	AA531607 AI655370 AI376907 AI811616 AW138145 AW139465 AA421656 AA239059 AW118141 AI214380 AW663302 AI024486 AI553789	
		AA650416 AI658947	

[illegible]

TABLE 21C:

Procy: Unique number corresponding to an Eos probeset

Ref: Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham I. et al." refers to the publication entitled "The DNA sequence of human chromosome 22" Dunham, et al. (1999) *Nature* 402:489-495

Strand: Indicates DNA strand from which exons were predicted

NT position: Indicates nucleotide positions of predicted exons

	Phy	Ref	Strand	N_posion
50	404040	8389428	Plus	35559-36255
	404583	9844011	Plus	81941-82434
	404737	9844011	Plus	71436-71441
	405064	1188605	Plus	35314-35402
	401057	9585518	Minus	63345-61096
55	401128	9699792	Plus	37349-37885
	405485	9529053	Plus	76555-80422
	417127	8134845	Plus	65443-65442
	401751	9826851	Plus	15195-139322
	401772	9562443	Plus	18327-184042
60	402385	9454515	Minus	8039-71185
	402385	9736841	Minus	818-4085
	402685	8017033	Minus	11814-2059,14230-14544
	402863	6136940	Minus	18901-24915
	402916	7406592	Plus	381-474,511-487
	403075	767037	Minus	114150-12772
	403325	8440025	Minus	105713-119526
	404256	9387203	Plus	149331-147796
	405189	7229507	Plus	168236-168795
	405445	605445	Plus	25161-24390
70	405388	2153224	Plus	16716-36278
	405496	8465658	Plus	347700-140582
	406151	9124019	Plus	12535-128331
	4076097	8576090	Plus	95473-95489,98900-99180
	406635	7714147	Plus	61325-8332

Table 22A lists about 811 genes up-regulated in ovarian cancer compared to normal adult tissues that are likely to encode extracellular or cell-surface proteins. These were selected as Table 22A from the ratio of "average" ovarian cancer level to "average" normal adult tissues was greater than or equal to 1.0. The "average" ovarian cancer level was the 95th percentile amongst all ovarian cancer specimens, the "average" normal adult tissue level was set to the 75th percentile value amongst various non-malignant tissues. The "average" ovarian cancer level was greater than or equal to 80 units, and the predicted protein contained a structural domain that is indicative of enzymatic function or of transducing an intracellular signal, or of being modifiable by small molecules (e.g., kinases, peptidases, phosphatases, or ion transporters). Predicted protein domains are noted.

TABLE 22A:

Pkey: Unique Eos probeset Identifier number

ExAccn: Exemplar Accession number, Genbank accession number

UnigeneID: Unigene number
 Unigene Title: Unigene gene title
 Protein Dom.: Predicted protein domain
 RI: Ratio of tumor to normal body tissue

	Play	Exon	Unigene ID	Unigene Title	Protein Dom.	RI
5	407223	H96850	HS.237924	gbyw03b12.1.1 Soares melanocyt		58.9
	430281	A878842	HS.237924	CG-69 protein	mlto_carr	46.7
	410418	D31382	HS.263525	transmembrane protease, sarfne	ldl_recept_a,lypsin	41.0
	431773	BE409442	HS.268557	plectstrin homology-like domai	PH	37.1
10	438424	A912498	HS.25895	hypothetical protein FLJ14958		35.3
	418039	W330191	HS.25807	hypothetical protein FLJ20258	SH3	35.2
	435022	AB005322	HS.311442	Rac2 protein-like 4	DEAD, helicase_C	24.4
	407722	BE252241	HS.38041	pyridoxal (pyridoxane, vitamin	ph8	28.2
15	451721	NM_006946	HS.26915	spectrin, beta, non-erythrocyt	spectrin,PH,CH	27.9
	416819	U77735	HS.80205	plm-2 oncogene	phbase	27.9
	430397	A904533	HS.105507	bicarbonate transporter relate	HCO3_cotransp	24.4
	450334	AF035969	HS.24879	phosphatidic acid phosphatase	PAP2	26.7
20	418945	BE246762	HS.89499	arachidonate 5-lipoxygenase	lipoxygenase,PLAT	25.3
	428420	BE514743	HS.146688	prostaglandin G synthase	MAPEG	25.1
	412574	X04106	HS.74451	calpain 4, small subunit (30k)	epsilon	24.4
	430023	AA158243	HS.227729	FK506-binding protein 2 (13kD)	FKBP	24.3
25	444672	Z95635	HS.11659	laminin, alpha 5	laminin_EGF, laminin_G,EGF	24.0
	413726	AJ278465	HS.75510	annexin A11	annexin	23.1
	430561	U51336	HS.16543	inositol 1,3,4,5-tetraphosphate 5'	oxidoreductase	23.0
	425099	BE439952	HS.196177	phosphorylase kinase, gamma 2	phkinase	23.0
30	431765	AF124249	HS.268541	novel SH2-containing protein 1	SH2	22.4
	428245	L10027	HS.118890	glycogen synthase kinase 3 ap	phkinase	22.4
	415435	AF228063	HS.86061	glycogen synthase kinase 1	DAGK	22.3
	422639	AB229377	HS.173724	creatine kinase, brain	ATP-gua_Pirans,ATP-gua_Pi	21.5
35	428859	AB07018	HS.15977	Target CAT		21.3
	418891	NM_002419	HS.85449	mitogen-activated protein kina	SH3,ph kinase, pyridoxal_deC	21.1
	410138	U48508	HS.25521	tyrosine receptor 1 (plekstrin	RYR,CTR,RyR,SPRY,Jan_T	21.0
	428266	BE359875	HS.279609	mitochondrial carrier homolog	mlto_carr	20.9
40	452875	BE275760	HS.30928	DNA segment on chromosome 19 (Euk_pont	20.8
	428997	BE820738	HS.173125	poly(ADP-ribose) polymerase F (y	p.p.p. isomerase	20.8
	422916			ENSP000002587:beta-ubiquitin l	HCO3_cotransp	20.6
	425760	D17628	HS.159479	galactosamine (N-acetyl)-6-sul	Sulfatase	20.7
45	400419	AF084545		Target	EGF,lg,lectin_c,sushi,XII	20.0
	419444	NM_002096	HS.90443	Target CAT	hex	19.5
	409133	U40343	HS.29556	cyclic-dependent kinase inhibi	ank	19.4
	447595	AW379130	HS.18953	phosphodiesterase 9A	PDEase	19.2
50	422708	AB017430	HS.119324	kinase-like 4	kinasin,homobox	19.0
	414837	U24268	HS.77448	aldehyde dehydrogenase 4 fami	aldohch	18.8
	429712	AW049325	HS.211914	ENSP0000023557:NAADH+ubiquino	oxidoreductase	18.5
	425848	BE242709	HS.159637	valyl-HRNA synthetase 2	GST_C,GST_M,Tropomyosin	18.4
55	451643	MA6437	HS.234799	breakpoint cluster region	RhoGEF,RhoGAP,PH,C2	18.1
	447859	AK021194	HS.19851	peroxisomal biogenesis factor	DAG_PE-bind,RhoGAP	17.3
	429457	AF084667	HS.169685	climexin (p13casin) 1	ldl_recept_L	17.1
	421612	AF161254	HS.106196	B26 antigen	PHURS	16.9
60	421363	NM_001381	HS.103854	docking protein 1, 62KD (downs	Acyl-CoA_hydro	16.8
	427239	NM_007274	HS.8679	cytosolic acyl coenzyme A thio	cadherin	16.8
	420568	F80247	HS.247735	protocadherin alpha 10	asp	16.8
	421445	AA513059	HS.104433	Home sapiens, clone IMAGE:4054	phbase,KAI1,UBA	16.7
65	425424	NM_004954	HS.157199	ELK1, molli kinase	kazni,QATP_M,OAATP_C	16.5
	446329	NM_012372	HS.14405	sodium channel family 21 (orga	myosin_head,Myosin_tail,l	16.4
	408620	MB1105	HS.46550	neutrophil heavy polypeptide 9, n	PX,SH3,OPR	16.3
	429109	AL008637	HS.195382	neutrophil cytosolic factor 4	PH,Oxytelord_BP	16.2
70	429183	AB014004	HS.197655	KIA00704 protein	DSPH,Ribonuclease	16.2
	444654	K26362	HS.171815	map kinase phosphatase-like pr	MIF-like_protein_L2	16.2
	427840	AF062923	HS.180015	D-4-tetradichrome isomerase	PMM	16.0
	425123	AW020274	HS.154695	phosphomannomutase 2	E1_dehydrog	15.8
75	416006	AA324251	HS.76930	branched chain keto acid dehyd	Acyl-CoA_dh,Acyl-CoA_dh_M	15.7
	412942	AL123444	HS.75074	acyl-coenzyme A dehydrogenase,	p450	15.5
	423362	Z80345	HS.127610	second mitochondria-derived ac	aldh3c_beta_ped	15.4
	426391	AW161050	HS.169611	cytochrome P450, subfamily XXV	7hm_2_EGF_cadherin,laminin	15.4
80	424568	AF050418	HS.150595	poly(ADP-ribose)-mediated factor 1	Collagen	15.2
	420029	BE258076	HS.244448	cadherin, EGF LAG seven-pass G	7hm_1	15.2
	435573	AF234887	HS.57652	collagen, type IX, alpha 2	ras_srf	15.0
	407619	AL050341	HS.371165	glucy2306.x1 NCL_OGAP_Lym6 Ho	complex1_240D	14.7
85	427326	AD287878	HS.8535	Home sapiens mRNA for KIAA1698	RhoGAP,SH3,PH	14.6
	424250	C00138	HS.8535	ras homolog gene family, membe		14.6
	458130	AA115911	HS.6838	hypothetical protein MGC11314	CPase_a_chain,PYC_OA,DAH	13.6
	449936	AA328293	HS.60088	NM_021074:Home sapiens NADH de	DUF1227	13.5
90	409230	AA652431	HS.51299	hypothetical protein	Foliate_mec	13.5
	423801	NM_015077	HS.132942	pyruvate carboxylase	helicase_CAT_hook	13.5
	419539	AB001502	HS.81753	programmed cell death 5	elF6	13.3
	419298	AA523479	HS.89890	folate receptor 1 (beta)	7hm_1	13.3
95	426108	AA723157	HS.13769	Srd2-related GTP activator pro	GDC-P	13.2
	446133	AF172157	HS.87908	Integrin beta 4 binding protal		
	418736	T18979	HS.87908	endothelial differentiation, I		
	436543	NM_002212	HS.5215	glycine dehydrogenase (decarbo		
100	431515	NM_012152	HS.258583			
	429469	MB4590	HS.27			

431462	AW583872	Hs.256311	granin-like neuroendocrine pep
444855	BE409261	Hs.12084	Ta translation elongation fact
423464	NM_016240	Hs.128856	CSR1 protein
450787	AK006160	Hs.25475	aquaporin 7
425539	AWA10063	Hs.184677	sodium carrier family 25 (mlt)
436014	AF281134	Hs.283741	osmosis component Rtp46
416886	AA297356	Hs.60324	serine/threonine protein phosph
433867	AK005956	Hs.3818	hippocampus-like 1
411428	U70566	Hs.65949	calcium channel, voltage-depen
432329	NM_002962	Hs.2960	S100 calcium-binding protein A
417887	AA114050	Hs.19949	casepase 8, apoptosis-related c
427448	BE246449	Hs.2157	Wiskott-Aldrich syndrome (ce
428520	AA438187	Hs.172631	integrin, alpha M (complement
446603	NM_014535	Hs.15519	cytoskeleton-binding protein-rela
427633	X55632	Hs.116804	enolase 3, (beta, muscle)
446629	BE091926	Hs.16244	mitotic spindle coiled-coil re
411757	U46922	Hs.77252	Fragile histidine triad gene
428593	AW207440	Hs.165973	degenerative spermatocyte (hom
432370	AA300334	Hs.274424	N-acetylneuraminic acid phosph
401542			C15001413-gt10645199refNP_
428782	X12830	Hs.193400	Interleukin 5 receptor
429999	AW513061	Hs.332981	ESTs, Weekly similar to I38022
422301	AT52163	Hs.114599	collagen, type VIII, alpha 1
410720	AF035154	Hs.65756	regulator of G-protein signal
407143	C14076	Hs.332329	ESIT
421321	NM_005309	Hs.103502	glutamic-pyruvate transaminase
425251	Z22521	Hs.155342	protein kinase C, delta
431354	BE048956	Hs.251673	DNA (cytosine-5)-methyltransf
420421	AF281133	Hs.343559	osmosis component Rtp41
416714	AF283770	Hs.79630	CD79a antigen (immunoglobulin-
427336	NM_005658	Hs.2134	TNF-receptor-associated factor
409799	D11528	Hs.76845	phosphoserine phosphatase-like
435319	I89977	Hs.5123	inorganic pyrophosphatase
400748			NM_022122Homo sapiens matrix
428948	BE514362		FKBP-binding protein 3 (23kD)
401215			C15000457-gt17512179refNP_
401281			DNFZP58802124 protein
427397	AB25685	Hs.177656	calmodulin 1 (phosphorylase ki
434396	AA442103	Hs.33084	solute carrier family 2 (facil
429608	AF21023	Hs.55173	cardiactin, EGF LAG seven-pass G
424415	NM_001875	Hs.46580	enolase 2, (gamma, neuronal)
447495	AW401864	Hs.18720	programmed cell death 8 (apopt
426928	AF037062	Hs.172914	retinol dehydrogenase 5 (11-c
405371			NM_005687Homo sapiens LIM do
416282	RS564	Hs.167257	brain link protein-1
452295	BE379336	Hs.28966	programmed cell death 10
430390	AB022186	Hs.241161	KIA00869 protein
435594	AK000790	Hs.240885	hypothetical protein FLJ20783
443814	BE281240	Hs.9857	carboxyl reductase
440242	AW295871		glucose transporter protein 10
447365	BE383676	Hs.334	Rho guanine nucleotide exchang
405843			NM_003105Homo sapiens sorli
422418	AK001383	Hs.116385	hypothetical protein FLJ10321
400232			NM_001895Homo sapiens casein
426828	NM_000020	Hs.172670	activin A receptor type II-like
431157	AB23689	Hs.132678	ESTs
427616	BE300330	Hs.118726	selenophosphate synthetase 2
406779	AA412048	Hs.279574	CGI-39 protein; cell death-reg
400389	AL135941		olfactory receptor, family 2
402207			Target Exon
435615	Y15065	Hs.4975	potassium voltage-gated channe
452344	D30394	Hs.23549	C-type lectin-like receptor-1
402053			C11001722-gt11436283refNP_
416841	BE243136	Hs.86947	a disintegrin and metalloprote
431512	BE270734	Hs.2755	lactate dehydrogenase A
403213			NM_019595Homo sapiens interse
412158	BE241740	Hs.785	integrin, alpha 2b (platelet g
423673	BE003054	Hs.1695	matrix metalloproteinase 12 (m
403949			C10000613-gt543592refNP_0
457670	AF119666	Hs.23449	insulin receptor tyrosine kina
418416	U11700	Hs.84599	ATPase, Cu transporting, beta
415954	AA201308	Hs.114117	lipocalin (DANA) B binding
427265	AW402701	Hs.1578	basophilic IAP repeat-coatlin
453023	AW028733	Hs.31439	serine protease inhibitor, Kun
425694	U51333	Hs.159237	hexokinase 3 (white cell)
433820	AB037108	Hs.6418	seven transmembrane domain orp
402478			Target Exon
444202	AL031685	Hs.12785	Cam_acyltransfer
425597	U28694	Hs.158324	Na_H_Exchange/ABC2_membri
413431	AW245428	Hs.75355	chemokine (C-C motif) receptor
415200	AL004328	Hs.78202	ubiquitin-conjugating enzyme E
414874	D28351	Hs.77515	SWI5NF related, matrix associ
423524	AF065589	Hs.129738	Inositol 1,4,5-triphosphate re
457558	AF063955	Hs.279552	potassium voltage-gated channe
			G-protein-coupled receptor

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45629	AIZ5701	Ms.193326	Fibroblast growth factor receptor
434314	BE399291	Mt.3797	RAB28, member RAS oncogene fam
402487	AF006823	Mt.24040	NC011261 [g]2658397[mt]CA470
446893	AA355615	Mt.338916	poliovirus capsid, stemly K
427672	AA355615	Mt.338916	deafly-associated protein 9
412048	AW966663	Mt.73090	nuclear factor of kappa light
110079	U54382	Mt.58589	glycogenin 2
420319	AW406289	Mt.36393	hyphobacterial protein
420302	NM_001759	Mt.35015	Factor for cytoplasmic protein
405474			NM_001093<sup>Homo sapiens acetyl
401507			CS10008<sup>Homo sapiens
431434	BE267636	Mt.254105	1000127 [g]111272 [g]pP793
431434	AW495474	Mt.327	endocytosis 1, (alpha)
432343	NM_002690	Mt.2561	leukodystrophy 10 receptor, alpha
408331	AA251995	Mt.334648	S100 calcium-binding protein A
421542	AA411607	Mt.118964	poly(A) polymerase activity
421542	AA411607	Mt.118964	ESTs, Weakly similar to KAA11
411070	UA0711	Mt.233037	tyrosin-RNA synthetase
412270	AA006262	Mt.151461	genomic nucleotide binding
424649	BE242033	Mt.151461	embryonic ectoderm development
400772			NM_003109<sup>Homo sapiens scott
458460	M53718	Mt.166373	nitric oxide synthase 3 (beta)
401510			NM_017434<sup>Homo sapiens distal
404596			Target Exon
451367	AA523729	Mt.26322	cell cycle related kinase
417810	028418	Mt.6269	hydroxyglutathione synthase
424263	AF1296	Mt.7565	phosphatase, cytoplasmic
424263	MT7640	Mt.1757	L1 cell adhesion molecule (hyd
430398	AF105202	Mt.241378	potassium voltage-gated channel
424339	BE257148		endonuclease
424339	AW183769	Mt.193655	2,3-kilobase cytosolic, putative
407055	Y10141	Mt.284292	glucosyltransferase DA11 gene, mur
433938	AF161356	Mt.284292	ubiquitin-cytochrome C reducta
409649	AA195218	Mt.55505	hydroxyphenyl flavonoid FL20242
409649			CG0217 [g]16083311 [g]AF3400
400333			NC1100830 [g]3746443 [g]AAC639
410181	AB06945	Mt.288218	NM_002175<sup>Homo sapiens NAGH
446633	AF111713	Mt.288218	junctional associated molecule 1
410181	AA141425	Mt.180565	cellulose kinase
410181	W42913	Mt.78069	ATPase, vacuolar, 14 kD
432579	AF043244	Mt.278413	nuclear factor 3 (apoptosis
422328	XB0459	Mt.1513	interferon (alpha, beta) and on
422328	U54382	Mt.1513	protein kinase 1, delta
450683	NM_001348	Mt.25619	death-associated protein kinase
414625	AA335738	Mt.76886	glutathione peroxidase 1
401935			Target Exon
424263	AW194740	Mt.84152	cytoskeleton-beta-5 synthase
425242	D13635	Mt.155287	KGA0010 gene product
400404	AF161221	Mt.8248	kallidinrin 1A
424332	AB93251	Mt.8248	Target CAT
424332	AL137531	Mt.258890	Homo sapiens mRNA: cdna DCF24
402623			NC002456 [g]9530918 [g]mt]CA05
404527			peptide YY, 2 (seminal plasma)
439953	AA204729	Mt.6793	platelet-activating factor induc
439953	AA204729	Mt.6793	cell specificity (phospholipase
439953	AA040353	Mt.3573	ATP-binding cassette, sub-fam
400933			NM_004347<sup>Homo sapiens catenase
403388			NM_002207<sup>Homo sapiens integr
422251	NM_016361	Mt.15871	L1 cell adhesion molecule 1, (beta
422251	AW957280	Mt.293694	ESTs, Weakly similar to HERC2
421658	XB0448	Mt.301760	frequentin (Drosophila) homolog
401885			Target Exon
426551			NM_000721<sup>Homo sapiens calcu
426551	NM_005136	Mt.268530	calcium voltage-gated channel
433146	AB033002	Mt.21413	solute carrier family 12, (pot
420390	AA202208	Mt.94986	ribonuclease P (3'5')
425281	AA044390	Mt.155482	hydroxyaryl glutathione hydrol
425281	X97175	Mt.155482	ATPase, vacuolar, 14 kD
407676	U32659	Mt.37274	interleukin 17 (cytokine 2) C
431131	N84730	Mt.250616	lipoic acid dehydrogenase 3 (NA
422612	NM_004278	Mt.27008	phosphatidyl inositol glycan, c
422612	AW786282	Mt.58884	ESTs, Weakly similar to microg
438090	AA477381	Mt.291530	ESTs, Weakly similar to ALUC, H
418843	AJ251016	Mt.89220	potassium intermediate channel
419244	AA435657	Mt.89781	ATP synthase, H transporing,
426746			Target Exon
426746	BE267636	Mt.192853	ubiquitin-conjugating enzyme E
421474	U76362	Mt.104637	solute carrier family 1 (gluta
419066	MA9596	Mt.89575	CG7898 antigen (immunoglobulin
419066	AF105202	Mt.153557	phosphatidylglycerol, 2-omega
444628	U01120	Mt.242	glucose-6-phosphatase, catalase
404198			ENSP000600211797<sup>Homo sapiens
408681	AL048462	Mt.194019	atracin
420621	AW406990	Mt.65425	cellulose kinase 1, (2beta)
415056	BE73867	Mt.23867	adenosine A1 receptor
			7bm.1

400471		Target Exon			6.8
406591		NM_003888*Homo sapiens retina		alkdeth	6.8
425427	A0552682	Hs.157205	branched chain aminotransferase	aminotran_4	6.8
410539	NM_002649	Hs.66581	protein disulfide isomerase	thiomod_Rho_GDIgnIR	6.7
430037	BE409649	Hs.227789	mitogen-activated protein kinase	phkase	6.7
450848	A0877994	Hs.428	lms-related tyrosine kinase 3	BL3_fig	6.7
414534	BE257293	Hs.76366	BCL2 antagonist of cell death		6.7
401454			NM_014228*Homo sapiens renal	plnase	6.7
408493	BE206854	Hs.46039	phosphoglycerate mutase 2 (mus	PGAM	6.7
433333	A016521	Hs.71816	v-akt murine thymoma viral onc	homoexobp_kinase,PH,plnase	6.7
430432	A0037758	Hs.241419	KIAA1337 protein	Paiched	6.7
406126			NM_002027*Homo sapiens regula	Ceul_necrop_zf_C4,hormone_	6.7
419493	AF001212	Hs.90744	proteasome (prosome, macropain	PCI	6.7
439569	AW002166	Hs.222399	CEP1 protein	CUB,EGF	6.6
401134			C1201198(g)(3183183)gpcr32142	bioplerin_H	6.6
442286	W31847	Hs.50335	cyclodione P450 monoxygenase		6.6
428376	AF119665	Hs.184011	pyrophosphatase (norganic)	Pyrophosphatase	6.6
433494	A0029395		beta-1,3-glucuronyltransferase	Glyco_tranf_43	6.6
427001	NM_005482	Hs.173135	dual-specificity tyrosine-(Y)-	phkase	6.6
437278	AA140017	Hs.290145	ESR1	cNMP_binding	6.6
414463	T69078	Hs.78177	alpha-1-microglobulin/bikunin	lipocalin,Kunitz_BP1	6.6
421871	AK001416	Hs.306122	glycoprotein, synaptic 2	Staroid_dh	6.6
427627	U73727	Hs.19718	protein tyrosine phosphatase,	Y_phosphatase,fn3,Ig,MAAI	6.6
433379			Target Exon	DNA_poi_A	6.6
446872	X97058	Hs.16362	pyrimidinergic receptor P2Y, G	7bm_1	6.6
432857	NM_016103	Hs.275682	GTP-binding protein Sara	ar/aras	6.5
420970	AA305079	Hs.1342	cytochrome c oxidase subunit V	COD5B	6.5
427221	T15409	Hs.174007	von Hippel-Lindau syndrome	VHL	6.5
402209			Target Exon	A2M_NA2M	6.5
400518			NM_002057*gi32117053HAA21		6.5
425606	US2112	Hs.198331	retin-binding protein	RasGEF	6.5
437955	AA043222	Hs.193334	EST1, Moderately similar to AL	C2	6.5
433392	AF038535	Hs.127588	synaptobrevin VII		6.5
402191			NM_021733*Homo sapiens testis		6.5
458493	A0701393	Hs.278728	Raf and Gcm-related 2 (rat hom	ras	6.5
431857		Hs.271742	ADP-acyltransferase (NAD; p	PARP,PARP_reg	6.5
457879	AB030816	Hs.38761	HRAS-like suppressor		6.5
408656	NM_005133	Hs.288626	RCE1, prenyl protein protease	AB1	6.5
458373	BE247706	Hs.86751	membrane-epinning 4-domain, s		6.4
432498	BE276633		RA56B, member RAS oncogene fam	ras,arf	6.4
400555			Target Exon		6.4
401960			Target Exon	Branch	6.3
432545	X52486	Hs.3041	uracil-DNA glycosylase 2	cyclin	6.3
445303	AW362198	Hs.12503	interleukin 15 receptor, alpha	csa1	6.3
404528			peptide YY, 2 (seminalpalsmin)	GDA1_CD39	6.3
428542	D79599		KIAA0167 gene product	ank,PH,ArfGap,ras	6.3
406868	AA505445	Hs.300697	immunoglobulin heavy constant		6.3
425472			NM_001933*Homo sapiens acetyl	CPasee_1_chain,biotin_lip	6.3
408601	U47928	Hs.85122	protein A	7bm_1	6.3
415008	NM_002777	Hs.928	proteinase 3 (serine proteinases	trypsin	6.3
430258	AU078844	Hs.236963	protein phosphatase 2A, regula	ank,lon_trans	6.3
430483	AJ272053	Hs.263310	vanilloid receptor subtype 1		6.3
459302	NM_002314	Hs.35956	LIM domain kinase 1		6.3
437644	AA749575	Hs.136748	lectin-like NK cell receptor	lectin_c	6.2
421707	NM_014921	Hs.107054	lectinomed-2	Lectophilin,OLF,7bm_2,Gal	6.2
414629	AA34824	Hs.70696	carboxylesterase 1 (monooxylein	Colesterase	6.2
453898	AWD03512	Hs.232770	arachidonate lipooxygenase 3		6.2
424053	AF067036	Hs.138520	collagen-filic tail subunit (ol	Collagen	6.2
457358	BE258532	Hs.261871	CTP synthase	GATase	6.1
421504	AW402937	Hs.105952	adaptor protein with pleckst	SH2,PH	6.1
406495			Target Exon	SRCR	6.1
453810	AW368882	Hs.33818	RacQ protein-like 5	DEAD,helicase_C	6.1
424880	NM_003028	Hs.153614	refillins pigmentosa GTPase re	RC1	6.1
423947	U16917	Hs.133314	RAR-related orphan receptor C	hormone_nec_zf_C4	6.1
409829	M33552	Hs.56729	lymphocyte-specific protein 1	Caldesmon	6.1
401180			eukaryotic translation elongat	lon_trans,IQ	6.1
452072	BE258857	Hs.27744	RAE3A, member RAS oncogene fam	ras,arf	6.1
425484	AA379538	Hs.272759	KIAA1457 protein	IP_trans	6.1
402453			C1002496(g)(7363439)refNP_039	7bm_1	6.1
457310	W28363	Hs.239752	nuclear receptor subfamily 2	globin,cNMP_binding,phkase	6.1
422059	AJ010053	Hs.343603	tlm-cap (telothelin)	N	6.0
402375			NM_006512*Homo sapiens sarc		6.0
434357	AW732284	Hs.3828	malonalate (diphospho) decarbo	GHMP_kinases	6.0
430299	W28573	Hs.106747	serine carboxypeptidase 1 prec		6.0
413762	AW411479	Hs.848	RK306-binding protein 4 (59kD)	FKBP_TPR	6.0
402393			ENSP00000008264*CDNA FLJ20404	RasGEF,PH	6.0
422922	NM_004656	Hs.198312	RAS protein activator 1a (1)	C2,PH,RasGap,BTK	6.0
456181	L30463	Hs.1030	ras inhibitor	RA,SH2,VP68	7.9
431493	AF91463	Hs.129873	EST1, novel cytochrome P450	p450	7.9
451553	NM_001089	Hs.26630	ATP-binding cassette, sub-fam1	ABC_tran,SRP54	7.8
415758	BE270465	Hs.78793	protein kinase C, zeta	pkkinase,DAG_PE-bind,phkase	7.8
419270	NM_005322	Hs.89839	EPH1	EPH1_bdi,phkase,SAM,fn3	7.8
422837	U25441	Hs.121478	dopamine receptor D3	7bm_1	7.8
401116			Target Exon	pkkinase	7.8

426440	BE382756	Hs.169902	solute carrier family 2 (faci	sugar_tr	7.8
419635	L11329	Hs.1183	dual specificity phosphatase 2	DSPc,Phosphatase,Y_phosphat	7.8
432747	NM_014404	Hs.278907	calcium channel, voltage-depen	PMP22, Claudin	7.8
403572			Ca01244;g359533p(g)461275	tubulin	7.8
437855	A1424921	Hs.122487	ESTs, Weakly similar to A54854	RasGAP	7.7
458890	U48213	Hs.155402	D allo of albumin promotor (at	DAGKc,abZIP	7.7
424107	AB014605	Hs.139548	kinesin family member 1C	kinesin,FHA	7.7
452695	AW780199	Hs.30327	mitogen-activated protein kina	cNMP_binding,ion_tras	7.7
433262	AUT1225	Hs.204171	KIAA1535 protein	nMMP	7.7
424198	AB029010	Hs.143025	KIAA1067 protein	nMMP,Calc-beta	7.6
406456			Target Exon	SROR	7.8
422423	NM_005897	Hs.157180	Intracellular A particle-prom	BTB,Kelch	7.6
422211			KIAA0430 gene product	ion_tras,A_beta	7.6
408710	Y10256	Hs.47007	mitogen-activated protein kina	phosphatase,GAM_decarbox	7.5
457615	W96321	Hs.111460	calcium/calmodulin-dependent p	phosphatase	7.5
402760	AL110261	Hs.157211	NM_021173?Homo sapiens eosino	Glyco_hydro_18,CBM_14	7.5
422428	AJ2532	Hs.1675	DNF275663621 protein	C1q,Collagen	7.4
423579	NM_004121	Hs.1675	gamma-glutamyltransferrase-like	G_glyc,Transcript	7.4
413104	L42374	Hs.75159	protein phosphatase 2, regulat	B56	7.4
419660	BE260337	Hs.194683	solute carrier family 7 (catio	aa_pernaseases	7.4
427774	BE244179	Hs.153022	TATA box binding protein (TBP)	TAF	7.4
402635			Target Exon	F2,kirgulin,Ig	7.4
444159	AF116846	Hs.10431	dead finger (Drosophila)-like	ARID,SNF	7.4
405714			ENSP00000221137.Olfactory rece	7m_1	7.3
422732	AA257161	Hs.8659	hypothetical protein DKF2Z434E	EGF,aminin,EGF,Xlink,S_m	7.3
421758	BE373336	Hs.1422	Gardner-Rasheed feline sarcoma	SH2,SH3,phkase	7.3
415995	NM_004573		phospholipase C, beta 2	PI-PLC-XPI-PLC-Y,C2	7.3
405137			Target Exon	C1012617-gj12695979jenti(CAA70	7.3
402460			keratin 17	keratin 17	7.3
431398	BE616547	Hs.2785	KIAA1118 protein	filament	7.3
429592	AB029041	Hs.209646	Target CAT	Troponin	7.3
429225	BE256337	Hs.198273	G protein-coupled receptor 12		7.2
422015	U18548	Hs.120334	RCE1, prenyl protein protease	Abi	7.2
454373	NM_005133	Hs.188326	N-Acetylglucosaminidase	RDK	7.2
440188	AK001812	Hs.7036	polymerase (RNA) II (DNA direc		7.2
432920	U37669	Hs.3128	sac61	ecy	7.2
446143	BE245342	Hs.306079	G protein-coupled receptor 30	7m_1	7.2
422201	NM_001505	Hs.113207	protein expressed in thyroid	lactamase_B	7.1
440859	NM_014297	Hs.7486	flag structure-specific endonu	XPGL_XPG_1,5_3_exonuclea	7.1
435069	AC004770	Hs.4795	ESTs	bsp_1,Repnolysin,Pop_M128	7.1
437161	A456447	Hs.26391	a disintegrin-like and metallo	phkase	7.1
426268	AF083420	Hs.168913	serpin/threonine kinase 24 (SI	S1,SH2,Ribosomal_L23,plin	7.1
445087	AW893449	Hs.12303	suppressor of Ty (S.cerevisiae	cadherin	7.1
415377	A117930	Hs.223687	casepase recruitment domain pro	phkase	7.0
421748	NM_014718	Hs.107050	KIAA0726 gene product	pyridoxal_deC	7.0
426691	NM_006201	Hs.171834	PCTAIRE protein kinase 1	ras	7.0
428599	AB033078	Hs.186613	sphingolipase 1-phosphatase	ras,arf	7.0
411898	BE409714	Hs.44856	hypothetical protein FLJ12118	Integrin_A,FG-GAP,Rhabd_g	7.0
427010	AW136332		muscle RAS oncogene homolog	NUDIX	6.9
457305	BE268048	Hs.236494	RAB10, member RAS oncogene fam	Ig	6.9
431630	NM_002204	Hs.265829	integrin, alpha 3 (Integrin CD4	SH2,SH3	6.9
457764	AW020234	Hs.4815	muscle (nucleoside diphosphate	hypoxanthine,EGF	6.9
435575	AF213457	Hs.44234	biogenetic receptor expressed	Idh,Idh_C,adh,short,Semia	6.9
456488	AW015098	Hs.301946	ESTs, Weakly similar to T30667	Galactosyl_T_2	6.9
428761	AF236119	Hs.153076	GRB2-related adaptor protein 2	PH	6.9
430396	C40742	Hs.241363	hydrolase-binding protein 2	Id,recap,a,h3,Id_rec	6.8
422066	AW249275	Hs.343521	malate dehydrogenase 2, NAD (m	C1q,Collagen	6.8
445937	AA52943	Hs.321231	UDP-Galactose-4-epimerase beta 1-4-g	dynamh_2,dynamh,GED	6.8
457459	AA52943	Hs.274370	hypothetical protein FLJ2260	TNFR_c6	6.8
402845			NM_003102?Homo sapiens sort	RAP2A, member of RAS oncogene	6.8
416931	D45371	Hs.80485	adipose most abundant gene tra	UDP-Galactose-4-epimerase beta 1-4-g	6.8
419815	NM_002462	Hs.76391	myxovirus (influenza) resistan	Glyco_hydro_1	6.7
432950	AL036771	Hs.279859	tumor necrosis factor receptor 4	z-C9orf2,phkase	6.7
459126	W22474	Hs.301746	RAP2A, member of RAS oncogene	SH2,SH3,phkase	6.7
429542	AF036860	Hs.205713	UDP-Galactose-4-epimerase beta 1-4-g	Reprolysin,bsp_1,Pop_M128	6.7
401488			Target Exon	p450	6.7
456243	AJ455001	Hs.82380	mange a tols 1 (CAK assembly	NADHdh_2	6.7
424321	W70408	Hs.1765	lymphocyte-specific protein ty	disintegrin,Reprolysin,Pe	6.7
405187			NM_014272?Homo sapiens a disin	TPR,z-C9orf2,PHD	6.7
413055	AV655701	Hs.75183	cyclochrome P450, subfamily IIE	FAD_Synth	6.7
449496	BE376077	Hs.130849	ESTs, Weakly similar to I50022	z-C9orf2,phkase	6.7
419667	AU077005	Hs.22206	a disintegrin and metalloprote	hoxa10	6.6
417103	Z33905	Hs.81218	hypothetical protein MGC3597	7m_2,bsp_1,GPS,HRM	6.6
407687	AK020111	Hs.375558	hypothetical protein FLJ11149	serologically defined colon ca	6.6
456469	NM_005109	Hs.95220	oxidative-stress responsive 1	glutathione S-transferase pi	6.6
405458	W62346	Hs.58819	ESTs	proteasome (prosome, macropain	6.6
428926	NM_001702	Hs.194654	brain-specific angiogenesis in	protein tyrosine phosphatase t	6.6
404953			C1002000-gj12735712et(XP_0	keratin 19	6.6
449401	AL135401	Hs.23357	serologically defined colon ca		
429562	Hs.256795		glutathione S-transferase pi		
421547	AA499058	Hs.1390	proteasome (prosome, macropain		
430035	NM_003463	Hs.227777	protein tyrosine phosphatase t		
406867	AA157857	Hs.182265	keratin 19		

	404946			Target Exon	3Beta_HSD	6.5
	435213	AAD92510	Hs.5985	non-kinase Cdc42 effector prot		6.5
	411201	T74588	Hs.8509	ESTs, Weakly similar to C3HU c	A2M_NA2M	6.5
	419344	U94905	Hs.277445	diacylglycerol kinase, zeta (1	ank.DAGKa.DAGKa.DAG_Pe-6i	6.5
	425194	T50172	Hs.2001	fibronectin A synthase 1 [rat	p450	6.5
	424681	AAD54400	Hs.151706	KIA0134 gene product	helicase_C_PKR	6.5
	417903	NM_002342	Hs.1116	lymphoxin beta receptor (TNF	TNFR_p6	6.5
	408935	AV55573	Hs.861	Target CAT		6.5
	438646	A973076	Hs.231658	matrix metalloproteinase 28		6.5
	431530	X51615	Hs.2798	leukemia inhibitory factor rec	tn3	6.5
	428883	AA436559	Hs.258802	ATPase, (Na,K) transporting, b	Na_K-ATPase	6.5
	404757			Target Exon		6.4
	403370			Interleukin 11	lypzin	6.4
	443611	NM_014397	Hs.9625	NIMA (never in mitosis gene a)	plnase	6.4
	424008	R02740	Hs.137555	putative chemokine receptor; G	7tm_1	6.4
	444912	AW247360	Hs.12124	putative prostate cancer cause	lactinase_B	6.4
	454460	X56545	Hs.743	fibroblast growth factor recep	lg plnase	6.4
	432269	NM_002447	Hs.2942	macrophage stimulating 1 recep	plnase, Sema,PSI,TIGAA_E	6.4
	458718	AJ359476	Hs.157059	ESTs		6.4
	405282			Target Exon	Cathe	6.4
	447245	AK001713	Hs.17860	hypothetical protein FLJ10851	E1_dehydrog	6.3
	442297	NM_006202	Hs.89901	phosphodiesterase 4A, cAMP-ape	PDEase	6.3
	400894			C110001293[93938014]refNP_05	7tm_1	6.3
	449446	NM_013385	Hs.7189	pleckstrin homology, Sec7 and	PHSec7	6.3
	430866	L36149	Hs.248116	chondrin (C motif) XG recep	7tm_1	6.3
	413394	NM_003595	Hs.26350	tyrosyl-protein sulfotransferase	Sulfotransfer	6.3
	436523	BE612930	Hs.5212	single-strand selective mononu		6.3
	422714	AB018335	Hs.119387	KIA0092 gene product	DUF221	6.3
	409924	AW255508	Hs.226131	homocodulin-interacting protel		6.3
	414551	A815639	Hs.76394	enoyl Coenzyme A hydratase, sh	ECH[Peptidase_U7	6.3
	413254	U40272	Hs.75253	isocitrate dehydrogenase 3 (NA	isoch	6.3
	415010	NM_004203	Hs.77783	membrane-associated tyrosine-	plnase	6.3
	449761	AB029638	Hs.22985	solute carrier family 22 (orga	magp_1	6.3
	432221	M21191	Hs.273415	aldolase A, fructose-bisphosph	glycolytic_enzy,Adeno_E3_	6.3
	414513	AB233400	Hs.76297	G protein-coupled receptor kin	plnase,RGS,plnase_C	6.2
	458516	BE010748	Hs.255097	ESTs		6.2
	417985	AA187445	Hs.33114	cyclothin, zeta (guanine red	adh_zinc	6.2
	447507	H55696	Hs.18747	POF7 (processing of precursor,		6.2
	418322	AA284166	Hs.94113	cyclin-dependent kinase inhibi	Y_phosphatase,DSPr	6.2
	428443	BE518108	Hs.184326	CDC10 (cell division cycle 10,	GTP_CDCM	6.2
	423229	AC033855	Hs.126332	protease, serine, 35	lypzin	6.2
	408903	BE244377	Hs.48876	farnesyl-diphosphate farnesyl	SOS_PSV,dsm,z-alpha	6.2
	426176	AB000482	Hs.167879	SH3-domain binding protein 2	PH,SH2	6.1
	421355	D50204	Hs.1623	pyruvate dehydrogenase (lipom	E1_dehydrog	6.1
	435517	S50271	Hs.241587	solute carrier family 5 (neuro	SNF	6.1
	435906	A686379	Hs.110796	SAR1 protein	arf/ras	6.1
	402786			C1001899[ap112722635]refXP_0	Glyco_hydro_18	6.1
	434202	BE382411	Hs.3784	guanylate kinase 1	Guanylate_kin,CoaE,Viral_	6.1
	402115			NM_0216243:homo sapiens histami	7tm_1	6.1
	407601	AC002200	Hs.37129	sodium channel, nonvoltage-gat	ASC	6.1
	404679			Target Exon		6.0
	450739	A1732707		ESTs, Weakly similar to ALU2_H	V1R	6.0
	437889	AB040949	Hs.6733	pancreas-enriched phospholipase	C2,PL-PLC-V,PL-PLC-X,RatG	6.0
	415742	BE410243	Hs.78789	thimet oligopeptidase 1	Peptidase_M3	6.0
	453190	AB002354	Hs.32312	KIA0355 gene product	PH,PHO,RUN	6.0
	435975	AW320861	Hs.6617	insulin triphosphatase (nucleo	HamIp_Rse	6.0
	412850	AW550635	Hs.74988	polymerase (DNA-directed), del	homocidic	6.0
	432805	X54630	Hs.3107	CD97 antigen	7tm_2,GPS,EGF	6.0
	418594	T74450		glycyl57c12,r1 Stratagene liver	A2M_NA2M	6.0
	417463	BE545343	Hs.82208	Acyl-CoA:sh,Acyl-CoA_sh_M	Acyl-CoA_sh,Acyl-CoA_sh_M	6.0
	419755	H19444	Hs.134846	BAT1-associated protein 3	C2	6.0
	457276	AF235097	Hs.227533	Homo sapiens chromosome X map		6.0
	423508	AJ056422	Hs.135183	centaurin-alpha	PH,ArtGsp	6.0
	432116	NS8718		glycyl55p2,r1 Soares, multipl		6.0
	427334	R44789	Hs.33191	Homo sapiens, Similar to trans		5.9
	424959	NM_005781	Hs.153937	activated p210c42Hs kinase	plnase,SH3	5.9
	453082	H18835	Hs.31608	hypothetical protein FLJ2044	ion_trans	5.9
	421168	AF182277	Hs.330730	cytochrome P450, oxidoreduct	cytochrome_P450, oxidoreduct	5.9
	422287	F18395	Hs.114346	cytochrome c oxidase subunit V	COX7A_Phage_G	5.9
	401736			C16000452[gi3127183]gHAA005	AMP-binding	5.9
	434785	AA648502		ESTs		5.9
	414862	AF273204	Hs.235376	XPHC2 protein	Exonuclease	5.9
	407338	AA773213		glucal68f10.s1 Stratagene lung	lg	5.8
	448426	BE018315	Hs.280776	tankyrase, TRF1-interacting an		5.8
	409586	AK000002	Hs.55079	Homo sapiens mRNA; cDNA DKFZp4	ADC_tran	5.8
	4530778	U61375	Hs.25450	solute carrier family 28 (nuc)	Nucleoside_tran	5.8
	423612	NM_002087	Hs.1658	guanine nucleotide binding pro	G-alpha_arf	5.8
	430845	AF024690	Hs.248056	G protein-coupled receptor 43	7tm_1	5.8
	424741	AF051941	Hs.343824	nucleoside diphosphate kinase	NDK	5.8
	412298	BE291579	Hs.75087	Fas-activated serine/threonine		5.8
	415701	NM_003876	Hs.78619	gamma-glutamyl hydrolase [con]	GATase	5.8
	423158	H97991	Hs.193313	Target CAT	MoA_NIB_PqqE	5.8
	414788	X78342	Hs.77313	cyclin-dependent kinase (CDC2-	plnase	5.8
	412915	AW087727	Hs.74823	NM_045413:Homo sapiens NADH de		5.7

5	420904	AL035964	Hs.100221	nuclear receptor subfamily 1,	hormone_reczf_C4	5.7
	415503	U36601	Hs.78473	N-deacetylase/N-sulfotransferase	Sulfotransferase	5.7
	433074	AL045019	Hs.323462	Homo sapiens cDNA FLJ112141	DEAD, helicase_C, dsm, Vira	5.7
	409124	AW525808	Hs.52727	N-acetylglucosaminidase, alpha		5.7
	428270	BE501549	Hs.107040	ESTs		5.7
10	435114	AA775643	Hs.288936	mitochondrial ribosomal protein	ODC_AZ	5.7
	422211	M18657	Hs.1867	proteasome (proteasomal) C	asp	5.7
	433054	A078088	Hs.13547	Target CAT		5.7
	423730	NM_002891	Hs.95890	polymerase (DNA directed), del	ICL	5.7
	415117	AF120499	Hs.78016	polynucleotide kinase 3'-phosph	Viral_helicase1	5.7
15	400986			Target Exon		5.7
	413163	Y00815	Hs.75216	protein tyrosine phosphatase,	Hs.3, Ig_V_phosphatase	5.7
	413858	NM_001610	Hs.75589	acid phosphatase 2, lysosomal	acid_phosphatase	5.7
	457308	AL415988	Hs.238272	inositol 1,4,5-bisphosphate re	lon_trans,RYDR,TTPR,MIR	5.7
	400551			C1001991*gtl(s624920(emb)CAB6	SROR	5.7
20	433472	AJ541246	Hs.3343	phosphoglycerate dehydrogenase	2-Hacid_DH,1,2-Hacid_DH_C,M	5.7
	402531	BE384319	Hs.54702	xylosyl protein beta1,4-galactosyl	Galactosyl_T_2	5.7
	448139	BE268315	Hs.23111	phenylalanine-tRNA synthetase	neur	5.7
	450207	T87615	Hs.14716	ESTs		5.7
	402266			NM_002850*Homo sapiens ATP-4h	ABC_tran	5.6
25	430713	AA331547	Hs.2842	autocatalytic translation elongat	GTP_EFTU,GTP_EFTU_D3,GTP_	5.6
	420911	U77413	Hs.100293	O-linked N-acetylglucosamine (TTPR	5.6
	405683			Target Exon		5.6
	449181	XS5783	Hs.22179	synaptobrevin V	C2	5.6
	414457	AW514320	Hs.76159	ATPase, H transporting, lysoso	ATP-eyn_LC	5.6
30	415193	AL048891	Hs.12185	hypothetical protein MGC14333		5.6
	434883	AW381538	Hs.19807	hypothetical protein MGC12959		5.6
	433135	AA443873	Hs.110477	deethyl-phosphatase mannopylosa	lysopl	5.6
	413049	NM_002161	Hs.823	heparin (transmembrane protease		5.6
	420899	NM_001628	Hs.100194	arachidonate 5-lipoxygenase-ac	MAPEG	5.6
35	423387	NM_001838	Hs.1652	chemokine (C-C motif) receptor	7tm_1	5.6
	434758	BE350332	Hs.134729	FXD domain-containing lon		5.6
	454112	NM_000868	Hs.40304	Integrin, alpha 4 (antigen CD4	Integrin_AFG-GAP	5.5
	405994			NM_021943*Homo sapiens ATPase,	E1-E2_ATPase,Hydrolase	5.5
	416322	BE019494	Hs.75217	pyruvate 5-carboxylate reduct	P5CR,Octopline_DH_N	5.5
40	446765	AW514373	Hs.76159	lysosomal protein Kinase 10	ptkinase,TYA	5.5
	411030	BE387193	Hs.67886	7.60 protein		5.5
	431498	AQ001777	Hs.258561	aspartyl aminopeptidase	Peptidase_M18	5.5
	433012	NM_004045	Hs.279910	ATX1 (antioxidant protein 1, y	HMA	5.5
	414807	X50726	Hs.77587	p-cyclic nucleotide 3' pho	ptkinase,POLO_box	5.5
45	424572	M18650	Hs.82088	Target Exon		5.5
	406617			glucosylase, alpha acid (Pomp	ehand,Fenile_reduct	5.4
	421893	XS5078	Hs.1437	asialoglycoprotein receptor 2	trekal,Glyco_hydro_31	5.4
	415525	T79257	Hs.823	2,4-dienoyl CoA reductase 2, p	hecl_Lc	5.4
	448093	AW977382	Hs.15888	protein tyrosine kinase 9-4b	actin_short	5.4
50	411574	BE242482	Hs.8780	CD1E antigen, e polypeptide	collin_ADF	5.4
	406432			polymerase (RNA) II (DNA direc	Sulfotransferase	5.4
	420921	Z43909	Hs.194638	calmodulin-like 3		5.4
	438337	M36707	Hs.239500	KIA0551 protein	ehand	5.4
	427162	AB011133	Hs.173864	TGF-beta1-induced anti-apoptotic f	ptkinase,PDZ	5.4
55	414216	D68970	Hs.75222	arachidonate 15-lipoxygenase,	oxidoreduct_4,myosin_head,b	5.4
	422083	NM_001141	Hs.111256	coagins VII	lipoxygenase,PLAT	5.4
	424373	AJ133796	Hs.146219	glob28305,r1 Soares_fetal_iv	C2	5.4
	449405	AA001350		Kelch-like ECH-associated prot	mlc_carr	5.4
	405983	D59822	Hs.57729	Interleukin 21 receptor	BTB,Kelch	5.4
60	435818	AJ237447	Hs.71174	hypothetical protein FLJ12116		5.4
	424357	AW361058	Hs.44856	KIA0522 protein	PH,4ZIP,IQ,Sac7	5.3
	423806	AB011094	Hs.125892	similar to silyltransferase 7	Glyco_transf_29	5.3
	432011	BE063080	Hs.274323	ESTs, weakly similar to d1207H	DEAD,GSPR_E	5.3
	450380	AJ037831	Hs.24372	tannin containing monooxygenase	FMO-like,pyr_redox	5.3
65	423378	Y02567	Hs.132821	Target Exon	p450	5.3
	427338			macrophage migration inhibitor	MP	5.3
	412276	BE262621	Hs.73798	met transforming oncogene (ker	ras,rf	5.3
	437967	BE277414	Hs.6947	prolaseroma (prosome, macrophal	PA28_alpha,PA28_beta	5.3
	424766	BE388855	Hs.152978	CGI-63 protein	adh_zinc	5.3
70	447766	NM_016011	Hs.19513	myosin IC	myosin_head,IQ	5.2
	453660	X36507	Hs.286226	mannosyl (alpha-1,3)-glycosyme	HLA_Mu_H_Jnm,Myc-LZ	5.2
	435321	BE318871	Hs.4967	protein kinase, interferon-ind	dsm,ptkinase	5.2
	423235	NM_002769	Hs.274382	synaptotagmin XII	C2	5.2
	445139	AB037848	Hs.12366	kinetin-like 3	Kinin	5.2
75	429214	AB012722	Hs.192626	thymidine kinase 2, mitochondr	thymidine_kinase_2	5.2
	432462	AJ020013	Hs.274701	ANNO2N protein	dNK	5.2
	424367	AJ739312	Hs.284163	glt:Human homeobox-like mRNA		5.2
	405697	Y15621	Hs.24612	CLP-dicacylglycerol synthase (p	Cytochrome/trans,Adeno_VII	5.1
	430321	AW111481	Hs.6509	ectonucleoside triphosphate di	SHMT	5.1
80	446108	AF039916	Hs.12330	glt:Human homeobox-like mRNA	GDA1_CD39	5.1
	419073	AW372170	Hs.163918	Homo sapiens cDNA FLJ12797	lg,bp_1,2U5	5.1
	409598	NM_001623	Hs.57697	hyaluronan synthase 1	Glycos_transf_2	5.1
	422599	AF078837	Hs.324861	RetA-associated inhibitor	SHL,ank	5.1
	424305	BE386095	Hs.112272	histone deacetylase 8	Hist_deacetyl	5.1
	427247	AW504221	Hs.174103	Integrin, alpha L (antigen CD1	wwa,Integrin_AFG-GAP	5.1
	429061	Y14039	Hs.195175	CASP8 and FADD-like apoptosis	DED,ICE_p20	5.1
	420848	XS2221	Hs.99367	excision repair cross-compleme		5.1

453337	R73417	Hs.25391	glyb2g12.1 Soares breast 2N
418910	Z2821	Hs.89466	Homo sapiens, Similar to dodec
425771	BE561776	Hs.159494	Bruton agammaglobulinemia lyso
425202			NM_017343-Homo sapiens deoxy
415452	BE560005	Hs.26433	thiolate-phosphate (UDP-N-acet
418231	AA326895	Hs.83848	triosphosphate isomerase 1
425165	NM_011483	Hs.154899	Target CAT
407676	NM_004519	Hs.40866	potassium voltage-gated channel
417831	H16423	Hs.82685	CD47 antigen (Rb-related anti
404716			NM_007313-Homo sapiens v-abl
405020			Target Exon
425236	NM_004798	Hs.168212	kinase family member 3D
433178	AB030699	Hs.253706	cystathionine lyase/CysLT2 r
429340	AW296219	Hs.115325	RAB7, member RAS oncogene fami
423414	NM_001181	Hs.6551	ATPase, H transporting, lysoso
425846	AA102174	Hs.159529	myosin D
413599	AJ005239	Hs.75438	quinoid dihydropteridine reduc
424168	L29277	Hs.321677	signal transducer and activator
436942	AF284422	Hs.119176	calion-chloride cotransporter
410775	AB014460	Hs.56196	(E.coli endonuclease III)-
428734	BE303044	Hs.192023	eukaryotic translation initiat
420340	NM_000734	Hs.97087	CD32 antigen, zeta polypeptide
433075	NM_002559		sorfin 1
403306	X23363		HER2 receptor tyrosine kinase
426811	BE239228	Hs.172609	nucleobindin 1
401577			NM_000761-Homo sapiens cytochr
409537	AA323948	Hs.55407	Homo sapiens mRNA: cDNA DKF4p
426831	BE292216	Hs.172973	S-adenosylhomocysteine hydrola
430904	U55402	Hs.248124	G protein-coupled receptor 31
423552	AF107028	Hs.129783	sodium channel, voltage-gated,
421487	AF027406	Hs.104865	serine/threonine kinase 23
421832			NM_004411-Homo sapiens glucoc
456748	AW137749	Hs.125902	ubiquitin specific protease 2
424771	BE397151	Hs.153003	serine/threonine kinase 16
404441			Target Exon
437053	AJ077018	Hs.3235	keratin 4
406644	N28522	Hs.8535	quinolate phosphoribosyltran
431204	F28841	Hs.250760	cytochrome c oxidase subunit V
405417	L36531	Hs.91296	Integrin, alpha 8
436735	L34989		mannosyl (beta-1,4)-glucosyl
441455	AJ271671	Hs.7854	zinc/ferritin regulated transport
446946	BE409053	Hs.259629	peroxisomal long-chain acyl-co
451964	AJ076998	Hs.132760	hypothetical protein MGC15729
403771			NM_003013-Homo sapiens sli (D
403248			ESTs, Weakly similar to I78855
410214	L29555	Hs.301698	slalytransferase 4A (beta-gal
407047	X59165		glt-Hsapiens SOD-2 gene for mu
422668	AF193364	Hs.119120	E3 ubiquitin ligase SMURF1
436057	AJ004832	Hs.5038	neuropathy target esterase
431262	NM_006672	Hs.251335	solute carrier family 22 (orga
406625	Y13647	Hs.119597	etacoyl-CoA desaturase (delta
426659	U55579	Hs.188599	G protein-coupled receptor 20
422716	AJ762964	Hs.205180	ESTs
414480	L00727	Hs.898	dystrophin myotonic-protein k
402687	S33329	Hs.181350	kallikrein 2, prostatic
425946	D42046	Hs.194655	DMX2 (DNA replication helicase
420028	AB014680	Hs.8785	carbohydrate (N-acetylglucosam
402912			Target Exon
443329	BE262943	Hs.9234	hypothetical protein MGC1936
426120	AA325243	Hs.168887	copine 1
430609	AA302921	Hs.247382	dimethylarginine dimethylamino
451320	AW118072		diacylglycerol kinase, zeta (1
447131	NM_004985	Hs.17465	retinoic acid receptor response
431222	X56771	Hs.273790	zeta polypeptide glycoprotein 3A
406458			C14000133-gp1082739ipr/C44
427804	AJ049554	Hs.180871	protein kinase C, alpha bindin
450748	AJ733593	Hs.247680	ESTs
427937	U03207	Hs.122511	centrin, EF-hand protein, 1
407978	AW385129	Hs.41717	phosphodiesterase 1A, calmodul
428773	BE256238	Hs.193163	bridging integrator 1
456444	AJ484517	Hs.31856	ESTs, Weakly similar to K0A414
405574			Target Exon
442414	BE408758	Hs.8297	ribonuclease 6 precursor
418289	AW403103	Hs.83951	Hermansky-Pudlak syndrome
421601	AJ650190	Hs.106070	cyclin-dependent kinase inhibit
422795	AB0331109	Hs.120965	KIAA1283 protein
433019	AJ205513	Hs.279915	translocase of inner mitochond
431522	AJ625859	Hs.258609	protein tyrosine phosphatase,
403846			seritin-related receptor, LQD
456881	AW028302	Hs.155079	protein phosphatase 2, regulat
418172	X61157	Hs.83636	adrenergic, beta, receptor kin
408433	AW162931	Hs.45002	ras-related C3 botulinum toxin
439921	AL110239	Hs.8770	LCAT-like lysophospholipase
427122	AW057736	Hs.322910	HER2 receptor tyrosine kinase

GSPIL_III	5.1
ECH	5.1
SH2,SH3,kinase,PH,BTK	5.1
mito_csr	5.1
Glyco_transf_4	5.0
TIM	5.0
ion_trans,KCNQ1_channel	5.0
lg	5.0
SH2,SH3,phnase	5.0
7tm_1	5.0
arLras	5.0
myosin_head,DAG_PE-bind_1	5.0
adh_short	5.0
SH2,STAT,STAT_bind,STAT_p	5.0
aa_permeases	5.0
HIV-GPO	5.0
WD40	5.0
ITAM	4.9
BMR	4.9
phnase	4.9
efhand	4.9
p450	4.9
Collagen	4.9
Adol-lyase	4.9
7tm_1	4.9
lg,Adeno_E3_Cr2	4.9
scd1a	4.9
FF	4.9
UCH-1,UCH-2	4.9
phnase	4.9
Aa_trans	4.9
filament-actin,Tropomyosin	4.9
ORPase,ORPase_N	4.9
dUTPase,COX6A_ras,ATP-ym	4.9
Integrin_AFG-GAP	4.8
	4.8
Zip	4.8
sugar_fr,Condensation	4.8
ECGF,lambin_G,LRRL,LRNT,L	4.8
SLT	4.8
Glyco_transf_29	4.8
scd1a	4.8
C2,WNV,HECT	4.8
cNMP_binding	4.8
sugar_fr	4.8
FA_desaturase	4.8
	4.8
phnase	4.8
tyrosin	4.8
UroD-Nalase,Viral_hole	4.8
Sulfotransfer	4.7
phnase	4.7
	4.7
C2	4.7
zf-C2H2,BAR,SH3	4.7
zona_pulchella	4.7
prolaseosome	4.7
PDZ	4.7
7tm_1	4.7
efhand	4.7
PDEase	4.7
SH3,BAR	4.7
	4.7
phnase	4.7
ribonuclease_T2	4.7
	4.6
COI	4.6
kazal_A2M,A2M_N	4.6
zf-Tim10_DDP	4.6
fr3_Y_phosphatase	4.6
td_recep_alu3,td_recep	4.6
BSS	4.6
phnase,PHRGs	4.6
ras	4.6
LACT	4.6
phnase,Furin-like,Recep_	4.6

427945	AW137156	Ha.181202	hypothetical protein FLJ10038	Collagen	4.6
451777	U08210	Ha.459	solute carrier family 18 (ves	sugar_tr	4.6
429938	BE29804	Ha.226377	phosphate cytidyltransferase	Cydidyltransf.COX6C	4.6
412974	R18978	Ha.75105	enoplamin-binding protein (btr	UO_con	4.6
414702	L22005	Ha.79532	cell division cycle 34	7m_1	4.6
425785	AJ000479	Ha.169543	endothelial differentiation, G	Rolanase.WW	4.6
422454	U40370	Ha.161362	protein (peptidyl-prolyl cis)	Methyltransf_4	4.6
408135	AA317248	Ha.42957	methyltransferase-like 1	carbamyl.Ccrbtrn.C_tarm	4.6
457388	AF033300	Ha.264157	carbamyl-like 22	Herpes_UL3	4.6
421140	AA298741	Ha.102135	signal sequence receptor, delt	Acyltransferase	4.6
434834	AF156774	Ha.324020	1-acylglycerol-3-phosphate O-a	SH2.SAM	4.6
413407	AF56293	Ha.75339	triositol polyphosphate phospho	chand_S_100	4.6
420463			NM_014024: Homo sapiens 5100 ca		4.5
17891	W79410	Ha.82867	protein phosphatase 1, regulat	ICE_p20.DED	4.5
421681	AA384922	Ha.195175	CASP8 and FADD-like apoptosis	emrintran_1_2	4.5
426516	BE26260	Ha.170197	glutamate-oxaloacetate transamin	alo_1a1.ect	4.5
418963	BE204371	Ha.89529	allo-keto reductase family 1,	phnase	4.5
423664	NM_004714	Ha.130998	dual-specificity tyrosine (Y)-	TNFR_c6,death.PHXlnk,Rh	4.5
427681	AB018263	Ha.180338	tumor necrosis factor receptor	rac.ar	4.5
423283	NM_016154	Ha.279771	Homo sapiens clone PP1598 unkn	FS_FL_type_C.plnase	4.5
10816	AL046341	Ha.75562	ABIC_membrane.ABC_tran	phnase	4.5
405546				phnase	4.5
16297	AA157634	Ha.78172	solute carrier family 25 (mito	mito_carr	4.5
421962	DE2061	Ha.288354	FabG (beta-ketoacyl-acyl-car	adh_short	4.5
15341	R02022		glycyl-HcA-1	phnase	4.5
456658	W81525	Ha.118329	ESTs. Moderately similar to GA	Neur_chan_LBD,Neur_chan_m	4.5
456662	AW327546	Ha.111024	solute carrier family 26 (mito	mito_carr	4.5
407853	AA317089	Ha.597	glutamate-oxaloacetate transamin	emrintran_1_2	4.5
455811	AW049394	Ha.5022	copper chaperone for superoxid	sodcu.HMA	4.5
453997	AW247615	Ha.37003	V-Ha-Cas Harvey rat sarcoma vi	ras	4.5
449029	N28989	Ha.22891	solute carrier family 7 (catio	aa,permeases	4.5
424829	NM_007207	Ha.1627	nerve growth factor receptor (death,TNFR_c6	4.5
425062	T22633	Ha.800478	ubiquitin-conjugating enzyme E	UO_con	4.5
429133	N13154	Ha.197116	solute carrier family 7 (catio	aa,permeases	4.5
426709	D31220	Ha.166168	peller pan (Drosophila) homolog	7m_1	4.4
414814	D14697	Ha.77333	farnesyl diphosphate synthase	polyppmny_LBP	4.4
432321	AB040967	Ha.112034	KUAI1534 protein	PH_Oxydant_3	4.4
402915			ENSP0000202567: B-carbonate t	HCO3_cotransp	4.4
418267	BE389337	Ha.83919	glucosylase 1	Glyco_hydro_53	4.4
403716	BE387267	Ha.247831	Homo sapiens. Similar to myosin	ethand	4.4
420874	X65357	Ha.336478	cyclin-dependent kinase 3	phnase	4.4
439962	AF174499	Ha.6764	histone deacetylase 6	Hist_deacetyl.Lzf-URP	4.4
400223			Eos Control	Shp1	4.4
450611	NM_004405	Ha.419	clat-hs homeo box 2	homeobox	4.4
412955	L06419	Ha.75993	procollagen-lysine, 2-oxogluta	Z0G-Fall_Oxy	4.4
435564	AF210652	Ha.16614	5(3)-deoxyribonucleosidase (dN		4.4
416121	X92762	Ha.79021	tafazzin (cardiomyopathy, dia	Acyltransferase	4.4
423323	AJ961628	Ha.127007	potassium channel, subfamily K	ion_trans	4.4
448191	NM_005881	Ha.20544	branched chain alpha-ketoadid	HATPase_6	4.4
456217	BE253181	Ha.81697	non-metastatic cells 3, protel	NOK.Arter_glycop	4.4
438415	BE263254	Ha.343258	proliferation-associated ZG4,	Peptidase_M24	4.4
429218	AA225065	Ha.198269	Target CAT		4.4
407453	AF209223		glt-Homo sapiens orphan G-pro	7m_3	4.4
425955	T95599	Ha.246549	ESTs. Moderately similar to S8		4.4
407230	AA157857	Ha.182255	keratin 19	Elament.bZIP	4.3
410197	NM_005518	Ha.83989	3-hydroxy-3-methylglutaryl-Co	HMG_CoA_synt	4.3
186409	BE1575	Ha.79300	ubiquitin-conjugating enzyme E	UO_con	4.3
447957	NM_014821	Ha.20126	KIAA0317 gene product	Filamin.HECT	4.3
421771	NM_001224	Ha.108131	casepase 2, apoptosis-related c	ICE_p20,CARD,ICE_p10	4.3
440886	AL137291	Ha.22451	hypothetical protein FLJ10357	PH_RhoGEF	4.3
414821	M03835	Ha.174204	Fc fragment of IgG, high affi	lg	4.3
431096	AA324358	Ha.249227	Homo sapiens DNA, cosmid clone		4.3
425892	NM_003803	Ha.2504	myomesin 1 (skelemin) (1850)	lg.h3	4.3
450126	BE318138	Ha.24447	sigma receptor (SR31747) bindin		4.3
131781	J05272	Ha.850	MRP (positive morphoprophyl) de	IMPDH_CIMPODH_N_CBS,NPD	4.3
406530			NM_005546: Homo sapiens IL2-in	SH2,SH3,phnase,PH,BTK	4.3
428363	AK000264	Ha.183950	hypothetical protein FLJ20277	GNT4	4.3
133554	AL037111	Ha.75641	galactase-1-phosphate uridylyl	Gulp_UDP_trans,Gulp_UDP_	4.3
432178	X76209	Ha.2913	Epib3	connasin	4.3
456529	AF014643	Ha.100072	connexin45.6	connasin	4.3
448988	Y09763	Ha.22785	gamma-aminobutyric acid (GABA)	Neur_chan_LBD,Neur_chan_m	4.3
426626	A124572	Ha.322879	inhibitor of kappa light polyp	of-C2H2	4.3
432566	AL137095	Ha.279861	CG-31 protein	thorad	4.3
428970	BE276891	Ha.194691	retinoic acid induced 3	7m_3	4.3
428953	AA306610	Ha.348183	tumor necrosis factor receptor	TNFR_c6	4.2
423922	AK001663	Ha.135458	muscle-specific beta 1 integr		4.2
426113	U86162	Ha.171290	hydroxy-methyl-Coenzyme A dehydro	adh_short	4.2
426566	AF131836	Ha.170453	tropomodulin	Tropomodulin,phnase	4.2
425179	A1224442	Ha.155020	putative methyltransferase		4.2
412715	NM_000947	Ha.74519	primase, polypeptide B4 (584)		4.2
439268	R05701		ghym5600: r1 Scars actin bra		4.2
404879			NM_030607: Homo sapiens glucose		4.2
400836			Target Exon	Apolipoprotein	4.2
430940	ZZ470	Ha.248145	melanocortin 5 receptor		4.2

	400563		Target Exon	Pep_M126_group	4.2
	430237	A1272144	DKFZP434P106 protein	abhydrolase	4.2
	425175	AF020202	UNC119 (C. elegans)-like	DAG_Pe_bnd,C2	4.2
5	400567	BE260459	putative GTP-binding protein s	nas	4.2
	419892	AJ252544	soluble carrier family 30 (cnc		4.2
	428394	AJ076472	glutaryl-Coenzyme A dehydrogen	Acyl-CoA_dh,Acyl-CoA_dh_M	4.2
	437696	ZB3844	hydrothermal protein d3JTE16.5	Hydrolase	4.2
	454334	NM_000691	aldehyde dehydrogenase 3 family	alcohol	4.2
10	411277	A751389	arginine-hydroxylase lyase	lyase	4.1
	451438	NM_012331	methionine sulfoxide reductase	PMSR	4.1
	415410	AF037332	sorting nexin 17	PX1n3,phknaase,SAMLEPH_ljb	4.1
	406538		Target Exon		4.1
	424340	AF141289	solute carrier family 7 (catio	slc_samperases	4.1
15	441164	AB023180	KIA0963 protein	helicase_C	4.1
	421318	U53973	rhodopsin kinase	phknaase,phknaase_C,GRS	4.1
	433540	A0302436	brain-specific Na-dependent in	sugar_n_BTT1	4.1
	411447	NT3703	ESTs	Glyco_hydrol_3l	4.1
	409693	AA010233	glutaryl-prolyl-4RNA synthetas	WHEP-TR5,GST_C,HGTP_antic	4.1
	403655		NM_003071-Homo sapiens SWI/SNF	SNF2_N,helicase_C,Zf-C3HC	4.1
20	411142	NM_014258	transmembrane protein 3	Galactosyl_T	4.1
	437016	AJ078761	guanine morphophosphate synthetas	GMP_synth_C,GATase	4.1
	428699	BE410690	emsl sequence (mammary tumor a	SH3,HS1_rep	4.1
	427202	BE272822	interleukin 10 receptor, beta	Tissue_fac	4.1
	421380	D31633	arginine vasopressin receptor	7tm_1	4.1
	434142	U41927	ubiquitin specific protease 5	Zf-UBP,UCH-2,UBA,UCH-1	4.1
25	427407	BE266649	ADP-ribosyltransferase (NAD, p	BRCT,PARP,Zf-PARP,PARP_po	4.1
	413749	AE293200	tyrosine kinase 2	phknaase	4.1
	411927	BE274009	glycogen synthase 1 (muscle)	Glycogen_synthase_L	4.1
	419726	U53038	bone morphogenetic protein 1	EGF_OUR,acidin	4.1
30	423814	AF105020	putative protein C-mannosyltra	PMT,MIR	4.1
	451355	NM_004197	serine/threonine kinase 19		4.1
	422958	NM_005245	protein phosphatase 2, regulat	B55	4.1
	428284	AS253762	NM_004545-Homo sapiens NADH de		4.1
	428286	AF117221	UDP-GalNAc4GlcNAc beta 1,3-ga	Galactosyl_T	4.1
35	443639	BE269042	proteasome (prosome, macropain	proteasome	4.1
	410039	AF207989	Homo sapiens, Similar to G pro	7tm_3	4.1
	431066	AF026273	interleukin 1 receptor-associat	phknaase,death	4.1
	452715	Z21693	ribosomal protein S6 kinase, S	phknaase	4.0
40	403892		NM_007037-Homo sapiens a dist	Reprolysin_top_1,Pep_M12B	4.0
	442549	A751621	TNF receptor-associated factor	Zf-C3HC,MATH,Zf-TRAF	4.0
	427239	BE270447	ubiquitin carrier protein	Ubl_con	4.0
	451125	AA015779	ESTs	Y_phosphatase	4.0
	425081	X74794	mitochondrion maintenance def	MCM	4.0
45	402171		Target Exon	C2	4.0
	402665		Target Exon		4.0
	420148	U34227	myosin VIIA (Usher syndrome 1B	myosin_head(IQ,MyTH4,SH3)	4.0
	421187	U58487	5-hydroxytryptamine (serotonin	7tm_1	4.0
	412658	AF096011	dishevelled 1 (Drosophila) to D	PDZ,DEP,DUX,Dishevelled	4.0
50	425786	U53524	protein tyrosine phosphatase, S	tn3,tyr_phosphatase,DSPE	4.0
	424288	AW137198	Phosphatidylethanolphosphatase		4.0
	425230	AW135360	ESTs	phknaase	4.0
	408449	NM_004408	dynamitin 1	PH-GEF,dynamitin,dynamitin_2	4.0
	422883	AF250258	ATP-binding cassette, sub-famil	ABC_7tm_phosphoRC,SRP54,Ca	4.0
55	422676	D28481	histamine receptor H1	7tm_1	4.0
	458639	BE247683	dual specificity phosphatase 1	DSPE	4.0
	402726		C13000717g112537g1p26196	DEAD,helicase_C	4.0
	405370		NM_005567-Homo sapiens LIM do	phknaase,LIM,PDZ	4.0
	413654	AA331881	peroxiredoxin 3	AhpC-TSA	4.0
60	423917	NM_014125	PROQ327 protein	sugar_3	4.0
	445332	AA611767	hypochlorite protein DKFZ564L	integrin_B,EGF	4.0
	424512	X53002	Integrin, beta 5		4.0

TABLE 22B:

Pkey: Unique Ecs probotid identifier number

CAT number: Gens cluster number

Accession: Genbank accession numbers

	Pkey	CAT Number	Accession
70	410191	11824_1	AE609645 AB182011 AA548024 A1278970 AA688086 AA858275 F21973 W95840 AW965644 X99726 AA431579 AA937087 AB850805 AB578365 BE565516 AA725824 A1000071 AW242322 AW007204 WE8289 AA431450 AW466973 BE222544 AA483454 A9168050 WS9795 AJ381017
	415341	1534442_1	AA78726 AB040976 AA89
	415995	1564_1	RO0862 242921 F36132
75			NM_004573 MS5878 BE242666 AW504110 AW408049 AW402205 AA747879 AW530959 AA439623 AB339994 AW751282 AW374413 AW578823 H18054 AA310456 16 12578 7T4300 AA533176 AW50138 AW950600 AA910221 AS24064 AW183098 AW678231 AT677111 AA229323 AA42290 AA465038 A
	418964	1089680_1	T74640 T74459
	424339	23827_1	BE257749 BE312111 AF219137 NM_015720 BE313698 BE382652 BE252205 BE251553 F12128 T86200 BE255805 BE254484 AA324183 H07952 AL134164 AB187802 A104071 A282924 AW192547 A1652760 A126471 A1083778
80	427010	27436_1	AW136332 AW207450 AW139531 AW139563 NM_012219 AF049338 AA4331986 AA084600 AW597599 BE351105 AA050260 A1063698 AA324154 A1312208 BE030901 AL118847 AW4458 A16518 AA453121 A14863 A14337355 BE174009 AA350765
	427239	27647_1	BE270447 AW409021 BE267288 BE207170 D56305 BE263223 BE408171 BE263243 BE392439 BE292736 BE261776 BE314300 BE267719 BE268815 BE13876 BE296291 BE297066 AA621052 BE407519 AW3344 BE622905 AW248281 AW250313 T19021 AA353115 AA316879 BE289633 BE621936 AA390724
	427326	277229_1	AE287878 AB041160 AA400787

42542	29266_1	D79889 NM_014770 U0131 AA32392 AA984512 H38328 AL120358 AL134787 AL134589 AIG37763 AIG71506 AA528909 AIG51627 AW243560 AA939009
428948	29373_1	BE514362 AIG75343 BE272670 BE616390 AW163444 AW161588 AW378754 AW238803 BE267205 BE047748 BE207213 BE312782 BE256301 BE289413 BE270346 BE280865 BE278633 BE291147 BE407786 BE378176 BE392818 AW377597 BE389591 BE353978 AW327453 BE393411 BE385795 BE275656 BE3
432118	34702_1	NS8718
432469	34657_1	BE270533 NM_016577 AF166492 BE276152 AF091031 AA908507 U06653 AIG70333 AA682567 AW593957 A148105 AW002401 AIG37463 AIG71185 AA304349 A13006 F23451 AHS51050 A233819 A1324119 A19618 AIG93314 Z46114
433075	35820_1	NM_022693 XS8248 AA233278 AA845376 AA705590 AA705533 BE327147 AW291971 AA071125 A1198417 AIG56213 A1168442 AIG33078 A475049 H85459 A90895 AA888000 AA18326 AA118378 N71981 AL043634 AA426361 AA418275 AA232975 AL036861 BE277220 BE387505 NS9710 AW375004 A
43494	3679_1	AB023990 U04534 C12115 H13005 H11553 H14256 A6665 Z40857 BE218899 A457785 BE550988 AIG93847 AAG61017 H40944 M79617 H59447 H80900 BE585719 BE550952 AW005546 AIG32686 AIG28848 H42324 R44075 AIG94849 AIG85638 AIG20772 BE590729 R43116 H40212 H40089 AA018091
434755	392764_1	AA548502 AA814385 AW957611 AA7458117
436735	425_1	L84869 AL022312 U131789 A781974 A1343437 AIG7512 AIG53032 AUST1173 H44868 AA743691 H47026 AIG31358 AAC23955 AAT13585 AW502618 AW500556 AW501353 AW499765 AA339125 H19141 H29645 R18883 AW455375 AA326081 AA406015 BE263559 NS2684 A
440242	489536_1	AW295871 A1005144 AA309877 T52634 AIG28684 AA875659 BE171353 AIG76733 AW510907 AIG742007
449405	80551_1	AA001350 A2023114 H83070 R06660
450739	844517_1	AIG73707 A742120
451320	86276_1	AA118072 AIG31982 T15734 AA224195 AIT01458 W20198 F26326 AA806057 N90552 AW071907 AIG71352 AIG75892 T03517 R88265 A124008 AA224388 AIG84316 AIG54586 T33652 A140719 AIG729211 T03490 AIG372637 T15415 AW205936 AAG30384 T03515 T33230 AAG7131 AA443303 T33623
459298	930107_1	R88701 R84600 AL157555_

TABLE 22C:

Play: Unique number corresponding to an Exon probelet

Ref: Sequence exon. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham L. et al." refers to the publication entitled "The DNA sequence of

human chromosome 22" Dunham, et al. (1999) Nature 402:489-495

Strand: Indicates DNA strand from which exons were predicted

N1_position: Indicates nucleotide positions of predicted exons

Play	Ref	Strand	N1_position
400471	9331670	Minus	105829-105750
400518	9786703	Plus	37246-37774
400521	9851071	Plus	40829-40934
400563	9844011	Plus	81941-82434
400565	9863505	Minus	93178-93429
400726	8118959	Plus	51524-51786
400748	8119053	Plus	84237-84398
400772	8131629	Minus	34896-35021,41078-41197
400833	8705148	Minus	167595-168138
400836	8854179	Plus	6771-1168
400843	9188605	Plus	5863-5870,7553-7784,8892-9023,9673-9807,10634-10789,15254-15403,23827-23958
400845	9188605	Plus	34428-34612
400846	9188605	Plus	38310-39474
400894	9385307	Minus	84507-85554
400933	7551535	Minus	106330-105503
400985	8085497	Minus	5856-6006,6236-6402
401118	9586714	Minus	111939-112126
401134	7210005	Plus	61210-51408
401180	9438548	Minus	150981-152128
401215	9858408	Plus	103739-103819
401281	9800073	Minus	13622-15136
401454	9169223	Plus	114659-114832
401488	7341775	Plus	54523-54686,55364-55451,55737-55846,59047-59175,59261-59356
401507	7534110	Plus	71055-71259
401510	7622246	Minus	46835-47126
401542	8072807	Plus	67655-67840
401577	9280797	Minus	139377-139674,141195-141281,142217-142340
401736	3219338	Plus	1771-1894
401885	8140731	Plus	148234-148321,150365-150559
401935	3603961	Plus	46320-46473
401960	3249127	Minus	67589-68091
402053	8083229	Plus	62703-63179
402115	8547582	Minus	101750-102018
402171	8575998	Minus	76357-76514,83258-83476
402183	7658390	Minus	100618-104298
402191	8576073	Minus	68410-69583
402207	8576119	Plus	41683-41681
402209	8576119	Minus	63315-63472
402211	7689783	Minus	67414-68229
402338	6357691	Minus	35915-37250
402393	9929688	Plus	19813-20084,20163-20263
402453	7534025	Plus	41-631
402460	9795884	Minus	109501-109254,110246-110591,113613-113960
402463	9795896	Minus	8818-8952
402478	9797301	Minus	108204-108335
402487	9757775	Plus	69894-69452
402532	9931258	Plus	101166-101419
402651	7950351	Plus	174215-174380
402665	8077033	Minus	11824-12090,14290-14544
402758	9213969	Plus	87638-87924

402260	9213869	Plus	136829-136952,137336-137521
402823	8217451	Plus	57916-58170,58475-58759,59580-59867
402912	7253904	Plus	145965-146257,150876-151388
402915	7405502	Minus	140-276
402916	7405502	Minus	361-474,541-687
403213	7630897	Minus	162572-162739,164442-164540
403248	7656333	Minus	167439-167606
403268	7230552	Minus	73332-72862
403379	9438244	Minus	117348-117560
403655	8736053	Plus	65668-65893
403672	7283286	Minus	96500-96881,96951-97280,97393-97594
403692	7367364	Minus	53903-53538
403711	7770482	Plus	11290-113045
403949	7711972	Minus	1731-1941
404199	6010176	Minus	1669-2740
404227	8152087	Plus	127737-127796,128080-128210,129888-130054,132545-132869
404228	8152087	Plus	135255-135486
404586	9958262	Minus	104807-105043
404676	9797204	Minus	56167-58342,58056-58183,58891-59048,60452-60528
404716	9797204	Plus	125954-126292,126591-127011,127774-127893
404716	9838969	Minus	123145-123417
404757	7706327	Plus	100933-101083,101580-101782
404879	5103013	Plus	78349-78473,78693-78893
404846	7382189	Plus	134445-134750
404953	7387324	Plus	16588-17031
404968	6899755	Plus	39287-39306
405020	7137674	Plus	106606-107309
405137	8570507	Plus	158969-159423
405187	7228926	Plus	117025-117170,118567-118736
405202	7230116	Plus	40209-40429
405282	3810573	Minus	10482-10689
405370	2078469	Plus	38998-39111
405371	2078469	Plus	47857-47758,48461-48596
405473	8439781	Plus	153074-153343,154501-154598,156879-156999,158863-159051,159910-160053,161109-161229,163035-163131,165163-165259,165869-166003,167375-167552,169252-169364,171127-171281
405474	8439781	Plus	172055-172175
405546	1054740	Plus	124010-124183
405574	3820481	Minus	33200-33646
405594	6960456	Plus	161628-161734,162823-163014,164439-164652
405583	4506157	Minus	21701-21864
405607	4309223	Minus	56765-57010,57696-58016
405714	4156179	Minus	42789-43553
406128	9159110	Plus	50425-50876
406370	9256130	Plus	125320-125482
406432	9256104	Plus	3804-3903,4025-4120,4929-5109
406441	9280715	Plus	26200-26458
406458	9786020	Plus	145874-146911
406495	7711328	Minus	174681-174978
406496	7711328	Minus	178947-179264,181779-182087
406530	7711474	Minus	11703-11860,14711-14829,14920-14984,16232-16448,16916-17067
406538	7711478	Plus	35196-35367,36229-38476,40050-40216,43522-43840
406591	8224220	Minus	2117-2227,2436-2540
406617	8439858	Plus	35430-35552

Table 23A lists about 779 genes up-regulated in ovarian cancer compared to non-malignant adult ovaries. These were selected as for Table 20A, except that the ratio of "average" ovarian cancer to "average" normal ovaries was greater than or equal to 4.0, the "average" ovarian cancer level was set to the 93rd percentile value amongst various ovarian cancer specimens, the "average" normal adult tissue level was set to the 93rd percentile value amongst various non-malignant adult ovaries, the "average" ovarian cancer value was greater than or equal to 200 units.

TABLE 23A:

Play: Unique Eos probe/identifer number

Ex. Acen: Exemplar Accession number, Genbank accession number

UG ID: UniGene number

Title: UniGene gene title

Protein Dom.: Predicted protein domain

R1: Ratio of tumor to normal ovaries

Play	Ex. Acen	UG ID	Title	Protein Dom.	R1
421296	NM_002666	Hs.103253	perlepin	perlepin_SS	37.8
427897	AA770561	Hs.146170	hypothetical protein FLJ22969	SS,TM,2F-DHHC	23.2
433028	AB005532	Hs.31442	Rac2 protein-like 4	DEAD,holcinase_C,Fork_head	27.6
441021	AW575716	Hs.7644	H1 histone family, member 2		27.2
422310	AA316622	Hs.98370	cytochrome P450, subfamily IIS	SS,TM,phosphatase,h3,hg	26.5
434017	AW023617	Hs.347130	hypothetical protein FLJ22709	SS,TM,myosin_head,RA,DAG	25.9
434242	AB124148	Hs.52895	hypothetical protein FLJ14096	SS,TM	25.8
435017	AA336522	Hs.12854	angiotensin II, type I receptor		25.0
409518	BC384836	Hs.3454	KIAA1821 protein	SS	23.3
410418	QJ1362	Hs.63325	transmembrane protease, serine	SS,TM,h1_receptor,atrypsin	22.8
43924	AB863897	Hs.125293	EST4	SS	22.7
46374	AA329256	Hs.24756	EST4, Moderately similar to al		22.6
431773	BC409442	Hs.268557	pleckstrin homology-like domain	PH,SS,LIM,Tropomyosin	21.4
420639	AF230582	Hs.28590	hypothetical protein MGC10870	SS,CS,UPF0135,Glyco_hydro	21.4
413436	AF230583	Hs.65061	sphingosine kinase 1	DAGK	21.2

424420	BE614743	He.146688	prostaglandin E synthase
422645	L40027	He.118890	glycogen synthase kinase 3 alp
436725	BE045223	He.136912	hypothetical protein MG107096
422088	H03117	He.111487	similar to mouse neuronal pr
428556	AW130399	He.86989	ESTs
434068	AA977835	He.127274	ESTs
423767	H18283	He.132753	F-box only protein 2
423852	AF032122	He.130712	Homo sapiens clone Z3929 mRNA
422179	AF078119	He.112657	dymin, axonemal, intermediate
441356	BE394351	He.182885	ESTs, Weakly similar to JC024
418569	WQ3191	He.28907	hypothetical protein FLJ20248
423631	H05373	He.165553	hypothetical protein FLJ2543N
439108	AW153034	He.84567	synaptophysin 3
451643	M54437	He.234739	breakpoint cluster region
434518	HE6995	He.37372	Homo sapiens DNA binding popt
413244	AW955951	He.159265	kuppel-related zinc finger pr
455642	AW451523	He.105752	putative c-Myc-responsive
458177	NM_012391	He.79414	RD6 antigen
490261	BE315042	He.19210	prostate epithelium-specific E
414337	U24266	He.77448	hypothetical protein MG011306
401278			aldolase
444804	A0084452	He.22158	Target Exon
406520	M81105	He.146550	hypothetical protein FLJ21988
421485	A553007	He.149152	myosin, heavy polypeptide 9, n
416983	AA455588	He.62406	ESTs, Weakly similar to RHOP M
442620	C00138	He.8535	hypothetical protein FLJ22573
406501	M14624		Homo sapiens mRNA for KIAA1668
416006	AA224251	He.78950	glutathione 4-beta-galactosyltran
455557	AW955839		branched chain keto acid dehyd
418819	U77735	He.80205	gbvCv4-BND044-110200-105-b07 B
444441	AW613941	He.301304	p1m-2 oncogene
409198	M8353		hypothetical protein MG03101
407605	WQ3512	He.6479	g1riforme sapiens DNA-binding pr
447304	Z98883	He.18079	hypothetical protein MG13272
402385			phosphatidylinositol glycan, c
407787	W15308	He.38623	Target Exon
432931	AF174487	He.233753	hypothetical protein
439233	AA031893	He.292787	Bcl-2-related ovarian killer p
423801	NM_015071	He.132942	hypothetical protein FLJ23109
433397	AE64523	He.105607	GI1Pase regulator associated wi
411570	BE144594	He.314341	carbonate transporter relatd
400206			ESTs
457941	A004525	He.14587	Eos Control
412874	X04106	He.74451	ESTs, Weakly similar to AF1518
400480			calpain 4, small subunit (30k
417595	AA424317	He.62259	C11002253-g[1]129081p[1]23287
428758	AA433988	He.95952	KIAA1681 protein
424707	BE261914	He.10944	CA125 antigen; mucin 16
444359	AW097180	He.143394	Homo sapiens cDNA FLJ14476 fs
435158	AW663317	He.85598	ESTs, Weakly similar to HS4L_H
407688	W25317	He.37616	DAZ associated protein 1
452503	R03917	He.301338	Human U9 splice variant 8 mRNA
427448	BE245449	He.2157	hypothetical protein FLJ11297
406230			Wiskott-Aldrich syndrome (ecze
432143	AD040183	He.123484	Target Exon
435573	AF234387	He.37652	Homo sapiens, clone IMAGE4178
413726	AJ278465	He.75510	cardiitis, EGF LAG seven-pass G
431974	AW972689	He.200934	annexin A11
428167	AA770021	He.16322	ESTs
450451	BE498031	He.46736	ESTs
412738	N34731	He.74582	hypothetical protein FLJ23476
445434	BE391690	He.9265	siah binding protein 1; FBP in
444008	BE344655	He.236572	hypothetical protein FLJ20917
444410	BE387360	He.33719	ESTs, Weakly similar to SFRM_H
444607	AW405635	He.293687	ESTs, Moderately similar to SE
404333			ESTs
401210			C7001735-g[7]776653b[3b]RAA95
424743	AD63410	He.293687	C12000519-g[7]776646b[6b]RP_05
434030	AW162336	He.3709	thrombospondin S18
450029	AW073380	He.267653	low molecular mass ubiquitinone-
439632	AW410714	He.334337	hypothetical protein FLJ10535
438185	Y19188	He.320461	hypothetical protein MG04248
432031	AF039196	He.272367	ESTs
405371	W37608	He.194492	halfheart protein (putative sin
459130	AA115811	He.6839	NM_005569-Homo sapiens LIM do
459577	A0002252	He.169758	ESTs
420029	BE258876	He.94446	ras homolog gene family, membe
446225	BE246743		hypothetical protein FLJ20245
432665	ZB3345	He.127610	polyamine-modulated factor 1
459216	AW024282	He.104938	hypothetical protein FLJ22635
451721	NM_006946	He.26915	acyl-CoA:cholesterol A dehydrogenase
421445	AA913059	He.104433	hypothetical protein MG015906
			spectrin, beta, non-erythrocyt
			Homo sapiens, clone IMAGE-4054

431354	BE046956	Hs.251673	DNA (cytosine-5)-methyltransf	SS,PWWP,FH0	9.7
433780	NM_012068	Hs.9754	activating transcription facto	bZIP,NTP_transf_2,SS,TBC	9.7
448133	AA723157	Hs.73769	folate receptor 1 (adult)	Folate_rec,SS	9.7
444202	AL031686	Hs.12785	KIAA0339 protein	SS,TM,NA_H_Exchange,ABC2	9.7
427640	AF092823	Hs.180016	D-dopachrome tautomerase	WIF,NA_H_UGT_L2,SS	9.6
419167	AI589535	Hs.94876	ESTs, Weakly similar to A35363	SS	9.6
424618	L23472	Hs.1802	major histocompatibility compl	TM,Ig,MHC_II_beta,SS,TMA	9.6
427497	AW139476	Hs.31240	ESTs	SS	9.6
429423	AA527718	Hs.88218	ESTs	SS	9.6
414756	AW451101	Hs.159489	ESTs, Moderately similar to JC	hexokinase2,hexokinase	9.6
407853	BE408359	Hs.43621	Homo sapiens, Similar to hypot	SS,SS,ar,rs,na,rs	9.5
408294	BE111732	Hs.12785	gCtMD-HT101-061099-032-037 H	Ammonium_transp	9.5
422332	AJ37618	Hs.337460	ESTs, Weakly similar to A47052	SS,TM,TGFb_propagatio,TGF	9.4
416866	AA227336	Hs.80324	serfs/threonine protein phosph	Metatophos,Metatophos	9.4
419823	AW271708	Hs.118918	ESTs, Weakly similar to M20M_H	SS,TM	9.4
422625	AW504638	Hs.155976	culin 4b	SS,SS,Culin,Culin	9.3
401264			C18000007(gg678655)ratNP_0	SS,laminin_Mem,laminin	9.3
407507	U73799		gCtHuman dyadactin mRNA, parlia	SS,TM,HCC3, cotransp,CAP_G	9.2
400833			C1100080(gg374644)gHAAEC99	SS,TM,7m_1	9.2
422064	AW452589	Hs.335742	ESTs	TM	9.2
424334	D30334	Hs.25549	C-type lectin-like receptor-1	lectin_c,SS,TM	9.2
421353	NM_001381	Hs.103854	docking protein 1, 62kd (downs	PI,URS,TM,PI,URS,hyprin,	9.1
427397	AF29585	Hs.177656	calmodulin 1 (phosphorylase ki	ehand,RmaA0,SS,ehand	9.1
431462	AW536572	Hs.256311	gran-1ike neuroendocrine pep	SS	9.0
434786	AAJ12046		ESTs	SS,myb_DNA-binding,myb_DN	9.0
422639	AF293777	Hs.173724	creatine kinase, brain	ATP_gua_P,Tranas,ATP_gua_Pi	9.0
407867	AI525268	Hs.164303	ESTs	TM	9.0
442472	AW908689		gCtMRD-ST0020-081199-004-c03 S	SS,TM,Ins-1-P_gynth,Ocd	9.0
455588	AI129913	Hs.174669	vesicle-associated membrane pr	synaptobrevin,SS,TM	8.9
454319	AW247736	Hs.101617	ESTs, Weakly similar to T32527	SS	8.9
429527	AA454184	Hs.289014	ESTs	SS,TM	8.9
422603	AA554820	Hs.105794	UDP-glucose:glycoprotein glucos	pherase	8.9
410338	WD2445	Hs.30205	gCtZellf11.1 f11 f20es melanocyt	WD40	8.9
452833	BE559681	Hs.30736	KIAA0124 protein	SS,Ig,SS,G_glu_transpept	8.8
417383	AF035032	Hs.181125	gCtHomo sapiens clone MCAIL my	SS	8.8
414413	BE294877		gCt501174162F1 NIH_MGC_17 Homo	SS	8.8
417165	AF124049	Hs.268541	novel SH2-containing protein 1	SH2,SS,TM	8.7
421694	BE387430	Hs.105890	byrsin-like		8.8
453583	AL079854	Hs.118598	Homo sapiens mRNA for KIAA1878	SS	8.8
418736	118979	Hs.87908	Smc2-related GTP activator pro	SS,helicase_CAT_hook,SS,	8.7
450586	AL137800	Hs.348012	Homo sapiens mRNA: cDNA DNFZp4		8.7
419725	U65048	Hs.92683	Homo sapiens clone 161455 Brea		8.7
415126	D60945		gCtULM141D04B Clontech human f	SST,M	8.7
403301			Target Exon	TM	8.6
418843	AJ251016	Hs.89230	potassium intermediate/alpha c	TM,CaMBD,SK_channel,TM	8.6
433396	AI742071	Hs.133205	ESTs	SS,TM	8.6
434333	AA186733	Hs.292154	stromal cell protein		8.6
407065	Y10141		gCtH.sapiens DAT1 gene, parlia	SNF,SS,TM	8.6
453851	AW172191	Hs.213117	ESTs	SS,Sema	8.6
422418	AK001393	Hs.116385	hypothetical protein FL10521	RhoGEF	8.6
447859	AK002194	Hs.19851	peroxisomal biogenesis factor		8.6
420636	AW595453	Hs.204959	hypothetical protein FL14896	SS,me	8.6
429099	BE439522	Hs.196177	phosphorylase kinase, gamma 2	pherase,SS,SNF2_N,helicase	8.6
419639	AK001502	Hs.91753	hypothetical protein		8.6
429712	AW245825	Hs.211914	ENSPO0000233627-NADH+ubiquino	oxidoreduct_g8,SS,TM,mm	8.5
452554	AW545434	Hs.58006	ESTs, Weakly similar to ALIE_31	SS,PAS,HLH	8.5
441076	N49809	Hs.11197	Homo sapiens, clone IMAGE:3343		8.5
428660	U38291	Hs.194301	microtubule-associated protein	M	8.5
421901	AB014554	Hs.109299	protein tyrosine phosphatase,	SAM,SS,SS,TM,POZ	8.4
441383	AW462011	Hs.128625	ESTs, Weakly similar to A46302	SS,TM,SP20,Tm_1	8.4
443801	AW205842	Hs.535394	litteral c1: licheninophagelarg	GATA	8.4
432862	AW004958	Hs.236720	aminoleucine protein	SS,MATHcd-TRAF_zf-CSHCH4	8.4
431849	AI670823	Hs.85573	hypothetical protein MGC10911	SS,TM	8.4
423652	AK001035	Hs.130881	D-cell CD1 lymphoma 11A (pne	SS	8.3
403365			Target Exon	SS	8.3
425694	U51333	Hs.159237	hexokinase 3 (white cell)	hexokinase,hexokinase2,he	8.3
423098	AA321980	Hs.204692	ESTs	SS	8.2
434552	AA633616	Hs.325116	Homo sapiens, clone MGC-2952,	SS	8.2
418361	AW525358	Hs.12450	gCt14H-F-BND-04u-d-03-0JL-1		8.2
427433	D82070	Hs.177972	chromosome 4 open reading fram	SS,pherase	8.2
420138	BE268854	Hs.177729	ESTs	SS	8.2
425391	AW181050	Hs.169611	second mitochondria-derived ac	SS	8.1
457613	AA598869	Hs.173707	ESTs	SS	8.1
427502	AI811865	Hs.7133	Homo sapiens, clone IMAGE:3161	SS,TM,ABC_tran,Glyco_tran	8.1
437215	AL117488		Human clone 23554 mRNA sequenc		8.1
423384	AL133632	Hs.127808	Homo sapiens mRNA: cDNA DNFZp4		8.1
447161	AB222113	Hs.92678	Homo sapiens clone CDAB0014 m	SS,TMLRR,aminoltran_1_2	8.1
431898	AK000020	Hs.272018	hypothetical protein FL2J0013		8.0
454291	AW364847	Hs.213534	ESTs, Weakly similar to MUC2_H	SS,XRCC1_N,BRCT,Jactamase	8.0
430054	AW364810	Hs.233764	human homolog of Drosophila Sc	SS,TM,lg	8.0
453002	NA_022914	Hs.365566	LM domain kinase 1		8.0
422765	AW407901	Hs.1578	baculoviral IAP repeat-contain	BIR,TX,SS,TM	8.0
425944	AK000664	Hs.164256	hypothetical protein FL2J0657		7.9
450873	BE464016	Hs.238956	ESTs	SS,zf-C2H2,mm	7.9

454246	AW045185	Hs.6596	ESTs	7.9
450535	AW403854	Hs.25237	mesenchymal stem cell protein	7.9
422305	AS92842	Hs.293438	ESTs, Highly similar to AF1984	7.9
425760	D17629	Hs.159479	galactosaminase (N-acetyl)-6-oxid	7.9
413534	BE148661	Hs.159479	gb:UVA.HT022:c111189.9-9.12 H	7.8
446391	AD48856	Hs.21627	gb:U05a05.a2_NCG_OCOP_Lu26 Ho	7.8
421726	AK001237	Hs.319088	hypothetical protein FLJ10375	7.8
427461	AA531537	Hs.332040	hypothetical protein MGC33010	7.8
448933	KU71630	Hs.9018	KIA-0144 gene product	7.8
443136	NM_001440	Hs.9018	exostoses (multiple)-like 3	7.8
427725	U66839	Hs.180533	mitogen-activated protein kinase Target Exon	7.8
409323	AA773820	Hs.63970	ESTs	7.8
419757	AA56983	Hs.196446	ESTs	7.7
458834	AA629286	Hs.332053	serum amyloid A1	7.7
452399	BE113301	Hs.29344	hypothetical protein, clone 24	7.7
435543	NM_002212	Hs.5215	Integrin beta 4 binding protein	7.7
418181	AB040972	Hs.301696	hypothetical protein FLJ11560	7.7
414534	BE257293	Hs.76366	BCL2-antagonist of cell death	7.7
455885	BE153524	Hs.180455	gb:PMO-H10339-241195-002-C03 H	7.7
427721	AB52843	Hs.180455	RAD23 (S. cerevisiae) homolog	7.6
430432	AB037758	Hs.241419	KIAA1337 protein	7.6
427273	AW139032	Hs.107376	hypothetical protein DKFZp434N	7.6
450334	AF035959	Hs.24879	phosphatidic acid phosphatase	7.6
413564	BC260120	Hs.63042	gb:GDI145999.F1.NH.MGC_19 Homo	7.6
410357	AF217517	Hs.63042	DKFZp564J157 protein	7.6
438539	BE346395	Hs.121589	ESTs	7.5
400286	AA180756	Hs.340316	C150009222.gi7499103.pri.gi7209	7.5
415472	BE243136	Hs.86947	ESTs, Moderately similar to AF1984	7.5
415841	BE243136	Hs.86947	a disintegrin and metalloprotease	7.5
419492	AA243547	Hs.19447	PDZ-LIM protein mystique	7.5
420970	AA305079	Hs.1342	cytochrome c oxidase subunit V	7.5
420485	AA458653	Hs.201881	Target Exon	7.4
448043	AA458653	Hs.201881	ESTs	7.4
401724	M77840	Hs.1757	C16001374.gi7550863.ref(NP_03	7.4
428952	AW579343	Hs.1757	L1 cell adhesion molecule (hyd	7.4
453023	AW028733	Hs.31439	serine protease inhibitor, Kun	7.3
400137	W94824	Hs.11985	Eos Control	7.3
436127	AA131325	Hs.88154	Riken cDNA 2010100012 gene	7.3
432747	NM_014404	Hs.278907	ESTs, Moderately similar to AF1984	7.3
448859	BE272446	Hs.265317	calcium channel, voltage-depen	7.3
407619	ALD50341	Hs.37165	hypothetical protein MGC2562	7.3
425299	AB229453	Hs.347468	collagen, type IX, alpha 2	7.3
401674	W94824	Hs.11985	hypothetical protein MGC213102	7.3
412289	AW935567	Hs.170162	C16001417.gi7550345.pri(T21	7.2
424158	AB025010	Hs.143026	KIAA1357 protein	7.2
412173	T71071	Hs.8882	KIAA1087 protein	7.2
438113	AA467908	Hs.8882	gb:GDI0565.1 Stratiotes llyer	7.2
429669	AB070108	Hs.15977	ESTs	7.2
439553	AW247529	Hs.6793	Target CAT	7.2
425041	AJ377130	Hs.152014	platelet-activating factor acc	7.2
448340	AA492010	Hs.32362	ESTs	7.2
406779	AA412048	Hs.275574	CGI-39 proteic; cell death-reg	7.1
431005	AA490544	Hs.127269	ESTs, Weakly similar to T02345	7.1
421273	AJ245416	Hs.103106	US onco-associated Sm-like pr	7.1
409649	AA159216	Hs.55505	hypothetical protein FLJ20442	7.0
430281	AB78842	Hs.237924	CGI-49 protein	7.0
444672	Z95636	Hs.11669	laminin, alpha 5	7.0
455928	NM_005309	Hs.103502	Target Exon	7.0
421321	AW799755	Hs.110553	glutamate-pyruvate transaminase	6.9
451937	AF119664	Hs.27259	retinoic acid induced 1	6.9
426675	AB084791	Hs.133122	transcriptional regulator prot	6.9
438627	AW073235	Hs.123473	hypothetical protein FLJ14524	6.9
438551	U51336	Hs.6453	ESTs	6.9
421758	BE337338	Hs.1422	insect 1,3,4-triphosphatase 5'	6.8
423228	AL137491	Hs.125511	Gardner-Rasheed fibrosarcoma	6.8
405346	AA54512	Hs.24301	Homo sapiens cDNA DKFZp4	6.8
432746	AB16771	Hs.257170	Rag C protein	6.8
452798	AA84791	Hs.348137	polymerase (RNA) II (DNA direc	6.8
453315	BE561988	Hs.257170	ESTs	6.7
440317	BE561988	Hs.257170	Homo sapiens, clone IMAGE:3542	6.7
438857	AS127912	Hs.130783	gb:G0134605.F31 NH_MGC_8 Homo	6.7
452072	BE258657	Hs.27744	Forssman synthetase	6.7
433938	AF161536	Hs.284292	RAB3A, member RAS oncogene fam	6.7
423106	N52572	Hs.13702	ubiquitin-cyclohexane c reducta	6.7
453101	AW952776	Hs.94943	ESTs, Moderately similar to AL	6.7
420307	AW026869	Hs.94943	ESTs	6.7
415056	AB024652	Hs.77687	ESTs	6.7
454262	AW612232	Hs.254835	adenosine A1 receptor	6.7
409227	AA806165	Hs.130323	ESTs	6.6
413908	BE409566	Hs.323813	Homo sapiens, clone IMAGE:3900	6.6
			Homo sapiens, clone MGC28607,	6.6

457274	AW074193	Hs.227152	mannan-binding lectin serine p	SS,TM,SS,TM,Cathrin Ig_c	6.6
419157	AA234540	Hs.23971	EST6	pkinaae	6.6
413424	A122969		EST6	SS	6.6
412464	T781411	Hs.22826	EST5, Weakly similar to 155214	SS,cathrin,crysal	6.6
430168	AW65643		DKF2P434I1735 protein	SS,TM,cd-nd,cd-nd	6.6
450305	AW851734		gm-MR2-CT0222-011199-007-e10 C		6.6
422682	W05238	Hs.94316	EST5, Weakly similar to T31613	SS,TM,DEAD,helicase_C,Lam	6.6
4563367	AW732847	Hs.76573	PKC-1-related HIT protein	SS,TM	6.6
450593	AF120355	Hs.25192	STPH homology and U-box conta	TPR,SS,TM,Rhomboid,lactam	6.6
420319	AW050289	Hs.96593	hypothetical protein	res,arf	6.6
431131	N84730	Hs.250616	isocitrate dehydrogenase 3 (NA	isodh,isdoh	6.6
431297	AA851771	Hs.3076	EST6		6.6
410082	AA081094	Hs.108311	Musashi (Disophila) homolog 1	SS,HECT,phesict	6.6
441307	AW071696	Hs.209065	hypothetical protein FLJ14225	SS,TM	6.5
454682	AW816029	Hs.209065	gm-MR3-5T0220-151299-027-b10 G	flament	8.5
407299	AA460305	Hs.289770	EST5, Weakly similar to 138022		6.5
422637	U25441	Hs.121478	dopamine receptor D3	7tm_1,SS,TM,7tm_1	6.5
407722	BE252241	Hs.38041	pyridoxal pyridoxine, vitamin	pkB,SS	6.4
417810	D28419	Hs.82609	hydroxymethylglutamate synthase	Porphobil_desam	6.4
445333	BE537841	Hs.44278	hypothetical protein FLJ12538	SS	6.4
402197				SS,TM,ATP1G1_FLN,MATB,jg	6.3
419390	A1701162	Hs.90207	hypothetical protein MGC11138	SS,TM,PMF22_Claudin,PMF22	6.3
447754	AW073310	Hs.163533	intron of HER4		6.3
444664	B26362	Hs.11615	map kinase phosphatase-like pr	DSPK,Rhodanese,SS,TM	6.3
421190	U92031	Hs.102482	muslin 5, subglp B, tracheobro	Cys_knot,wvs	6.3
432872	A1505954	Hs.279623	selenoprotein X, 1	DUF25,SS,Ribosome_L3,PDZ	6.3
430023	AA158243	Hs.227729	FK506-binding protein 2 (13kD)	SS,FKBP,SS,PDGF,C2,PI-PLC	6.3
413343	BE350206	Hs.334346	hypothetical protein MGC13045	SS,DnaJ	6.2
417852	AJ250562	Hs.82749	transmembrane 4 superfamily me	transmembrane4,SS,TM	6.2
403128			KIAA1033 protein	SS,TM,tubulin,EGF,FS_F,1	6.2
413055	AV655701	Hs.75183	cytochrome P450, subfamily IIE	pk40	6.2
427812	AA770424	Hs.988162	EST6	SS	6.2
457761	AAW01809	Hs.4779	KIAA1150 protein	SS,LIIM,SS	6.2
450399	H62087	Hs.31659	thyroid hormone receptor-associ	SS	6.2
426048	AT768853	Hs.134478	EST6	TM	6.2
407223	H98565		glyw03b12x1 Soares melanocyt	SS,SS,TM,SS,DDOST_48kD	6.2
445634	AJ524849	Hs.344612	EST5, Weakly similar to KELL_1	wvd	6.2
441197	BE244638	Hs.166	sterol regulatory element bind	HLH	6.1
421707	NM_014921	Hs.107054	lectinome-2	Lectophilin,OLF_7tm_2,Gal	6.1
435750	AB028012	Hs.4990	KIAA1089 protein	SS,TM	6.1
432353	NM_010558	Hs.274411	SCAN domain-containing 1	SCAN	6.1
427326	AJ287878		glucy2305x1 NCL_CGAP_Lym6 Ho	SS,TM,7tm_1,SS,TM	6.1
447128	A1271898		cyclin K		6.1
419444	NM_002496	Hs.90443	Target CAT	for4,SS,TM,ATPase_sub_a	6.1
457078	AA776538		glucy2305x1 NCL_CGAP_Lym6 Ho	SS,PHUQ,RasGEF,RasGEFNR	6.1
410446	AA199530		ADP-ribosyltransferase (NAD p		6.1
413857	W19144	Hs.271742	ADP-ribosyltransferase (NAD p	PARP_PARP_reg,SS,TM,Pept6	6.1
407143	C14078	Hs.332329	EST	SS,TM	6.0
442237	NM_002302	Hs.85901	phosphoserine 4A, cAMP-spe	SS,phkase,tubulin	6.0
405724	AJ55542	Hs.294143	EST5, Weakly similar to T22914	SS,TM,phkase,Activin_rec	6.0
436685	W25661	Hs.5288	Homo sapiens mRNA; cDNA DKF2p4		6.0
441583	AT791499	Hs.205742	EST5, Weakly similar to ALUA_H	WD40_Plec_P2A,M,SS	6.0
419802	AB028989	Hs.85550	mitogen-activated protein kina	SS,Sulfatase	6.0
414927	T31507	Hs.186476	EST6	WD40_Plec_P2A,M,SS	6.0
434314	BE352921	Hs.3797	RAB26, member RAS oncogene fam	SS,Sulfatase	6.0
414157	BE297801	Hs.103949	EST5, Moderately similar to i5	ras,ar,SS	6.0
424415	NM_001975	Hs.145580	onkion 2, (gamma, neuronal)	SS	6.0
405487			Target Exon	enolase,SS,Allophrin-1,Air	6.0
447365	BE383676	Hs.334	Rho guanine nucleotide exchang	SS,TM	6.0
417900	BE250127	Hs.82905	CCO20 (cell division cycle 20,	SH3,PH,RhoGEF	6.0
442237	NM_002302	Hs.85901	phosphoserine 4A, cAMP-spe	WD40,SS,TM,3,EGF,3,1q	6.0
426440	BE327556	Hs.189022	solute carrier family 2 (facil	PDCase	5.9
418256	AW845318	Hs.12271	f-box and leucine-rich repeat	sugar_3,SS,TM,sugar_3r	5.9
431543	AW959519	Hs.259768	adenylate cyclase 1 (bran)	SS,SS,TM,HSP_DNA-bind	5.9
433344	AA476827	Hs.171012	hypothetical protein FLJ22349	TM	5.9
428539	AA476827	Hs.171012	solute carrier family 25 (mto	HLH	5.9
403938			Target Exon	mto_carr,SS,TM,profilin	5.9
456950	AF111170	Hs.306165	Homo sapiens 14q32 Jagged2 gen	Ephrin	5.9
451481	AA302028	Hs.235856	hypothetical protein DKF2p434H	SS,TM,DSL	5.9
443837	AW732784	Hs.3628	muscarinic (Gq/12pho) desabo	GHMP,PKase,SS,TM	5.9
443553	AL040535	Hs.9573	ATP-binding cassette, sub-fam1	ABC_tran,SS	5.9
433333	A1016521	Hs.71816	v-akt murine thymoma viral onc	homoebx,gknaase,PH,phkna	5.9
430660	AW955967	Hs.274348	HLA-B associated transcript-3	ubiquitin,SS,TM,G_patch_a	5.9
440934	AJ684149	Hs.172035	hypothetical protein similar 1	SS	5.9
421542	AA411607	Hs.118954	EST5, Weakly similar to KIAA11	SS,SS	5.9
431534	AL137531	Hs.258950	Homo sapiens mRNA; cDNA DKF2p4	SS,TM,ras	5.9
429608	AF231023	Hs.55173	cathenin, EGF LAG seven-pass G	SS,TM,7tm_2,cathenin,GPS,	5.9
434364	NM_016240	Hs.128556	CSF1 protein	Collagen,SS	5.9
422379	AA832660	Hs.133854	EST6		5.8
443887	NM_004729	Hs.9533	Ac-leuc transposable element	zf-8ED	5.8
450122	BE313765	Hs.343443	EST5, Weakly similar to 138022	SS,TM,phosphatase,LOHA	5.8
404807			Target Exon	UPF0027	5.8
445303	AW362198	Hs.12503	Interleukin 15 receptor, alpha	SS,suhs,SS	5.8
445631	AK001822		Homo sapiens cDNA FLJ10950 fs		5.8
412091	R06185		glyc94603.1 Soares fetal iv	SS,TM,IBR,IBR	5.8

446536	W74413	Hs.15251	hypothetical protein
432866	BE35875	Hs.279509	mitochondrial carrier homolog
402393			ENSP00000085284*CDNA FLJ20404
413041	BE061580	Hs.16122	gb:MRB102049-051289-201-c07 B
414558	AW955085	Hs.335147	gb:U-HF-ENB-ale-a-10-0-4ULr
402916			ENSP00000202587*Sciarabonate t
459133	UA0343	Hs.29556	cyclin-dependent kinase inhibi
404757			Target Exon
403873	BE083422	Hs.55851	gb:QV2-TT0003161199-013-H08 T
411219	AW832917		
421871	AK001416	Hs.306122	glycoprotein, synaptic 2
434057	118913	Hs.124023	Homo sapiens cDNA FLJ14218 fs
416735	AK020978	Hs.78741	hypothetical protein FLJ20116
446562	BE273566	Hs.15358	hypothetical protein FLJ20254
407117	AA146625		gb:z07107.a1 Stratagene pancor
444835	BE409261	Hs.12084	Tu translation elongation fact
421543	AK003519	Hs.105606	hypothetical protein FLJ20512
407757	BE049414	Hs.165215	hypothetical protein MGC5395
419125	AA624252	Hs.130881	B-cell CLL/lymphoma 11A (zinc
437141	BE304917	Hs.31097	Target CAT
408925	AV155783	Hs.661	aquaporin 7
450767	AB006190	Hs.25475	ESTs
432496	D45676	Hs.187959	ESTs
429367	AB047867	Hs.278311	plexin B1
422708	AB017430	Hs.119324	kinasin-like 4,
417442	AA199940	Hs.124039	ESTs
432751	AF152099	Hs.278911	Interleukin 17C
432004	BE018302	Hs.2894	placental growth factor, vascu
454151	AA047169	Hs.154088	hypothetical protein FLJ22756
456145	BE259427	Hs.21446	KIAA1716 protein
417877	NM_016055	Hs.82389	CGI-118 protein
451558	NM_001089	Hs.25530	ATP-binding cassette, sub-fam
402785	AW149126	Hs.17319	hypothetical protein FLJ13719
407204	RA1933	Hs.140027	ESTs, Weakly similar to ALU_1
452848	AF044624	Hs.30792	hook2 protein
435343	AF036616	Hs.114611	hypothetical protein FLJ11808
453271	AL049534		gb:CDZ454M16.1_1 434 (tymory
401609			C16001614.g[7801278]emb[CAS91
447827	U73727	Hs.19718	protein tyrosine phosphatase,
402125	RT1768	Hs.343567	axonal transport of synapto v
450437	X13556	Hs.43298	hypothetical protein MGC10471
415514	F11301	Hs.138329	ESTs
437926	BE383605	Hs.300816	small GTP-binding protein
405653	U24683		immunoglobulin heavy constant
421678	AA410008	Hs.106730	chromosome 22 open reading fra
42472	R93096	Hs.279930	mitochondrial carrier homolog
414918	AT219207	Hs.72222	hypothetical protein FLJ13459
434906	BE410573	Hs.283636	Homo sapiens, clone IMAGE-4053
414757	U48322	Hs.77252	fragile histidine triad gene
450314	AF281134	Hs.283741	exosome component Rps46
421656	AF033308	Hs.106890	Homo sapiens clone 23771 mRNA
408015	AW136771	Hs.244349	epidermal differentiation comp
445871	AT02901	Hs.145592	ESTs, Weakly similar to FCRA M
411813	NM_014931	Hs.72172	KIAA1115 protein
425058	AW295349	Hs.8038	ESTs
429720	MP0061		gb:EST01239 Subtracted Hippoca
453988	AK003512	Hs.232770	arachidonate lipoxygenase 3
449225	R59108	Hs.6777	ESTs
423233	BE048021	Hs.11067	ESTs, Highly similar to T46395
423538	BE258332	Hs.276362	male-enhanced antigen
408215	BE514230		synectin 10
406244			Target Exon
436041	AA035316	Hs.272891	Nipocalcitol-like protein 4
422013	N50696	Hs.253354	ESTs
442451	AA089090	Hs.129616	ESTs
427859	AA416856	Hs.98170	ESTs
435540	BE367032	Hs.14468	hypothetical protein MGC14226
427847	AW11425	Hs.150655	serine/threonine kinase 12
414466	AK48811	Hs.127765	ESTs
431630	NM_002204	Hs.255629	integrin, alpha 3 (antigen CD4
415976	RA3144	Hs.21919	ESTs
447374	AF253462	Hs.16376	KIAA1319 protein
431275	T56371	Hs.10041	ESTs
40343			C7002191*gb[5063028]h[AAD389
431461	BE29671	Hs.256310	likely ortholog of mouse ZFP28
421779	AB951159	Hs.108276	wingless-type MMTV integration
416878	NM_001037	Hs.167370	conotoxin-like antigen (NT-450)
457310	W26363	Hs.239752	nuclear receptor subfamily 2
417193	AB922189	Hs.288390	hypothetical protein FLJ22795
432545	X52466	Hs.3041	uracil-DNA glycosylase 2
455373	AZ7389		Homo sapiens, clone IMAGE-3553
409164	AA706639		gb:agp00609.1 Stratagene hNT n
442296	NM_007725	Hs.8186	lung cancer candidate
438670	AZ76803	Hs.123428	ESTs

	400297		ENSPO0000000452-BAD protein (B	SS,hormone_rec,zf-C4	5.3
	449514	AW970440	Hs.23642	SS,FX,ar,fipocain,PHD,z	5.3
	427336	NM_005658	Hs.2134	MATHSS,MATH_ZM,N_AZM,NT	5.3
	414551	AB156362	Hs.76354	ECM,Peptidase,U7,SS,TM	5.3
5	447960	AW954377	Hs.26412	SS,TM,CHL,N,CHL,N2,CHL,N3	5.3
	430605	AJ245433	Hs.247323	SS,TM,G-patch,ubiquitin,a	5.3
	456849	AA522304	Hs.153177	SS,TM	5.2
	4401206	AJ012026	Hs.241562	SS,TM,GST,C,calbindin,ase	5.2
10	424437	BE244700	Hs.147049	CUT,homobox,beta-lactama	5.2
	427815	BE072019	Hs.12851	SS,TM,Tm_1	5.2
	417903	NM_002342	Hs.11116	TNFR,cd,SS	5.2
	420476	AW971863	Hs.136232	SS,HLH	5.2
	405950	BE251944		SS,TM	5.2
15	436325	AL390088	Hs.7393	SS,Synapsin_C,SS	5.2
	444439	AA528883	Hs.143545	SS,TM,FAF-AH_p_1	5.2
	412515	AW087727	Hs.74623		5.2
	418891	NM_002419	Hs.85448	SH3,kinase,pyridoxal_deC	5.2
	438323	UM0714	Hs.239307	DUF101,SS,rRNA-azym_t,bJR	5.2
20	423296	AW295956	Hs.11900	SS	5.2
	457843	AW138211	Hs.128746		5.2
	425522	NM_004568	Hs.195312	C2,PH,RasGAP,BTK,SS,C2,PH	5.1
	429225	BE250037	Hs.198273	WD40	5.1
	412104	AW205197	Hs.240951	SS,STM	5.1
	444750	U28588	Hs.32325	SS,STM	5.1
25	427725	AB93786	Hs.131035	SS,STM	5.1
	430390	AB023186	Hs.241161	SS,SS,STM,FX,PH,PLDc,arnes	5.1
	421658	XQ4048	Hs.301760	PH,SS,STM	5.1
	426528	AF037062	Hs.172914	ethand	5.1
	428224	AD15405	Hs.98659	ethand,short,SS,adh_short,TG	5.1
30	458876	AA50895	Hs.195347	SS,STM,actin_c	5.1
	402632				5.1
	417672	AW111479	Hs.848	Fz,kinase,lg	5.1
	419451	AS071117	Hs.90535	FXBP,TPR,SS	5.1
	456155	R85182	Hs.7175	SS,STM	5.1
35	422396	W21872	Hs.7907	SS	5.1
	413903	BE346394	Hs.279194	ESTs,Weakly similar to CA24_H	5.0
	447598	AW998918	Hs.199530	ESTs,Weakly similar to AF1568	5.0
	425958	AA364923		ESTs,Weakly similar to T19486	5.0
	440511	AF132959	Hs.7236	ESTs	5.0
40	452661	AAW48413	Hs.257152	SS,TM	5.0
	412900	AW550582	Hs.74598	SS,TM,Peptidase_M10,fn2,h	5.0
	446603	NM_014835	Hs.15519	SS,TM,MAGE,Ribosomal_S17,	5.0
	402884			SS,STM	5.0
	446680	AW245890	Hs.21753	SS,STM,Peptidase_M10,fn2,h	5.0
45	431515	NM_012152	Hs.258583	SS,STM,MAGE,Ribosomal_S17,	5.0
	427204	AA405044	Hs.215725	SS,STM	5.0
	425169	AW252900	Hs.128514	SS,STM	5.0
	412940	BE255701	Hs.819	SS,STM	5.0
50	440839	AI42078	Hs.135582	SS,STM	5.0
	443814	BE281240	Hs.9857	SS,STM	5.0
	434243	AA828082	Hs.200358	SS,STM	5.0
	435505	AF151815	Hs.4973	SS,STM,SS,TM,ABC,tm,ABC,	5.0
	417116	Z43916	Hs.7634	SS,STM,filamentUF,AL	5.0
55	403555				5.0
	420856	BE513294	Hs.205736	C2002219-gli12737280,ye(XP_0	4.9
	405594			HLA class II region expressed	4.9
	405334			NM_021949,homo sapiens ATPase,	4.9
	419483	AF001212	Hs.90744	Target Exon	4.9
60	413784	BE162704		proteasome (prosome, macropain	4.9
	409169	F00291	Hs.50889	gb-PM1-H10484-301299-001-408 H	4.9
	446933	AL137659	Hs.297214	(clone PWSL C2-34) myosin light	4.9
	409139	AS019171	Hs.3321	HSPC141 protein	4.9
	456672	AA020216	Hs.114727	ESTs,Highly similar to IRX_11	4.9
65	420842	AJ036882	Hs.50501	ESTs,Highly similar to IRX_11	4.9
	421908	NM_013375	Hs.109428	Homo sapiens, clone MGC 16327,	4.9
	419667	AW077005	Hs.92208	hypothetical protein MGC10586	4.9
	443496	AJ036973	Hs.9482	TATA-binding protein-binding p	4.9
	409532			a disintegrin and metalloprote	4.9
	456143	HI1097	Hs.61960	target of myb1 (chicken) homol	4.9
70	427527	AB090507	Hs.153261	NM_004374,homo sapiens casease	4.9
	414265	BE410411	Hs.75964	hypothetical protein	4.9
	423933	AF94382		immunoglobulin heavy constant	4.9
	452302	AF173867	Hs.28906	endoplasmic reticulum glycopro	4.9
75	409938	AW974648		Homo sapiens clone TCCCA00164	4.9
	408845			glucocorticoid modulatory elem	4.9
	425976	C75094	Hs.334514	gb-EST386752 MAGE resequences,	4.8
	434962	AK01574	Hs.4291	NM_003105,homo sapiens sortil	4.8
	418572	AT9174	Hs.95172	NC22 protein	4.8
80	440569	NM_014297	Hs.7486	hypothetical protein MGC3136	4.8
	453446	BE299956		protein tyrosine phosphatase,	4.8
	412159	AF286958	Hs.9271	golgi peripherd membrane prot	4.8
	439799	AW276811		paired related homobox prot	4.8
				protein expressed in thyroid	4.8
				gb-600944574F1 NH_MGC_17 Homo	4.8
				glial1071 protein	4.8
				kbxp6562XZ NC2_OGAP_Ov99 Ho	4.8

5	420233	AA256714	Hs.194964	hypothetical protein FLJ22578	SS	4.8
	414576	AK004005	Hs.76480	ubiquitin-like 4	SS,TM,LRRC7,Sema	4.7
	433669	ALD47879	Hs.80475	ESTs, Weakly similar to ALU2_H	SS,TM,RNA_pol_L,RseGAP,C2	4.8
	446984	AW75165	Hs.22753	hypothetical protein FLJ2316	SS	4.8
10	428912	AL43354	Hs.26857	ESTs, Weakly similar to A46302	SS	4.8
	418945	BE245762	Hs.89499	archidionate 5-epoxygenase	lipoygenase,PLAT,SS	4.8
	404333	AI378424	Hs.288761	hypothetical protein FLJ21749	SS,TM,IP_trans,pkinase,pk	4.8
	425515	AF032614	Hs.158341	transmembrane activator and CA	TM	4.8
15	458940	BE205262	Hs.287711	hypothetical protein FLJ22692	SS	4.8
	458367	AA08470	Hs.83135	Homo sapiens, Similar to RIKEN	SS,RNA-synt_2d	4.8
	433254	AA582082	Hs.199410	ESTs	TM	4.7
	437671	AA53047	Hs.9850	hypothetical protein MGC1842	SS	4.8
20	425338	HI1716	Hs.126248	Homo sapiens cDNA FL14444 ts	SS,TM,LRRC7,Sema	4.7
	447946	AA56164	Hs.165827	ESTs	SS,PTN,MK7m,T_1,DAGKc,DAG	4.7
	447205	BE517015	Hs.11006	ESTs, Moderately similar to T1	SS,TM,LRRC7,Sema	4.7
	416880	I95840	Hs.53567	EST	SS,TM,SS,TM,Peptidase_M22	4.7
25	440150	AW95738	Hs.7201	Homo sapiens, clone IMAGE:3940	SS,TM,SS,TM,Peptidase_M22	4.7
	426268	AF083420	Hs.158913	serine/threonine kinase 24 (St)	pkinase,pkinase	4.7
	429253	Y11739	Hs.139313	winged-helix nude	SS,TM,SS,TM,Peptidase_M22	4.7
	425261	AA785727	Hs.34068	ESTs, Weakly similar to A3932	SS	4.7
30	430246	AA08072	Hs.7201	membrane-associated lysine-	SS,SS,TM	4.7
	419120	BE271922	Hs.79347	ESTs, Weakly similar to zinc f	SS,TM,DENN,Cydydytrans	4.7
	416487	AW150458	Hs.79347	KIA02211 gene product	SS,TM	4.7
	413837	AW163525	Hs.187828	Bin-cap (telothanin)	SS,TM,SS	4.7
35	419887	AW222662	Hs.187828	ESTs	SS,TM,SS	4.7
	410277	R89621	Hs.26249	ESTs, Weakly similar to T203_H	ATP-synt_F,SS,TM,CH,Flam	4.7
	415169	W42913	Hs.78089	ATPase, vacuolar, 14 kD	ATP-synt_F,SS,TM,CH,Flam	4.7
	410892	AW097862	Hs.222056	Homo sapiens cDNA FL11572 ts	SS,TM,SS,TM,TSPN,bp_3,SE	4.7
40	407754	AA527448	Hs.26857	Homo sapiens cDNA FL114105 ts	SS,TM,SS,TM,TSPN,bp_3,SE	4.7
	405877	AW502498	Hs.15220	zinc finger protein 105	pkinase,SH2,SH3	4.7
	431629	AA077025	Hs.265827	interferon, alpha-inducible pr	SS,TM	4.7
	438800	AB037108	Hs.6418	seven transmembrane domain op	SS,TM	4.7
45	423822	R50681	Hs.53609	Huyl fibrinogen locus 9C	SS	4.7
	418900	BE207357	Hs.3454	KIA11821 protein	SS	4.7
	402400			Target Exon	SS,TM,RNase_HII,bZIP,DUF2	4.7
	419625	U91616	Hs.91640	nuclear factor of kappa light	ark,SS,TM	4.7
50	433319	AA583232	Hs.199410	ESTs	SS	4.7
	424959	NM_005781	Hs.153937	activated p210c42b kinase	pkinase,SH3	4.7
	432750	NM_014440	Hs.278910	interferon 1, epsilon	IL1	4.7
	429554	AK030333	Hs.164476	hypothetical protein FLJ20626	SS,LPof-C2H2,KRAB,SS,KRAB	4.7
55	447245	AK021113	Hs.17680	hypothetical protein FLJ10851	E1,dehydrog	4.6
	427101	R87591	Hs.172684	ESTs	SS,TM	4.6
	447544	AA401573	Hs.288284	hypothetical protein FLJ22378	SS,TM	4.6
	420286			NM_022857-Homo sapiens ATP-3i	ABC_tran	4.6
60	412841	AT511557	Hs.101335	hypothetical protein MGC11352	SS,TM	4.6
	422056	AW242275	Hs.343521	malate dehydrogenase 2, NAD (m	ldh,ldh_C,adh_short,Sema	4.6
	414874	D26351	Hs.77515	Inositol 1,4,5-trisphosphate re	TM,RYDR,ITPflon_trans,Mi	4.6
	416373	AA750770	Hs.84344	C93-135 protein	SS,TM,PAP22_C,acidin,2OG-F	4.6
65	424487	T08154	Hs.6239	KIA16695 protein	SS,SS,TM,Glyco_hydrol_31,G	4.6
	426571	AA391642	Hs.6239	gbc:EST94816 Activated T-cells	SS,TM,TNFR_c6	4.6
	433941	AA620612	Hs.107187	ESTs	SS,TM,TNFR_c6	4.6
	427177	AF230824	Hs.107187	divalent cation tolerant prote	SS,TM,TNFR_c6	4.6
70	450883	NM_013448	Hs.22619	death-associated protein kinase	pkinase,GTP_EFTU,EFG_C,GT	4.6
	427361	AW732480	Hs.7678	cellular retinoic acid-binding	SS,TM,aminotran_1_2LRR	4.6
	426421	AF261133	Hs.343589	exosome component R41	RNase_PH,RNase_PH_C	4.6
	414513	AW239400	Hs.76297	G protein-coupled receptor kin	pkinase,RC3,pkinase_C,SS,	4.6
75	431458	AK011777	Hs.26857	aspartyl aminopeptidase	SS,Peptidase_M18,SS,TM,LY_	4.6
	432553	AW301003	Hs.51483	ESTs, Weakly similar to hypoth	SS,TM,adh_short	4.6
	404661			C0000386-gli12737280reflKP_0	SS,TM,adh_short	4.6
	412790	NM_014767	Hs.74583	KIA04275 gene product	lactyl,thymoglobulin_1,af-	4.6
80	452423	AL045001	Hs.82360	mammalian h.1 (Cdk assembly	af-C2H2C4	4.6
	426222	BE391706	Hs.168073	DKFZP272M231 protein	GSH_synthase	4.6
	435534	AJ245026	Hs.111099	hypothetical protein MGC10574	CLP_protease	4.6
	409114	AA070021	Hs.119273	glucocorticoid 1 Smilgen neuro	SS,TM,lysin	4.6
85	429049	AW452126	Hs.119273	KIA42056 gene product	SS,TM,lysin	4.6
	424271	A991887	Hs.305882	5-oxoprolinase (ATP-hydrolysi	SS,TM,pkinase,Activin_rec	4.6
	418741	H83265	Hs.8881	ESTs, Weakly similar to S41044	flavodoxin,FAD_binding,MD	4.6
	450453	M32718	Hs.166373	nitric oxide synthase 3 (endo)	DEAD_helicase_C_dom,Mra	4.6
90	430774	AL045019	Hs.12109	Homo sapiens cDNA FLJ11214 ts	WD40	4.6
	444853	AW245312	Hs.12109	WD40 protein C1ac1	homeobox,SS,homeobox,home	4.6
	420508	AJ270953	Hs.98428	homeo box B6	SS,TM,LY,homeobox	4.6
	405931	AA525253	Hs.9100	Homo sapiens cDNA FLJ10310 ts	RA,SH2,RC3,SS,TM,Nucleos	4.6
95	456181	L36453	Hs.1330	ras inhibitor	SS,TM,HC03_cotransp	4.6
	439270	BE268278	Hs.28393	hypothetical protein MGC2592	SS,SS	4.5
	440104	AA132838	Hs.238984	hypothetical protein MGC2803	SS,SS	4.5
	423279	AW559681	Hs.250943	suppressor of Ty (Scerewissia	SS,SH2,Ribosomal_L22,phn	4.5
100	445017	AW833449	Hs.12303	Target Exon	SS,SH2,Ribosomal_L22,phn	4.5
	431832	AW276856	Hs.192715	ESTs	SS,TM,cathepsin,cathepsin	4.5
	433886	AA813556	Hs.28412	ESTs	Est,SAM_PNT	4.5
	426735	T0716	Hs.120446	ESTs	SS	4.5
105	417825	AW838994	Hs.6363	heparan sulfate 6-O-sulfotrans	Cystositol_BP_PH	4.5
	456900	BE061053	Hs.133483	gco:QV0-ET0041-271099-437-d09 B	SS,TM	4.5
	423858	AL137326	Hs.133483	Homo sapiens mRNA: cDNA DCF24	CA	4.5
					SS,TM	4.5

5	421680	AL031186	Hs.289106	Human DNA sequence from clone	SS,SS,rm,zf-RanBP,rm,GA	4.5
	408157	AA047685	Hs.62946	ESTs	kinase	4.5
	434303	AW204058		transforming growth factor bet	SS,TM,SSF,G-FAP,gwajhto	4.5
	440745	AW033627	Hs.143301	ESTs	SS	4.5
10	419534	U94505	Hs.277445	cloniglycyrol kinase, zeta (1	ank,DAGka,DAGkc,DAG_Pe-ki	4.5
	447208	BE315291	Hs.237971	hypothetical protein MGC5627		4.5
	364163	R84938		gby16504.1 Soares retina N2		4.5
	458636	AK001528	Hs.347255	Homo sapiens, Similar to DGE0		4.5
15	410817	U02781	Hs.33918	protein disulfide isomerase re	SS,thione	4.5
	434558	AW294102	Hs.39168	ESTs	SS,TM,LRCT,LR	4.5
	440548	AL117408	Hs.7274	DKFZP434P1750 protein		4.5
	450200	AW978525	Hs.173088	ESTs	zfUBP,zf-CHC1A	4.5
20	432434	AL161977	Hs.2994	PCTAIRE protein kinase 3	SS,kinase	4.5
	440042	AW073367	Hs.133898	ESTs	SS	4.5
	454328	AW372097	Hs.278429	hepatoellular carcinoma-assoc		4.5
	458196	AB02408		ubiquitin A-S2 residue ribosom	SS,TM,bz,FKBP,TPR	4.5
25	433472	AS14245	Hs.3343	phosphoglycerol dehydrogenase	2-HsdL,DX12-HsdL,OH_LCM	4.5
	408826	AW295527	Hs.255479	hypothetical protein MGC5566	A_deaminase,A_deaminase	4.5
	448033	AW877382	Hs.15898	2,4-dienyl CoA reductase 2, p	adh_short,NDK	4.5
	426272	AAW45071	Hs.189284	ESTs	SS,DEAD,helicase_C,SS,DEA	4.5
30	453610	AW058892	Hs.33918	RacQ protein-like 5	SS,DEAD,helicase_C,SS,DEA	4.5
	441327	AK001706	Hs.7778	hypothetical protein FLJ10751	SS,TM,tm_1	4.5
	426581	AA054400	Hs.151706	KIA0134 gene product	helicase_C,PRK,SS,TM,tm_	4.5
	434443	AS44042	Hs.9347	regulator of G-protein signal	TM,Na_FL,phras	4.5
35	426877	AW948856	Hs.97165	ESTs	SS	4.5
	412482	AA099330	Hs.334885	mitochondrial GTP binding prot	SS	4.4
	425236	AW067800	Hs.155223	stannocalcin 2	Stannocalcin,SS	4.4
	422229	AK003865	Hs.125532	protease, serine, 26	trypsin,SS	4.4
40	412338	AA151527	Hs.69465	hypothetical protein FLJ12436	SS,TM,TG,Sema,PSI	4.4
	419395	BE268326	Hs.90280	5-aminimidazole-4-carboxamide	AlCARFT_1MPCHas,MGS,AlCAR	4.4
	424662	AF031405		gb:AF031405 Soares fetal liver		4.4
	439875	AW328081	Hs.6817	inosine triphosphatase (nucleo	Hamp1_ike,SS	4.4
45	425220	BE522023	Hs.15463	Homo sapiens, clone IMAGE2959	SS,thione	4.4
	423220	BE394920	Hs.125462	aldolase	WD40,TM,Activin_recep,phn	4.4
	411574	BE242842	Hs.6780	protein tyrosine kinase 9-like	cottlin_ADF,SS,TM	4.4
	446947	BE161508	Hs.337228	ESTs, Weakly similar to AXHU e	SS,TM,lg,kinase	4.4
50	407755	AW151323	Hs.69465	Homo sapiens, serpin pininoyl	SS,TM,ambiotan_1,2	4.4
	414849	AW372721	Hs.291623	ESTs, Weakly similar to unname	TM,kinase	4.4
	458171	AA020016	Hs.192090	ESTs	SS,TM	4.4
	424443	AW151281	Hs.284161	hypothetical protein from EURO	SS,TM,SS,TM	4.4
55	427022	AA024053	Hs.23158	ESTs	SS,zf-CH2	4.4
	404344			CD02191+g15053028(gb)AD388	SS,ABC_tran	4.4
	427458	BE208364	Hs.29283	ESTs, Weakly similar to UGHU p	SS,FS_F8_type_C,EGF,TGT	4.4
	419764	BE265234	Hs.93183	vasodilator-stimulated phospho	WH1	4.4
60	446872	X07058	Hs.18362	pyrimidinergic receptor P2Y, G	TM,1,SS,TM	4.4
	435615	Y15065	Hs.4975	potassium voltage-gated channel	Ion_trans,KCNQ1_channel	4.4
	403945			Target Exon		4.3
	435593	R88872	Hs.4964	DKFZP58J1524 protein	Herpes_HEPAss	4.3
65	421899	AJ011895	Hs.109281	Nef-associated factor 1	Virus_HS,bZIP,G-gamma,Myo	4.3
	428245	AW15768	Hs.155314	KIA0095 gene product	SS,TM	4.3
	423348	AA324687		gb:EST27558 Cerebellum II Homo	SS,TM	4.3
	452105	AA022838	Hs.6570	ESTs, Weakly similar to S1089	SS,TM,TBC,rm	4.3
70	431834	AB013481	Hs.272714	STG protein	SS	4.3
	429499	AA453609	Hs.95350	ESTs	SS,TM	4.3
	453486	BE520712	Hs.33026	hypothetical protein PP2447		4.3
	459393	BE492083	Hs.193264	hypothetical protein MGC3234		4.3
75	405364			ENSP0000029138?Cervine mado		4.3
	428346	AJ242431	Hs.118282	PAP-1 binding protein	SS,TM	4.3
	435327	BE301871	Hs.4667	mannosyl (alpha-1,3)-glycopro	SS,HLH_Myc_N_tern,Myo-LZ	4.3
	413053	AW532663	Hs.65377	ESTs, Moderately similar to Ki	TM,SS,TM,EF_TS,UBA,transm	4.3
80	409993	D05022	Hs.57729	Ketch-like ECH-associated prot	BTB,kat5,SS,TM	4.3
	409936	AK001691	Hs.57655	hypothetical protein FLJ10829	SS,TM	4.3
	421592	AF009801	Hs.105941	bagpipe homeobox (Drosophila)	homeobox,SS	4.3
	424251	AA877466	Hs.143696	coactivator-associated arginin	SS,SNF2_N,helicase_C,brm	4.3
85	414788	X09432	Hs.77215	cyfin-dependent kinase (CDC2-	kinase	4.3
	432805	X94630	Hs.3107	CD97 antigen	SS,TM,tm_2,GPS,EGF,G,SS,TM	4.3
	424927	AW973666	Hs.153850	hypothetical protein C32102.4	SS	4.3
	456063	T16837	Hs.4241	ESTs	fusion_gly,homeobox,TM	4.3
90	417323	R88669	Hs.102447	TSC-2-like	PWWF	4.3
	406621	X57609	Hs.181125	immunoglobulin lambda locus	SS	4.3
	431493	AT91493	Hs.129873	ESTs, novel cytochrome P450	SS,p450,SS	4.3
	412528	BE391579	Hs.75097	Fac-activated serine/threonine	SS,kinase	4.3
95	431659	BE409117	Hs.266335	RNA telomerase associated	rm,SS,ROCI	4.3
	419579	W46529	Hs.296200	hypothetical protein AF053356	MSP,domain,SS,TM,CUG,NTR	4.2
	410076	T05387	Hs.7991	ESTs	SS	4.2
	408673	AA812424		heat shock 27kD protein 1	HSP20,SS	4.2
100	424702	AL157689	Hs.152449	hypothetical protein DKFZp434K		4.2
	418419	X55239	Hs.85094	centromere protein B (80kD)	CENP-B,HTH_5	4.2
	447377	X77343	Hs.334334	transcription factor AP-2 alpha	TF_AP-2,TF_AP-2	4.2
	419931	D45371	Hs.80485	adipose most abundant gene tra	CtgCollagen,SS	4.2
105	411674	AW881123	Hs.183918	RNA telomerase associated	SS	4.2
	419073	AW027170	Hs.183918	Homo sapiens cDNA FLJ12797 fs	hs,ssap_1,ZU5,SS,TM,Nuc	4.2
	406867	AA157857	Hs.182265	keratin 19	filament,bZIP,SS,filament	4.2
	432183	AA151952	Hs.46679	hypothetical protein FLJ20739	SS	4.2

5	418910	Z52821	Ha.89466	Homo sapiens, Similar to dodec	EOH,SS,TM,aminotran_3,ABC	4.2
	437300	AL040504	Ha.25063	PRO0461 protein	SS,TM,phkase,cyclin,F-bo	4.2
	426615	AA003678	Ha.6473	gbzuu70a1.1r1 Soares_testis_NH		4.2
	421453	AA234652	Ha.104555	neuropptide FF-antide peptide	SS,bZIP,zf-C2H2,bZIP,zf-C	4.2
	428516	AA075048	Ha.104555	gbzaml6c10.1 Strataegia pancer		4.2
10	444744	BE394732	Ha.147562	ESTs	SS	4.2
	412575	AA113177		gbzcm23605.a1 Strataegia pancer	TM,ER,lumen_recept	4.2
	435592	AF038960	Ha.206713	UDP-Gal-betaGlcNAc beta 1,4-g	Galactosyl_T_2,lg,SS,TMA	4.2
	426204	Ha.348188		hypothetical protein FLJ20262		4.2
	421453	AK001171	Ha.326422	hypothetical protein MGCA549	SS,Methylphos	4.2
15	456153	AW972270	Ha.144054	ESTs	SS,TM	4.2
	455340	AW901435		gbzRC0-NN1012-270300-031-a10 N		4.2
	457288	AW272279		ESTs, Moderately similar to AL		4.2
	432311	BE083080	Ha.274323	similar to stalytransferase 7	Glyco_transf_29	4.2
	409556	NM_005133	Ha.288626	RCE 1, prenyl protein protease	ABL,SS,CPase_1_chain,HMG	4.2
20	424919	BE314461	Ha.153768	U3 snRNP-associated 55-4Da pr	WD40,SS,KH+domain	4.2
	416328	H65052	Ha.337621	ESTs		4.2
	416137	AK534834	Ha.72461	Homo sapiens PAC clone RPS-108		4.2
	417334	AA337572	Ha.157240	hypothetical protein MGCA737	SS,TM,ion_trans	4.2
	451920	AA224483	Ha.27239	DKFZP586K0204 protein	SS,TM,SS,TM	4.2
25	413049	NM_002151	Ha.823	hepzin (transmembrane protease	hepzin,SS,TM,ATP1G1_PLM_	4.2
	458988	AW110451	Ha.283570	C2-119 protein		4.2
	408954	M21305		FGENES predicted novel secretate		4.2
	451595	AW965569	Ha.20996	ESTs	SS,WD40	4.2
	449728	AB20751	Ha.107635	ESTs	SS	4.1
30	432245	T99901	Ha.336781	ESTs	TMA,ABC_tran	4.1
	432238	AL133057	Ha.274135	Homo sapiens mRNA: cDNA DKFZp4	WD40,LR	4.1
	430037	BE409649	Ha.227769	mitogen-activated protein kina	phkase	4.1
	442196	AB262646	Ha.31844	hypothetical protein FLJ12566	SS,CAN	4.1
	422251	Z22321	Ha.155342	protein kinase C, delta	phkase,DAG,PE-bind,phkna	4.1
35	415014	AW954054	Ha.245951	ESTs		4.1
	404088	BE559877	Ha.183232	hypothetical protein FLJ22638	SS,zf-C3HC4,SPRY,zf-B_box	4.1
	418837	UD4263	Ha.89040	preproendoprin	Ophidn_nuraprep,SS	4.1
	410239	AS58350	Ha.61273	hypothetical protein MGC2650	SS,ART,TM	4.1
	446975	BE246446	Ha.16695	ubiquitin-activating enzyme E1	Thf,U,ABACT	4.1
40	433968	AA847843	Ha.62711	High mobility group (nonhiston	SS,HMG_box	4.1
	446241	AW811054		gmR2-5T0131-21 1099-008-c06 S	SS	4.1
	414355	AJ271671	Ha.78554	zincfin regulated transpore	Zip,SS,TM,Cydylyltransf	4.1
	450848	AB777954	Ha.428	fin-related tyrosine kinase 3	tk3,lg,SS,Ribosomal_L13	4.1
	429218	AA225065	Ha.192869	Target CAT	SS,Nop	4.1
45	425437	AK000492	Ha.181780	hypothetical protein FLJ20241		4.1
	426613			Target Exon	SS,phkase,LR,LR,CRCT,Ribo	4.1
	431239	AL039971	Ha.251216	hypothetical protein DKFZp434A	ank,WH2	4.1
	436057	AJ004832	Ha.5038	neuropathy target esterase	cNMP_binding,SS,TM,cNMP_b	4.1
	415193	AL040891	Ha.12185	hypothetical protein MGC14333	SS,TM,aminotran_1_2,LR	4.1
50	424610	BE372782	Ha.207443	hypothetical protein MGC10846		4.1
	432968	BE814192	Ha.279869	melanoma-associated antigen re	SS,TM,RCG,DIX	4.1
	428156	BE263038	Ha.182698	mitochondrial ribosomal protai	SS	4.1
	414094	AW168771	Ha.71574	hypothetical protein FLJ14926	SS,PSCR,EF,IBD	4.1
	424564	AW181271	Ha.153951	ARPI (actin-related protein 1,	actin,SS	4.1
55	431410	AW299534	Ha.105739	ESTs		4.1
	433968	AW181481	Ha.111577	Integral membrane protein 3	TM	4.1
	432351	AJ270313	Ha.127762	hypothetical protein MGC12962		4.1
	426120	AA325243	Ha.165887	copine 1	C2,SS,aminotran_5	4.1
	416877	BE386296	Ha.85568	hypothetical protein FLJ23436		4.1
60	425970	AK001500	Ha.165186	hypothetical protein FLJ13852	SS,PSCR,Epimase,zf-C2H2	4.1
	434848	BE236304	Ha.32148	AD-015 protein	SS,TM,SS,TM,LR,RF,Peptid	4.1
	458715	AK000073	Ha.16725	hypothetical protein FLJ10111	IBR,zf-C3HC4,SS,TM,LR,FK	4.1
	435851	AA700946		ESTs		4.1
	425538	BE270918	Ha.164026	Homo sapiens, clone IMAGE:3534	SS,Sfz2,X_hellbase_C_brom	4.1
65	444416	AW280305	Ha.11155	hypothetical protein	zf-C3HC4,SpaA,PHD,TM,sym	4.1
	429831	BE296216	Ha.17273	S-adenosylhomocysteine hydrola	AdoHcyase,SS	4.0
	444596	BE560652	Ha.11417	Rab acceptor 1 (prenylated)	SS,TM,lg_chan,ANF_recept	4.0
	435985	AW956781	Ha.293937	ESTs, Weakly similar to FXD2_47	SS,PWWP,TSG22	4.0
	447402	BE14526	Ha.19490	hypothetical protein FLJ24542	SS,TM	4.0
70	450184	W31056	Ha.237817	Homo sapiens, clone IMAGE:3447	SS	4.0
	426058	AF029778	Ha.166154	jagged 2	DSLEGF,wc,granulin,SS,T	4.0
	459255	AA932444	Ha.239500	hypothetical protein MGC13114	SS	4.0
	403182			Target Exon	SS	4.0
	432078	BE314877	Ha.24553	hypothetical protein FLJ12541	SS,TM	4.0
75	459187	BE504370		ESTs, Weakly similar to CA13_H	SS	4.0
	452747	BE153655	Ha.61460	lg superfamily receptor LNHR	SS,TM,lg_HLH	4.0
	444633	AF111713	Ha.250218	junctional adhesion molecule 1	lg,SS,TM,HLH	4.0
	434171	BE247688	Ha.347349	KIAA0948 protein		4.0
	422155	AW249152		sirtuin (silent mating type I)	SR2,HLH,Myc_N_term,Myc-L	4.0
80	433262	AS71225	Ha.264171	KIAA1535 protein	SS,TM,cNMP_binding,lon_tr	4.0
	442539	AF078037	Ha.324051	Rub-associated inhibitor	SR5,ank,SS,TM,Hg,lg	4.0
	452560	AW373011	Ha.54558	hypothetical protein FLJ22222		4.0
	437563	AJ217204	Ha.144968	ESTs		4.0
	423234	AA531128	Ha.115903	ESTs	SS	4.0
	433135	AA436373	Ha.110477	dicholyl-phosphate mannosyltra		4.0
	447405	AW401854	Ha.18720	programmed cell death 8 (apopt	pyr_redox,SS,Ests	4.0
	452857	BE072814	Ha.258519	ESTs, Moderately similar to S6	SS	4.0
	427834	AA506101	Ha.285813	hypothetical protein FLJ11807	SS,TM	4.0

418953	BE304571	Ha.85529	aldo-ko reductase family 1,	aldo_ket_red	4.0
437340	AL353935	Ha.135917	hypothetical protein OXKZp7610	TBC,2BP,WD40,WD40	4.0
455928	BE170313		gq-OVA-H10536-040500-153-q02 H	SS	4.0
450007			Target Exon	SShomobox	4.0
424825	AF207069	Ha.153357	procollagen-lysine, 2-oxogluta	ZOG-Fell_Oxy_Glycoas_trans	4.0
438143	BE500581	Ha.269552	ESTs		4.0
433173	Z35093	Ha.3196	surfeit1	SURF1,SS,TM,SURF1,SURF4	4.0
412550	RS2452	Ha.26370	gryg98g77.r1 Soares Infant hr		4.0

TABLE 23b:

Pkey: Unique Eos probe/est identifier number

CAT number: Gene cluster number

Accession: Genbank accession numbers

15	Pkey	CAT Number	Accession		
	408215		BE614236 AA037674 N35629 AA338536 AI193603 AA781096 AI680061 AI61258 AW276647 BE212263 AI348919 AI855031 AI200708 AI359617 I0478_1		
			AA626361 AF160210 AA446461 AI356346 AI343638 AI343640 AI275091 MT8746 AW262379 AW520002 AA503756 AI934519 AW272086 N26520		
20	408294	1050553_1	BE141732 U75823 BE141331 AW178418 AW178430 BE141343 BE141298 BE141702 BE141285		
	409114	110086_1	AA070021 AA126205 AA032771 AA102169 AA083530 AA082183 AA115915 AA085147 AA123905 AA063336 AA079206		
	409164	110421_1	AA076639 AA064707 AI035200 AI551598		
	409616	114348_1	AA076248 AA120958 AA122152 AA076249		
	409616	116091_1	AW974648 AA552153 AA0549671 AA078592		
25	409590	116270_1	BE261944 AF115641 AA318136 AA134872 AA319849 WD4622 AI291655 AW879302 AA130778 BE314003 AA306246 AW660808 AA353648		
			AA226977 C02043 AA135937 AA078870 AA377355 AA318785 AA318785 AA331960 BE005960 AW370250 AW370244 T85303 AA795250		
			AI567682 AA032839 AI056920		
	410445	120374_2	AA195630 AI143895 AW961629 AA322482		
	411215	123058_1	AW932617 AW832913 AW832996 AW832788 AW832915 AW832776		
	411674	1253746_1	AW861123 AW861123 AW856717 AW861116 AW856705 AW856788 AW866774 AW856787 AW856780 AW856782 AW856788 AW856772		
30			AW856784 AW856786 AW856776 AW856535 AW856757		
	412091	1216564_1	R06185 AW891805 AW901832 AW901895		
	412173	1280870_1	T17017 AA032279 AW857658		
	412575	130769_1	AA113177 AW854515 AA113847		
	413534	1376357_1	BE146951 BE146780 BE146788 BE146957 BE146774 BE146963 BE146907		
35	413534	1376722_1	BE250120 BE148538		
	413664	1387163_1	BE142704 BE142705 BE162732 BE162702 BE162694		
	413963	139363_1	AW163355 AW162705 AW163385 AI829359 BE277278 AA132590 AW157329 AA584408 AW157252 AI602198 AW003514 T24436 AI765598		
			AW157459 AB187040 AI595082 AW689924 AI829284 AI040993 AI343083 AW684650 AW299513 AA132529 AI340991 AB182836		
40			AS41293 AI550609 AA279		
	414413_1	1443696_1	AA77945 AW0116655		
	415126	1523506_1	DE0945 D61346 DE1568 D80539		
	419120	182026_1	BE271922 N54771 AA234233 AA471354 BE171081 AA253482 AA470113 AA823272 H24470 AW504757 N51688 AI400700 AA578548 AA714130		
			AA069917 AW1670348 AW664465 AW647553 AW571643 AA649943 AW474826 AW767165 AA326817 AI493859 AW952245 AA347139 AA805093		
45	422155	21235_1	AW249152 AW249153 BE298858 AW192672 AF095714 R05553 AF083107 AF160214 NM_012237 BE258447 BE253088 AA297721 H69848		
			W39153 AA070372 H14246 AA1079367 R24561 AW403997 AA297034 AA297092 F11858 AI372597 AA297787 Z42780 AA257072 T81280 T83544		
			AA297053 H26053 A26		
	423348	227276_1	AA324687 AA325155 AW962038		
50	425858	257265_1	AA354923 AW983483 BE182774 C21461		
	426571	262823_1	AA381642 AA381654 AW983560 AW969848 AA381728 AA381608		
	427326	272229_1	AA287878 AB004160 AA400787		
	429092	285620_1	AW879141 AA421182 AT341404 AA173923 AA430600		
	429720	308153_1	MT95091 AA773950 AA586573 AA457225		
55	430168	313927_1	AW968343 AA468507 AA478223 AW513008 AI762122 AI564512 AA862642 AA468976		
	431424	333110_1	AQ222989 AA083560 AA504839 AA805261		
	432319	363095_1	AA583222 AA001715		
	432933	377703_1	AT54388 AW251910 AI056058 AI056059 AI863364 AI863355 AW131720 AI874922 AI499042 AI890006 AI823178 AW469487 AA520354		
	433941	377883_1	AA620612 AA984983 AA949503		
	434303	383224_1	AW204059 AA24378 AI696963 AA829077 AW613033		
60	434743	3925_1	AA363410 AI256019 H00141 T77848 AA045363 AL079911 AI750972 Z46002 AA642523 AI232826 AA215407 AI683329 AA292122 NA2783		
			AW055958 AF086956 N93340 N63271 AA131836 AWE07273 AA571323 AA421961 T34951 AW656080 MT8807 N34977 AA521151		
			AA778886 AA044784 AA700		
	434796	393400_1	AA812046 AW974514 AA784999 AA649302		
65	435851	411522_1	AA703946 AA702712 AA479620		
	436163	41515_6	R94838 AL047151 AA310339 AW63200 AI569552 AI307823 NA49975		
	437215	43473_1	AA117488 AL044479		
	439399	467696_1	AA276811 AA829050 AA829190		
	439246	47021_3	AA068072 AW610838 AA955235 AA852987 AI939209 AA206609 AW190187 AA555262 AF086057 F35814 AW516382 AA377885 N50847 F27148		
70			AA721186 AA417778 AA003145		
	440317	48187_1	BE581888 BE580615 BE562102		
	442462	542322_1	AA077451 H734151		
	442472	543731_1	AW066569 AW066562 AF049582		
	445625	54558_1	BE246743 AA435943 AW024744 AW242217 AA975476 AW385185 R07536 R73462 AV654529 T57442 AI399986 R50073 R48743 AT69689		
75			AA863005 AA317806 AW878000 AW189563 AW962007 AW471273 R73463 AI335104 AI590161 AA69257 AB54604 H21954 T25141 AA85793		
			R50074 AT08253 A12		
			AA068072 AW610838 AI332996 AW655331 AW130957 AW193951 AI347975 AW081323 AW662527 AI343924 AI380749 AA308163 T66966		
	445931	6457_1	AI655000 AW148837 AB040455 AA410598 AI520726 BE050135 AW572000 AS24755 AW593995 AI336927 AI335928 AI357036 R60592		
			AI90588 R11124 T1		
80	447128	70934_1	A1271888 BE048502 AW52509 AA24810 X84721 AW58001 AI533947 AA149583 H00719 AT765229 AW973696 F25787 F35749 AI568815		
			AW915380 AA54539 C02021 AA961610 AW059537 R71712		
	448241	756181_1	AW811064 AW811160 AA478413		
	448993	79225_1	AA171630 BE546871 AW407710 BE153882 BE546739 AA063597 BE140503 BE218514 AW56702 AI656234 AI636283 AI567265		
			AA040858 BE207794 AA053085 R09173 AA292343 AA454988 AA293504 AI695741 AI527478 AA339460 AT60441 AA346416 BE047245		
			AA730380 AA390485 AA454		

453446 967533_1 BE290996 BE297115 BE270415 BE295214 BE296526
 454682 1228976_1 AW816029 AW813292 AW816156 AW813333 AW816159 AW813302 AW813344 AW813172
 455035 1249762_1 AW851734 AW851676 AW851693 AW851713 AW851722 AW851676 AW851731 AW851648 AW852215
 455340 1235204_1 AW891455 BE295457
 455557 1325974_1 AW955839 AW959097
 455600 1335877_1 BE061053 BE000589 BE000957 BE091618
 455885 1360385_1 BE153524 BE153576 BE153583
 455928 1383898_1 BE170313 BE168339 BE158280
 455973 201205_1 A1279811 A101071 A1274686 A1279813 AAS8460 AA287256 BE171665
 457268 104543_1 AW272279 AA61542 AA640015
 457978 448502_1 AA776538 BE439540
 458196 503719_1 BE020426 AA007424 A279233 A302762 N33153 BE045678 A863332 AW173558 AD002328 Z30793 D25594 BE326823
 459167 82053_1 BE504370 A243453 A1055556 AW02878 A1070213 A1300626 AW072219 A1369492 A1349587 AW779061 W78149 AA055693 AA974162 A1394380
 A830098 AW054857 A1870008 AW207658 AW655508 AW300595 A192392 AW628019 A274365 AA906922 N92547 AW054727 AW206667
 459271 969297_1 ALD45934 AL039532 H55631

TABLE 23C:

Phy: Unique number corresponding to an Eos probe set

Ref: Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham L et al." refers to the publication entitled "The DNA sequence of human chromosome 22" Dunham, et al., 1993 Nature 402:489-495

Strand: Indicates DNA strand from which exons were predicted

NL_position: Indicates nucleotide positions of predicted exons

Phy	Ref	Strand	NL_position
400460	8389428	Plus	32559-36295
400607	5887666	Plus	3112-4159
400833	8705148	Minus	19759-188138
400945	9158265	Plus	34428-34612
400923	7637836	Minus	94518-94559
400933	7651935	Minus	105330-105503
401210	7712287	Plus	160895-167133,169760-169877,171563-171733
401264	9787154	Plus	132610-130527,133367-133504
401278	9789936	Plus	98428-98573
401609	7705041	Minus	9877-11907
401674	7685953	Plus	137876-138227,139157-139298,139440-139599,139660-140159
401724	7656694	Plus	150083-150241
402187	8576113	Plus	195466-195585
402365	9454515	Minus	70928-71185
402353	8929608	Plus	19513-20054,20163-20263
402400	8945145	Minus	80123-80232
402632	9931268	Plus	101166-101419
402884	9926552	Plus	47890-49191
402916	7466502	Minus	361-174,541-687
403055	8748804	Minus	1095321-10225
403128	7331425	Plus	122894-123018,123134-123283,123372-123555,123779-123940,124059-124256
403182	9838273	Plus	102163-102245,102545-102725
403338	7711785	Plus	48336-48022
403945	7711669	Minus	32141-32263
404036	6587760	Minus	65247-67529,112537-114863
404333	9802821	Minus	137948-138024,138111-138300
404343	9838093	Plus	122604-122931
404344	9838093	Plus	127865-128394
404365	9964977	Plus	50151-50319,50859-51098
404561	9787073	Plus	33374-33675,33769-34008
404757	7705327	Plus	100933-101053,101550-101782
404807	4165210	Minus	124246-124422
405334	3135285	Plus	139386-139856
405346	2981263	Plus	101962-102171
405354	2231075	Minus	46325-46491,49136-49252
405371	2078469	Minus	47657-47768,48461-48596
405594	6950456	Plus	161628-161734,162823-163014,164439-164652
405928	7717155	Minus	2523-3259
406230	4782469	Plus	77176-72515
406244	7417725	Plus	39422-39595
406301	8575868	Plus	57291-57494
406487	7711336	Plus	82039-82092
406495	7711338	Minus	174651-174578
406613	2957168	Plus	5029-5147

Table 24A lists about 117 genes down-regulated in ovarian cancer compared to non-malignant adult ovaries. These were selected as for Table 23A, except that the numerator was set to the 75th percentile amongst various non-malignant ovary specimens, the denominator was set to the 96th percentile value amongst various ovarian cancers, the numerator was greater than or equal to 75 units, and the ratio was greater than or equal to 2.0 (i.e., 2-fold downregulation in tumor vs. normal ovaries).

TABLE 24A:

Phy: Unique Eos probe set identifier number

Ex. Accn: Exemplar Accession number, Genbank accession number

UG ID: UniGene number

Title: UniGene gene title

Protein Dom.: Predicted protein domain

R1: Ratio of normal ovaries to tumor

Phylo	Ex. Acon	UG ID	Title	Protein Dom.	RI
428232	BE272452	Hs.183109	monamine oxidase A	Amino_oxidase,pyr_redox,F	16.9
433553	AJ732037	Hs.277901	ESTs	SS	10.8
444931	AW52098		general transcription factor I	SS,Glypican	8.7
451573	AW130351		ESTs	SS	8.3
428570	BE242256	Hs.2441	KIAA0022 gene product	lectin_c,SS,TM	7.9
435110	AB99482	Hs.42151	ESTs	SS	7.5
410295	AJ741357		nidogen (enactin)	SS,EGF_Jd1,ncspt,b,hyro	6.9
438549	BE386801	Hs.21858	tridecylolide repeat contain	SS,serpin,SS,WD40,FYVE	6.5
407969	AA046217	Hs.105370	ESTs	SS,Pept_M12B_propep,ReproI	6.2
414541	BE235116	Hs.76392	aldohyde dehydrogenase 1 fam1	aldohd	5.7
449438	BE511301	Hs.246554	Homo sapiens cDNA FLJ11640 fs	SS	5.0
441422	RA3777	Hs.21364	ESTs	SS,TM	5.1
413391	AJ223328	Hs.75335	glycine amidinotransferase (L-'	Amidinotransf	3.9
428022	Z39565	Hs.27865	ESTs	SS	3.6
423444	AJ320829	Hs.97266	protocadherin 18	SS	3.6
416039	AA376989	Hs.78989	alcohol dehydrogenase 5 (class	adh_zinc,HCV_NS4a,TM,adh_	3.5
425854	AA437061	Hs.14050	prokinectin 1 precursor	SS	3.4
436772	AW975688		metallothionein 1E (functional	SS,TM,7tm,2_HRM	3.2
415162	AF035718	Hs.78051	transcription factor 21	HLH	3.1
427794	AA709186	Hs.59070	ESTs	SS	3.1
433072	AJ928037	Hs.158832	ESTs	SS	3.1
418318	U41732	Hs.84072	transmembrane 4 superfamily me	transmembrane4	2.8
410029	NM_007308	Hs.58324	a disintegrin-like and metallo	Reprolysin,1p_1_Pep,M12B	3.2
431933	AI187057	Hs.132554	ESTs	TM,SS,TM	2.9
420303	AA258282	Hs.278436	KIAA1474 protein	SS	2.8
437480	M64336		ghHomo sapiens retinoic acid-	SS,wnl	2.8
426611	A441021	Hs.104761	ESTs	Sec7,PH	2.8
433782	AW933237	Hs.236438	hypothetical protein DKFZp761K	SS,Pept_M12B_propep,ReproI	2.7
453828	AW970960	Hs.293821	ESTs	z-CCCH,SS	2.7
418444	AJ952899	Hs.85155	butyrate response factor 1 (EG	wec,LRP,SSLRR	2.7
435767	AB011192	Hs.35094	extracellular matrix protein 2	kazal,SS,kazal	2.7
413824	BE177019	Hs.75445	SPARC-like 1 (nast3, hevlin)	laminin,B,laminin_EGFJam	2.7
413025	NM_000426	Hs.323511	Homo sapiens cDNA: FLJ23176 f	SS,gliptase,SAM	2.7
414504	AW069181	Hs.115175	startle-alpha motif and leucin	Sec7,PH	2.7
439857	NM_015310	Hs.67563	KIAA0424 protein	HATPase,c_HATPase,c	2.6
421639	NM_012082	Hs.106309	Friend of GATA2	EGF,laminin_h_3,glu	2.6
442498	US4617	Hs.8364	Homo sapiens pyruvate dehydrog	SS	2.6
410494	K38394	Hs.64015	protein S (alpha)	SS	2.5
425958	AA583299	Hs.40527	ESTs	SS	2.5
449648	AW205607	Hs.253499	ESTs	SS	2.5
435519	AJ218950	Hs.125461	hypothetical protein FLJ11539	SS	2.5
433690	AJ373949	Hs.279610	hypothetical protein FLJ10493	SS	2.5
424319	AW951028	Hs.58732	ESTs, Weakly similar to ALUB_H	SS	2.5
420174	AB24144	Hs.199749	ESTs	PID,Herpes_UL6	2.4
421709	AA159394	Hs.107056	CEO-6 protein	WH2	2.4
417622	AW298183	Hs.82318	WAS protein family, member 3	SS,TM,zona,pellucida	2.4
433655	AW930427	Hs.342874	transforming growth factor, be	SS,PX,PH,PLDc,PH,PLDc,PX	2.4
408468	AB097112		phosphatidylinositol transfer	SS,TM,SS,TFIID_30d0	2.3
400829			C11000244.g111056030001NP_0	nas	2.3
453125	AW775544	Hs.115497	hypothetical protein FLJ22655	HLH	2.3
437862	AW971807	Hs.5884	Homo sapiens mRNA: cDNA DKFZp5		2.3
425462	AA91852	Hs.46783	Homo sapiens cDNA: FLJ23822 f		2.3
417094	NM_008895	Hs.81182	histamine N-methyltransferase	Acyl-CoA_dh	2.3
403247			Target Exon		2.3
441916	AA993571		ESTs	Glypican,SS	2.3
422746	NM_004484	Hs.119651	glypican 3	SS,GTP_CDC,GS	2.3
416777	AF146760	Hs.79844	DKFZP564M1416 protein	SS,TM	2.3
409403	AA588224	Hs.8634	Homo sapiens cDNA: FLJ22547 f	SS	2.3
418956	AJ234631		KIAA0768 protein	Vinculin,Stathmin	2.3
410073	AW408163	Hs.58488	catenin (cadherin-associated p	hormone_rec-z-C4,hormone	2.2
419461	AA526201	Hs.288869	nuclear receptor subfamily 2,	SS,gliptase	2.2
423019	AJ232754	Hs.195058	similar to calyculin/calmodulin	SS	2.2
425123	AJ267615	Hs.38022	ESTs		2.2
453305	R39224	Hs.267997	EHM2 gene		2.2
411617	NM_003243	Hs.342874	transforming growth factor, be	zona_pellucida,SS,TM,zona	2.2
408537	U14966	Hs.185946	ribosomal protein L5	Ribosomal_L16p	2.2
414466	AA345211	Hs.75205	cyclothione P450, subfamily XIA	p450	2.2
408915	NM_016651	Hs.48950	hepaticellular carcinoma novel	SS	2.2
420929	AB694143	Hs.326248	programmed cell death 4	MA3,LRP	2.2
456972	AJ654347	Hs.2017	ribosomal protein L38	SS,TM	2.2
409549	AB020516	Hs.54866	phospholipase C, epsilon 2	C2,PLIP-PLC-Y,PLC-X	2.2
410209	AJ583661	Hs.60548	hypothetical protein PR01635	SS,TM,Fork_head	2.2
449500	AW956345	Hs.12926	ESTs	SS,TM	2.2
447886	W53516	Hs.10432	ESTs, Weakly similar to I38022		2.1
441712	AW931827	Hs.7946	KIAA1289 protein	SS	2.1
445025	AJ768895	Hs.295727	ESTs, Weakly similar to ALUB_H	SS,BAG,Upp0001	2.1
444161	N52543	Hs.142940	ESTs	SS	2.1
427156	BE521719	Hs.173602	KIAA0603 gene product	SS,TALDTC	2.1
433995	AH160015	Hs.125469	ESTs	SS,TM,RasGEF,actin,RasGEF	2.1
408443	N33937	Hs.10336	ESTs	SS	2.1
448274	AJ268097	Hs.67317	Homo sapiens cDNA FLJ11775 fs		2.1
426554	NM_004010	Hs.169470	dystrophin (muscular dystrophy	ZZ,CH,WW,apactin,bZIP,SS	2.1
443906	AA348531	Hs.7913	ESTs		2.1

444815	AA151539	Hs.1227	aminolevulinic acid, delta-, dehydratase	SS,ALAD	2.1
420278	AA767718	Hs.93581	hypothetical protein FLJ10512	SS, TM, Sema, PS, Ig	2.1
404245			NM_007116.1	Stratogen, C, h3, SS	2.1
439420	AA443966	Hs.31595	ESTs	SS, TM, PMP22, Claudin, SS, TM	2.1
410066	AL117664	Hs.58419	DKFZ7586L2024 protein	EGF, TIL, SS	2.0
414476	AA301867	Hs.76224	EGF-containing fibulin-like ex	EGF, TIL, SS	2.0
421437	AA357989	Hs.16262	ESTs	SS	2.0
447659	AAJ17472	Hs.107250	hypothetical protein DKFZp566H	SS	2.0
444862	AI209158	Hs.143329	ESTs	SS, TM	2.0
426086	T94907	Hs.186572	ESTs	PH, C, spectrin	2.0
436980	AB64710	Hs.201945	ESTs	SS, ATP-synt, C	2.0
424651	AI65206		ESTs	SS	2.0
432939	AL038924	Hs.278849	KIAA0436 gene product	cf-C3HC4, myosin, head, DIL	2.0
449088	AB554048	Hs.195556	ESTs	SS, MACPF, auct, h, J, recept	2.0
428642	NM_014899	Hs.10432	KIAA0876 protein	B18, ras	2.0
415977	L35351	Hs.12266	Integrin, alpha 8	TM, integrin, A, FG-GAP	2.0
450435	AI699975	Hs.201935	ESTs	laminin, B, laminin, EGF, Jam	2.0
450696	AB54223	Hs.16025	hypothetical protein FLJ23191	SS	2.0
421255	BE326214	Hs.93813	ESTs	TM	2.0
432467	T03667	Hs.293388	Human DNA sequence from clone	SS	2.0
408654	BD18382	Hs.46721	UCPI protein	SS, Ependymin, SS	2.0
412611	AA732036	Hs.164478	hypothetical protein FLJ21939	SS	2.0
453355	AW25374	Hs.31412	myopodin	SS	2.0
424665	AW36576	Hs.139851	caveolin 2	SS, TM, Caveolin, Caveolin	2.0
458147	AW75257		ghrl, 3-CTD214-161299-045-B06 C	SS, TM, PWM	2.0
447566	NS0432	Hs.102648	ESTs	SS, TM, pkinase, F3, F8, type_	2.0
414496	W73953		ESTs	SS, TM, pkinase, F3, F8, type_	2.0
425618	AW110112	Hs.9552	Homo sapiens cDNA: FLJ22042 fi	SS, TM	2.0
415166	NM_003852	Hs.79058	carboxypeptidase Z	Zn, carb, Opept, F, 2, Oxygene	2.0
422157	AW557295	Hs.112318	6.2 kd protein	SS	2.0
452263	AL133047	Hs.24715	Homo sapiens mRNA; cDNA DKFZp4	SH	2.0
416919	AA222336		ESTs	SS, DUF25	2.0
444846	AB71055	Hs.148477	ESTs	SS, TM	2.0
418781	T41160	Hs.8404	ESTs		2.0

TABLE 24B:

Pkey: Unique Eos probe/ Identifier number

CAT number: Gene cluster number

Accession: Genbank accession numbers

Pkey	CAT	Number	Accession
404848	106033_1		AI095712 AL039752 BE000365 AA376878 N75269 AA345398 AA340553 AW960002 R76169 R70638 AA540770 AI378587 AI338002 AI762398 NA7873 AI065549 AA741112 AIW450680 AA658668 R76154 AW242828 NS8555 AW080313 AJ378491 AI807102 AA417043 AI655444 AW253286 AW297099
410236	11922_2		AA741357 AB700000 W75997 H50726 AW659709 AA988817 AL037804 W67847 BD105553 AI033256 N76810 N31548 AI032204 NS5278 AW075272 AI032081 R35753 W93372 AA700790 AI036587 NS2985 R82468 AW580252 AL036750 AI052219 R36621 W07047 AA088621 AI249109 W68776 W65374 AA15
414496	145392_1		W73633 AA28112 W77887 AW889237 AA148524 AT749182 AT754442 AI338392 AI253102 AI070493 AI370541 AI697341 H57338 AW188021 AI376658 W72716 A051402 AI188071 AI335900 N21488 AW770478 W92522 AI691028 AI913512 AI144445 W73819 AA063438 N26900 W95221 AI688132 H58
418919	186233_1		AA232635 AI373703 AA233330
418956	186262_1		AI234531 AI703302 AW502216 AA776957 R49415 AI420777 AA665394 AI036019 AA775469 AB72390 AA0980 AI094453 AA826397 AA535994 AI585251 AB804295 AA897791 AA232893 AI346880 AI356232 AA235138 F31396 AW079977 H1 6405
424661	241981_1		AI453208 AA732315 AA344619 AA804035 AW522967 AA488889 AA635644 BE245127 AA669979 AA761874 H28767 AA510081 AA837086 AI766406 W76175 AB21825 AA746092 AA743152 AI478562 H88863
436772	426554_1		AI097568 AA731063 N67054
438780	46001_1		MI4536 AI025512 AI382387 BE061777 AA089966 BE169030 T41176 AW594624 BE502415 AA121893 AI259223 T40311 AI684569 AA257011 AI078277 AI241318 BE327710 AW597521 AW895268 AA84990 BE327514
441916	528799_1		AA935371 AA971516 AI937262
444931	62357_1		AA52086 AA426880 T58512 T58561 AB51255 NA0838 H87921 AW264447 AA428067 AA364094 AW955655 D62894 AW341452 AA243652 AI846418 AB16803 AB71252 AI376942 AI740496 AA452836 AI277917 AI481941 AA456147 AB745656 AI003975 AI245674 AI433703 AI202068 AI289985 AI38
451973	875588_1		AW130551 AW538899 AI003973
458147	488821_1		AW752597 AW948781 AW849062 AW849040 AW752699 AW752604 AW752709

TABLE 24C:

Pkey: Unique number corresponding to an Eos probe/ Identifier

Ref: Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham I. et al." refers to the publication entitled "The DNA sequence of

human chromosome 22" Dunham, et al. (1999) Nature 402:489-495

Strand: Indicates DNA strand from which exons were predicted

NI_position: Indicates nucleotide positions of predicted exons

Pkey	Ref	Strand	NI_position
400829	8570385	Plus	152176-152616
402347	765803	Minus	76626-77146
404245	7405725	Plus	36016-37073-37813,38946-39314,40355-40651,42738-43026,43351-43696,45698-46030,51110-51415,52779-53072,54648- 54935,55201-55509,55926-56240,56355-56672,57078-57401,59965-60282,62600-62926,63363-63686,66693-67025,68180- 68497,68909-69232,71372-71695,720

Table 25A provides UnigeneID, UnigeneTitle, Pkey, and Exemplar Accession for sequences in Table 26. The information in Table 25A is linked by SEQ ID NO: to Table 26.

Table 25A:

Pkey: Unique Eos probe/ Identifier number

Ex. Acon: Exemplar Accession number, Genbank accession number

UG ID: UniGene number

Title: UniGene title

SEQ ID NO: Sequence identification number for sequences in Table 26

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Play	Ex. Acon	UG ID	Title	SEQ ID NO
462538	U85011	Hs.30743	preferentially expressed antigen in melan	SEQ ID NO: 1-2
421476	A082243	Hs.37258	ESTs. Moderately similar to S2530 fibro	SEQ ID NO: 3-4
436982	A018305	Hs.5378	spondin 1, (spondin) extracellular mat	SEQ ID NO: 5-6
456627	AW08642	Hs.97984	SRY (sex determining region Y)-box 17 (S	SEQ ID NO: 7-8
422956	BE545072	Hs.122579	ECT2 protein (Epithelial cell transfor	SEQ ID NO: 9-10
410102	AW248508	Hs.278777	ESTs: homolog of FCN-3 (Ciona savignyi)	SEQ ID NO: 11-12
422959	NM_005756	Hs.184542	G protein-coupled receptor 64	SEQ ID NO: 13-22
426227	AA321649	Hs.2248	small inducible cytokine subfamily B (C)	SEQ ID NO: 23-24
451110	AJ955040	Hs.265398	PAR-6 beta (partitoning defective 6 h	SEQ ID NO: 25-26
426187	AJ07333	Hs.265229	G protein-coupled receptor 40	SEQ ID NO: 27-28
424605	NM_002497	Hs.153704	NIMA (never in mitosis gene a)-related k	SEQ ID NO: 29-30
431159	AB035898	Hs.150587	kinesin-like protein 2	SEQ ID NO: 31-32
426427	M96699	Hs.169540	TTK protein kinase	SEQ ID NO: 33-34
425371	D49441	Hs.155081	mesothelin	SEQ ID NO: 35-36
418806	AA084248	Hs.85339	G protein-coupled receptor 39	SEQ ID NO: 39-40
465646	AB60321	Hs.203845	KCNK15 potassium channel, subfamily K, m	SEQ ID NO: 41-42
427344	NM_000869	Hs.2142	5-hydroxytryptamine (serotonin) receptor	SEQ ID NO: 43-44
445537	AJ24501	Hs.12944	EGF-like domain, multiple 6	SEQ ID NO: 45-46
424620	AA101043	Hs.151254	kallitrein 7 (chymotrypsin, elastin com	SEQ ID NO: 47-48
412078	X69599	Hs.73149	paired box gene 8	SEQ ID NO: 49-52
409178	BE363948	Hs.50915	kallitrein 5	SEQ ID NO: 53-54
448243	AW069771	Hs.170195	integrin, beta 8	SEQ ID NO: 55-56
426514	BE616533	Hs.170195	bone morphogenetic protein 7 (osteogeni	SEQ ID NO: 57-58
419452	U33635	Hs.90572	PTK7 protein tyrosine kinase 7	SEQ ID NO: 59-60
431130	NM_006103	Hs.2719	HEC4 epidermis-specific, whey-acid pr	SEQ ID NO: 61-62
415539	AJ73381	Hs.7472	DMP-R10	SEQ ID NO: 63-64
423961	L31666	Hs.136348	parosin (OSF-zos)	SEQ ID NO: 65-66
417433	BE270256	Hs.82128	ST4 oncofetal trophoblast glycoprotein	SEQ ID NO: 67-68
422867	L32137	Hs.1594	cartilage oligomeric matrix protein (pro	SEQ ID NO: 69-70
408542	AA563820	Hs.2686	hypothetical protein FLJ22418	SEQ ID NO: 71-72
444381	BE367335	Hs.283713	ESTs. Weakly similar to S64054 hypoth	SEQ ID NO: 73-74
452747	BE153855	Hs.61460	Ig superfamily receptor LNIR	SEQ ID NO: 75-76
450375	AA039447	Hs.155223	a disintegrin and metalloproteinase doma	SEQ ID NO: 77-78
426215	AW063419	Hs.155223	sirocalcin 2	SEQ ID NO: 79-80
430044	AA464510	Hs.152812	ESTs	SEQ ID NO: 81
447033	AJ357412	Hs.157601	ESTs	SEQ ID NO: 82-87
410418	L31382	Hs.63325	transmembrane protease, serine 4	SEQ ID NO: 88-89
411274	NM_002776	Hs.6423	kallitrein 10	SEQ ID NO: 90-91
422260	AA315953	Hs.105484	regenerating gene type IV	SEQ ID NO: 92-93
409041	AB033025	Hs.50081	Hypothetical protein, XP_051850 (RQA4119	SEQ ID NO: 94-95
428654	AK001666	Hs.180905	similar to GALL1 (rat [Drosophila]-like	SEQ ID NO: 96-97
404977			leucine-like growth factor 2 (somatomedi	SEQ ID NO: 98-99
427747	AA411425	Hs.180655	serpin/thrombin kinase 12	SEQ ID NO: 100-101
412140	AA219691	Hs.73625	RAB6 interacting, kinesin-like (rablines	SEQ ID NO: 102-103
431846	BE219524	Hs.271580	uropathin 1b	SEQ ID NO: 104-105
425465	L18654	Hs.1904	protein kinase G, iota	SEQ ID NO: 106-107
432938	T27013	Hs.3132	steroidogenic acute regulatory protein	SEQ ID NO: 108-109
421451	AA291377	Hs.50831	ESTs	SEQ ID NO: 110-117
431478	AL309172	Hs.317432	branched chain aminotransferase 1, cytos	SEQ ID NO: 118-119
411945	AL033527	Hs.92137	L-tyrc-2 protein (MYC2)	SEQ ID NO: 120-121
424078	AB008625	Hs.139033	paternally expressed 3	SEQ ID NO: 122-123
406400			kallitrein 8 (neurospirovasin) (KLJ3)	SEQ ID NO: 124-125
428450	NM_014791	Hs.184339	HNA0175 gene product	SEQ ID NO: 126-127
438167	RZ0363	Hs.24286	chemokine binding protein 2 (CCBP2), mRN	SEQ ID NO: 128-129
416530	U82801	Hs.79381	kallitrein 6 (neurospiro, zyme)	SEQ ID NO: 130-131
430691	C14187	Hs.167208	aristalase-related homeobox protein ARX	SEQ ID NO: 132-133
406081	AW461597	Hs.167208	protein of basic-helix-loop-helix-PAS pro	SEQ ID NO: 134
411773	NM_000679	Hs.72026	protease, serine, 21 (testidin)	SEQ ID NO: 135-138
407792	AJ077715	Hs.36384	putative secreted ligand homologous to l	SEQ ID NO: 139-140
428093	AW594506	Hs.104330	ESTs	SEQ ID NO: 141-144
431630	NM_002204	Hs.265629	integrin, alpha 3 (antigen CD49C, alpha	SEQ ID NO: 145-146
421692	AF111658	Hs.105259	sodium carrier family 3a (sodium phospho	SEQ ID NO: 149-150
431441	U81961	Hs.2794	sodium channel, nonvoltage-gated 1 alpha	SEQ ID NO: 151-152
431389	BE184455	Hs.251754	secretory leukocyte protease inhibitor (SEQ ID NO: 153-154
436972	AA234579	Hs.25640	claudin 3	SEQ ID NO: 155-156
422504	X91133	Hs.204238	lipocalin 2 (lipocalin gene 24p3) (NGAL)	SEQ ID NO: 157-158
410001	AB041036	Hs.57771	kallitrein 11	SEQ ID NO: 159-160

TABLE 26B:

Play: Unique Eas probe/identifier number

CAT number: Gene cluster number

Accession: Genbank accession numbers

TABLE 25C.

Play: Unique number corresponding to an Eos protein

Ref: Sequence source. The 1 digit numbers in this column are Genbank identifier (GI) numbers. 'Dunham L. et al.' refers to the publication entitled 'The DNA sequence of

human chromosomes 22' Dunham, et al. (1999) *Nature* 402:489-495

Strand: Indicates DNA strand from which exons were predicted

N_L position: Indicates nucleotide positions of predicted exons

Play	Ref	Strand	N _L position
404977	3738341	Minus	43081-43229
406400	9256298	Plus	1553-1712, 1878-2140, 4252-4385, 5922-6077

Table 26

Seq ID NO: 1 DNA sequence

Nucleic Acid Accession #: NM_006115.1

Coding sequence: 236...1765

1	11	21	31	41	51	
GCTTCAGGCT	ACAGCTCCCC	CGACGCCAGA	AGCGGGGCGCT	GCAGCCCTCC	AGCACCCCTC	60
CGGACACACC	CACCGGCTTC	CCAGGGGTGA	CTCTTCACCA	GCAACTTCGC	GGTGTGTGTA	120
ACTCTCTGAG	GAAGAATATT	TGTGATATT	ACTCTCAGCA	GTCTCTGCGA	ACAGTGTACT	180
GAGGACTAGA	AATCCAGAGT	TGGAGGTCTC	TGAGGCCAGC	CTAAGTCGCT	TCAAAATGGA	240
ACGAGGGGCT	TTGTGGGGTT	CGATTCAGAG	CGATATCATC	AGCATAGTGT	TGTGACACAG	300
CCCAACGAGA	CTTGTGTGAG	TGGCAGAGCA	GGGCTGCTGT	AAGATATGAG	CCCTGGCCAT	360
TGCCGCCCTG	GAGTTTCTGC	CCAGGGAGCT	CTTCGGCGCA	CTCTCTCAGG	CAGGCTTTGA	420
CGGAGCACAC	AGCCAGACCT	TGAGGCAAT	GGTGCAGGCC	TGGCCCTCTA	CTCTGCTCCC	480
TCCTGGAGTG	CTGATGAGG	GACACATCTC	TCACTGTGAG	ACCTTCAAAG	CTGTGCTCTG	540
TGACTATTGAT	GTGCTCTTGT	CCAGCAGAGT	TGGCGCCAGG	TGTGAGGAAC	TTCAATGTCT	600
GGATTTCAGG	AGAGACTCTC	ATCGAGACTC	CTGAGCTGTA	TGTCTGTGAA	ACAGGGCCAG	660
TCCTTACTCA	TTTCCAGAGC	CAGGAGCAGC	TCAGCCCATG	ACAAAGAGAC	GAAATATAGA	720
TGTTTGTGAC	ACAGAGGCAG	AGAGGCCCTT	CATTCCAGTA	GAGGTGTCTG	TGAGACTGTT	780
CCCTCAGGAA	GGTGGCTGTG	ATGAATTTGT	CTCCTACCTC	ATTGAGAAAG	TGAGGCCAAA	840
GAAGAATGTA	CTACGCTCTT	CTCTTAGAGA	GTCTGAGATT	TTTGCATATG	CCATGACAGA	900
TATCAAGATG	ATCTCCAAAA	TGTGTGAGCT	GGACTCTATT	GAAGATTGAG	AAGTGAAGTG	960
TACTCTGAAG	CTACCACTCT	TGGGCAAAAT	TTCTCTTATC	CTGGGCCAGA	TGATTAATCT	1020
GGATGACTCT	CTCTCTCTCC	ACATCTCATG	ATCTTCTCAT	ATTCTCCGCG	AGAGGAAGAA	1080
CGATTAATTC	GGCAGATATC	CTCTCTGAGT	CTGAGCTGCT	CAAGCCCTCC	AGCTCTCTTA	1140
TGTGACTCTT	TTATTTTCTC	TTAGAGCGCG	CTGAGTACAG	TGTCTGAGCC	ACGTAATGAA	1200
CCCTCTGGAA	ACCTCTCTCA	TAACTAATCT	CGGCTCTTGT	GAAGGGGATG	TGATGACTCT	1260
GTCCAGAGAT	CCAGAGCTCA	CTGACTAGAT	TGTCTGTAGT	CTAAGTGGGG	TCATCTCTGAC	1320
CAHTATAGCT	CTGACATCTC	TCTAATCTCT	CTCAATGAGA	GCTTCTCCCA	CCCTCTCAGG	1380
CTGTGCTCTT	GATGAGTGTG	GGATCAACGA	TGATCAGCTC	CTTGGCCCTC	TGCTCTCTCT	1440
GAGCAGCTGC	TGCCAGTTA	CAACTTAAG	CTTCTAGGGG	AATTCCACTT	CCATATCTGC	1500
CTTCCAGAGT	CTCTGCGAGC	ACCTCAACGG	GCTGAGCAAT	CTGAGCCAGG	TGCTGTATTC	1560
TCTCTCTCTG	GAGATGATAG	AGGACATCTG	TGATCAGCTC	CACTCTGAGA	GGCTTCTGCT	1620
TCTCATGCGC	AGGCTCAGGG	AGTTGCTGTG	TGAGTTTGGG	GGCGCCAGCA	TGCTCTGCTG	1680
TAGTGCACAC	CCCTCTCTCT	ACTGTGGGGG	CAGAACCTTC	TATGACCCGG	AGGCCATCTT	1740
GTGCGCCCTG	TTATGCTAGA	ACTAGCTGGG	TGCACATATC	AAATGCTCTA	TTCTCTATAC	1800
TGAGCACTA	AGGCGAGAT	GTGCATGCAT	CTTGAAGCAA	CAAGAGGCC	ACAGTTCTAG	1860
ACAAATGTTT	AGTGTGATGT	AGGAAAAACT	GTTCAGTGAAG	GAUAAAAACT	TCAGACAAAT	1920
GTTCAGTGAAG	GAUAAAAAGG	GGAGTTTGGG	GATAGACAGA	TGTTTGATTT	AGGAGTTAAT	1980
GTGACTTTTG	GGGAGATACA	TCTATAGAG	TGAGAGATAG	AATCTGAAAT	TCTAAGAGGA	2040
GATTCCTGCT	TGGGAGATCA	ATGTAGGAGT	TAACTCCCTG	GTAGACTGTT	GTAAGAGAAC	2100
TGTTGAJAAT	AAGAGAGAGC	AATGTGAAGC	AAAAAANAANA	AAAAAANA		

Seq ID NO: 2 Protein sequence

Protein Accession #: NP_006106.1

1	11	21	31	41	51	
MEERRRIGSI	QRYIENSVW	TSPLRLVELA	QGLLKDEAL	AJRALELLRP	ELFPPLPMAA	60
FDGRHSQTLK	AMQVAMPFTC	LEFLGVLMKG	HHLEHTFKAV	LDGLDLVLLAG	EVPRPRMKGL	120
VLDLRKNSHQ	DPWTVWNSP	ASLVSEFPPE	AAQPMFKRRK	VDGLSTEARQ	PFIPFVEVLG	180
LFPLGSCADE	LFSTLIERVK	KKKSVRLCTC	KKLKITPMW	QDHLHLEW	QKQSEIPLV	240
TCWVLPFLA	KFSPFLQMI	NLRLLLSHI	RSSEVISPEK	EPQYIAQFTS	QFSLAQCLQA	300
LYVSLFFFLR	GRDLDLRIW	NFLELTLSIT	NRLSESDVW	HLSPSPSVSQ	LSVLSGLSWG	360
LDVSPPEPLQ	ALLERASATL	QDLVEDECGT	TDQLLALLPL	SLHSCSQULT	LSFYGNISIT	420
SLAGSLQLHL	IGLBNLEIR	HFPELSEVET	HTGTLRLRL	ATLHARLREL	LCGLGRPSW	480
WLSANPCPIC	GRTYTPPEP	LLCPKPFVN				

Seq ID NO: 3 DNA sequence

Nucleic Acid Accession #: Eos sequence

Coding sequence: 264...782

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CTCTGCTCCA	CTCACACCCC	GAAGCTGACT	GGTCCACGCA	CAGCTGAAGC	ATGAGGAJAC	60
TCATCGGGGG	ACTAAATTTT	CTTAAATATT	AGACTTGCAC	AGTAGAGACT	TCAACTGACC	120
TTCTCTCAGC	TGAGAACCTG	TTCAGATATA	TACATCAAGT	CAGTGAAGTC	TCCAGCACCC	180
TGCGGCTGGG	ACTATCAGGA	GACAGAGTGC	CAGGCTGGTT	CTCTGAAGTG	CCAGAGCCCC	240
AACTTCTAGC	GAAGAGCTGA	ATCAAGATGA	CAGAGACTAT	CGAGCTCTGC	CATGCTGATT	300
TGATCGGGGT	GGTGTCCCTC	TTCCTGCGAG	CTGTGCTCTC	CACGSCCATC	AACTACTGCG	360
TCAGCAGGCA	CATGCGCCAC	AGAGATGAGC	AGATACTGAA	AGCGGCGAGT	CTCAGATTTC	420
CCAGGCGCCAG	CCCTGCGCAC	CATCATCCAC	CTCTGTGCA	GAGATATGAG	GAGACTGAGA	480
CAGAGAGAGA	CATCCGATAT	TCGTATTCCC	TTTACAGGCA	TGACAGGCAC	ACACCTCTGC	540

5	ATAGCTTGGA	TAGCTCTCG	AGTTGCGCTC	CTGCTGCGCA	GGCCACAGAG	GATGTGGATT	600
	ACACACAGAT	GCTCTTTTCT	GACCTGGTAG	AACTAAAAAA	THACTTCCCG	CTGAGCATAG	600
	AGAACCTTAA	GGAATCTGCA	ATGTCAATCC	AGAAAGACAG	AGGCGCAATT		720
	TCTGTGTAATT	TGTCAACCTCT	GCTCTGTCCTG	AGCCAGCGGA	ATATGATCAA	GTGGCCATGT	780
	GAATTCCTAAA	TATTTTAAAT	GGGGTCCAGT	TCTCATGGA	TCTTCACTT	TAATTTGTAG	840
10	GGAAATGCGA	TTTTTCCCCT	TAAACCAAGG	CATGGGCGCTC	ACAGTCTTAT	GGAGACAGCG	900
	CAAAAGAGAT	GTGGAGAGG	AACTGTGAAA	ATACACAGAG	GTCTCTAGAG	CCCATGGACT	960
	CTCTGTCTGT	ACCCAAAGAA	GCTCTTGCTT	CCTCAAAAC	AAAAACAGG	CTTGGCTGGG	1020
	AAACAGGCCG	AATGCCCGCG	CAAGAAAGGT	TGAGATCAGA	TGTTTAGAG	AACTTTCAAG	1080
	TAAGGTATGA	GAACTATAGA	GTCCATCAGC	AGAGATAGTA	GTGAAGTCTC	TCCCAGAGGA	1140
15	AAATTTTAAA	AGAGTTGAT	AGAGTTCTAT	TGCGAACTCT	TGTGCTTAAA		1200
	TGACTTCCCT	TGAGCTCTT	TAATATTGG	CAATAACAA	CTTCTTTAAA	AGTTTAAAT	1260
	AAATAGCAA	CCACACCA					
20	Seq ID No.: 4 Protein sequence						
	Protein Accession #: Bos sequence						
	1	11	21	31	41	51	
	MLTEYVMEVNH	GLIVAVVSLF	LQACPLTAIN	LLSRHMAHK	GLILKAASL	QVPRSPSGRH	60
	HPFAVKEMKE	QTEDRIPMS	DSLYRHIDST	PSDELSSCS	SPPAQATSD	VDYTVQVFSQ	120
25	Seq ID No.: 5 DNA sequence						
	Nucleic Acid Accession #: AB051390						
	Coding sequence: 34...2457						
	1	11	21	31	41	51	
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30	CTGAGCGCGA	CTCGCGACT	CGTGGCCGCTG	GGCTGTCCCG	TGGCGCGCGC	GCTGCGCTTC	120
	TCCGACGAGA	CCCTGCGACA	AATGCCCAAG	TCAGAGGGCT	ACCTCGACCG	GCTGCGCTTC	180
	CGCCAGCGCA	CGGCGCGCGA	GGCTCAACCG	GGATTCGAGC	TCCCTCGTGG	GGGCGACCTC	240
	GACTCTTACA	AGCGCGGAAC	CAGCTCACCG	GTAACACTTT	CAGCTGCTCC	TCCCTCTCC	300
	TTACAGAGAT	TCACATTAAT	TGCCCTCAGA	GAGAACGAGG	AGGGTAGATA	GGAGAGAGAG	360
35	CATGCTGCGA	CTCTCCAGAT	CATAGACAGC	GTTCAGAGCA	GAGAAAGAGC	AGTTTAGTAG	420
	GTTCGATCA	CTCAGAGAGG	TCCAGCGAGG	AGGACCCCGC	TCCATCTGCT	TGGATAGACA	480
	CCACAGCGGG	GACAGCGCTG	CGTGAATCTG	AAAGCGCAGA	TGGTCAAAA	AGCGACTAT	540
	TATTTTCAAG	ATAGAGGCTC	TCTGACCAAG	AACTCTTGTG	AACAAGATTC	CACATTGTAT	600
	GGGTTGACTG	GAAGAACCAT	CTTACAGAGC	TGTGCTCGCG	GAACTGCCAA	GTACAGAGCA	660
40	CACTTTTATG	GGAAATGCTG	CGAGAGACA	CAACCAAGGG	ATTACCTCGC	TCCGCGCAAC	720
	CAGTGGTCTG	CGATCATGGG	AGGATCCCAAC	TCCAGAAATT	ATGTACTGTG	GGAAATAGGA	780
	GGATATGCCA	GCGAAGGGGT	CAACACAGTT	CGAGAAATGG	GCTCAACCGT	GAAGATGGAG	840
	GAGAAATATC	GACACACAGG	TACATCTGAG	CTCACCGCTA	TCGAAGCGCA	AGCCCATAGC	900
	CCAGCTTGAG	AGGCTCTCAA	CGTAGAGACA	CGACCTTCAG	CTGAATTTTC	CTGTGACAGA	960
45	ACGCGCAATT	TAATGTCTCT	CCTGACCATG	ATGGGCGCTA	GTCCCGACTG	GAACTAGGCC	1020
	TTATCTGAGC	AAAGTACTGTG	CCAGAGAGAA	TGTGGCTGGG	TCAGAGAGGT	GCTGCAAGAC	1080
	CTGATCTCTT	CGATCTCTCT	CGACACAGC	GGGTTGACTC	ATGATGCTCC	CAGAAAGCTC	1140
	ACATCTCCCT	AGGAGAAATAT	CCGCGCCCTG	ACAGACCTGG	ACCATCTCCA	GATCTCTTTC	1200
	TATGACCCAG	AGGGTGGGTC	CATCACTCAA	GTAGCCAGAG	TTGTATCGA	GAGAAATCGA	1260
50	CGAGAGGGTG	AAACATGCAA	TATTTTACCT	GAGAAATGGC	ATGATATGTG	AGTGAACCTG	1320
	GCTCCAGAGG	AGAAAGATGA	AGATAGACCT	CTGGAAGCTC	GCATCTCTCT	CAACTGTCTG	1380
	CCATGTCTCG	CCTCGACCTC	CTCCACCTGT	GACAAAGGAG	AGAGAGTGGC	ACAGCGCATG	1440
	CTGAAGAGAC	AGCTGACACT	CAAGTCTCCC	TGCTCTGACA	CCAGAGACTT	CCAGCGCTTC	1500
	ATGGGCGCTG	GCTGCAATGA	GAGAGAGGCG	TCCACTCTCA	CTGATCTCCA	GTGGATACCC	1560
55	TGTCGTCCTT	CGAGCATCTC	GTGCGCATG	GCGATAGGTT	CCCGAGAGAG	ATGTGTAGAG	1620
	CAGTCTCCGG	AGGAGGCTCT	CGTGTGCGAG	CTGCCCACTG	AGGAAACGGA	GAAGTGCAAG	1680
	GTCAACAGAG	ATGTCTCTCC	CGACAGCTGC	CTGAAAGACG	AGTGGCGGGA	GTGGAGAGAG	1740
	TGCAAGGCCA	CTTGCGCATC	GGCGCTGAG	AGGCGCACCC	CGATATGCAA	GATGACACCC	1800
	CGMAATGGCT	CGATATGCTT	AGCCAGAGCA	TCACAGCGAG	AGATAGTCAT	GATGCGAAGG	1860
60	TGCCACACCA	TCCCATGCTT	GCTGTCCCAA	TGTTCCAGAT	GGAGTGACTC	CAGCTGTGAC	1920
	TGCGGAGAGG	CAATGCAAAC	CCGACAGCGC	ATGTCTCAAT	CTCTGCGAGA	ACTTGGAGAG	1980
	TGCAAGAGAG	ATGTCGAGAG	GTGCGTAGAG	TGCTATCTCT	CCGATATGCC	CATGTAGCTT	2040
	GAGCTCACCG	AGTGTGCCCA	TGTATCGGAA	TGTAAACAGT	CATGTGGGAA	AGGCGCACGT	2100
	ATTCGAACCC	GGATATGCAA	AATGAGGCTT	CAGTTTGGAG	GTGACCCCTG	CCGAGAGACT	2160
65	GTGCAAGCGAA	AAAGATGCCG	CATCCGAAAA	TGCTTTCGAA	ATCCATCCAT	CCAAAGACTA	2220
	CCGTCGAGAG	AGTCCGAGAG	CCTCTGAGAG	TTCCATCGAG	GAAGTAGAGT	CAGGACACTA	2280
	GAGCGTCTTC	CAGTGTGTAG	GATGCGCCCA	TGAGACGGCT	GTTGAGATG	CAACAACTG	2340
	TGCGAGGGTG	GAATTCAGGA	ACGTTACATG	ACTGTAAAGA	AGGATTCGAA	AGCTTCCGAC	2400
	TTTACCGAGT	GCAAGAGCAA	GAGAGGAGAT	AGAGCTAGAT	ATGTCTATCC	TTGTAGACCA	2460
70	GGTGAAGAGT	AGTCAACCAAT	ATCTGCTGAT	ATTCAGAGAT	CCAGAAAGCT	TGGATTAATT	2520
	CTTGTTTAAA	GACAAATTTA	ATTTGTGTAO	CTAGTTTCA	TTTTTCAAGT	TTTTTTCGCG	2580
	CAGTAGTCTT	GTGATGCCA	GAGACATCTT	TCTCTGAATC	TCTCTGATGG	GTACAGGCTG	2640
	AGTGGGCGCG	CCTACCTCTC	AGCCAGGCTC	TCTCTGCGGA	GGATTAGAGT	CAGGACACTA	2700
	GTACTAGCTT	GATCTGAGAG	CCTCTGAGAG	TTCCATCGAG	CCAGAGAGGA	CCGAGACTGT	2760
75	GACTCACTCT	ACATGAGAGG	GCAACCATGT	CTGAGAGTGA	CTATGCTGTA	GTCCAGAGGT	2820
	GGGGCAGGTA	GAAACATTC	ACAGATGAGG	ACAGCAGAT	COCCACATTC	TCACTTTTGG	2880
	CGTGTGCAAT	GAAACCATTT	TTTGCCCATC	TCTCTTAAAT	GAACCTTAGG	GTCTCTTTTC	2940
	AACTGCTCTC	AGTCAACAT	AGTCTCTGAG	GAAAGACAG	GCTGTGAGC	TAGAGAGGTA	3000
	CGATTAGTGT	TGGTGGTCTT	AGTTCTTTTC	ACTAGAGAAAT	TGGGATATCA	TCTCTCTCAC	3060
80	CGCTGATAT	GCTGTCTGAT	GCCTCCCCCA	CAAAATATAA	TAATATAAT	ATGCTGCTGT	3120
	TATTTAAATA	TAGAGTACTT	AGTTTTCACA	CTGAGATATA	TAATAGACT	TAGAGATGTA	3180
	TTTTCTGCTG	CTTCTGAGG	TTACAGAGAG	TTCTCTGAGA	TTCTCTGAGA	AGGAGGCTGT	3240
	CTGACCTTTT	TGGTATATAA	TCCATTATGG	AACAGAGCAA	AGGAGAGCAA	AATTTGGTCT	3300
	TTTAGAGACC	AATTTGCCATA	AATTTTAAAA	TCTTCTACCA	CACATCTAGA	CTTTCAAGTT	3360
85	TGCAATACAG	TTTTTAGCAA	GAAACATTTA	TGTCTATACA	AGCATTTTTC	TAACTGTGCG	3420
	CAAGGCCCC	CCATGTGATT	CCTTCAACCA	AATCACTCT	CTGTACTTTA	AAATTAATTT	3480

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 TGCTCCACAC CAGGGCTGTG GTCTCCCGAG ACATGCATAG GATAGGCCAC AGGTTTAGCC 3660
 TGCTCTCCA GCAATATAT CACAGACAGA TTGCGGAGAA CTGACACACA AGGGATAGTG 3720
 TAAAGGAGCA TTCTCTCAGT TGGGTCCATC AGCAGTTTCT CTCTCTGCAT TTATTGTTGA 3780
 AACTATGTTT TCTATCTCTT CTTTATATAG CTTTATATCT GCTTAAATCA AATGTGTGAC 3840
 ATTGTGTAGA CACTAGACAT CATCTGAATA ACTACGAAT TTGTATTATA CACTACAGA 3900
 TATTTCGAAA TACA CATAG TATATCTCTG AATATGTACT TTAAACACA AGAGACTAT 3960
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 AGATTTTTAA CTACAAAAAT G .

Seq ID NO: 6 Protein sequence
Protein Accession #: BAB18451

1 11 21 31 41 51
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 25 MRSLPAPLKL SRTPALLALA LPLAALAFS DETLDRVPS EYCSIRLRA QGTRREYITE 60
 FLRLVSDNDP PYKPGTSYRV TLRAPPPHY RGPLTLALRE NRGDKREHH AGTFQILDER 120
 ETQFMHWCPV AYKPLTFRRA TRLQWFLAP PASTGCVLK ASVQVRIIT PQGRSLRTH 180
 LCRSDITFDG VDRKPLIDCC ACATAYKRLT FYQMSKETH PKDYPRNRH KSAIIGGHS 240
 KHYVLYEYGG YASGGVQVQA ELGSPVMSRE EIROOSDEVL TVIKAAQWP AQOLPNVRA 300
 30 PAEPEYVDRT RHLMSPILTM GPEDPVRNGL SAEGLCTICE GPVQKRVQSL IPMDAGTDS 360
 VYTESPHTLT IPEKRIPLT ELGHRQSPYF DPDSGTLTV ARVLEILAL KGRGNTVPE 420
 NVDDIVADLA PEREDBDTP ETCIYSNPS WSACSSSTCD KGRKRRRLR KAQLDLSPC 480
 POTQDPQPCM PGSCSDDEGS TCTMSBHTM SPGCSISQMG KRSREYVRQ FPEDGVSCTL 540
 35 PTEREKTCTV NECPSPASCL MTEWGEWDEE SATCOMMKR KHRMIDENPA DSGMCAETS 600
 QAEKQKQPCG RTPLCLSPH SENSICSTCT GKGWRTKRP LKSLALGDC NDLVRTEK 660
 MLPCPDIDCE LTMWSQWSEK NKSGCKEIVI RTMILQMEP FGGAFCPETV QREKCRIRK 720
 LRNPISQKLR WRHARESRS EQLKEESDGE QFPGCRMLP TAMSECTKLC GGLIGERYMT 780
 VKRRPKSSQF TSCDKDKGIR ACNVHPC

Seq ID NO: 7 DNA sequence
Nucleic Acid Accession #: NM_022454
Coding sequence: 205...1449

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 AGAACACCGG CGCGCGCTTC GGGCGCGAG AACCCGCGAG CCTCGCGGC ATTCGATGTC 120
 CTCATTCCCT ACTCCATCCC CGGGTCTCGS GAGCGCGCGC CGTCGCGCGG AGGGTTGAG 180
 50 GAGCGCGGCG AGGCGCTGGAG GCCTATGAGC AGCCCGGATG CGGATACGCC CAGTGACGAG 240
 CAGAGCCAGA CCGACGAGCCG GCTGCGCGCG GTATAGTGCG GCTGTGGGCC CTGCGCCGTG 300
 GCCAGTTCAC TGAGCCCATC CGSGAGGATG AAGTGTGAAG GCGAGCGGCG GCGGAGAGC 360
 GAGACACCGG CGCGCGCGCG GSCCTGAGCC AAGCGGAGGT CCGATATCGC CGCGCGCGATG 420
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 CTGACACAGC CGAGGTTGAG CAGAGTACTG GCGAAGTTGT GBAAGGCTCT CAGCTACGCG 540
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 55 CCGCACTACA AGTACCGGCG GCGCGCGGCG AAGCAGGTGA AGCGGCTGAA CGGAGTGGAG 660
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 CGGCTGTGCA TGAGCGGCTT GCGGCTCCAG TCTCCGACAG AGGGCTCTCC CGCGCGCGCG 780
 CGCTCTCTCG CTGCTGAGCG TACCGGCTCG CAGCGAGCTC GAGCGAGTCT GAGCGGCGCT 840
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 65 ATGCAGCGCG AACAACAGCA CAGACACAGC CACACAGACC ACCCGCGGCG CGCGCGAGAG 1140
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 GAGCTCTCTG GAGAGGTGGA CGCAGCGAAA TTGAAACGAT ATCTGACCTT CGTGTGCAAG 1260
 70 CTTGAGATGG GCTCTCCCTA CAGGGGATCT GACTCGGTTG TGAATCTCCC GACAGACGAG 1320
 GGGGCGATT CCGTGGTGGT GTCCGAGCGC AGCTCTCGCG TATATTACTG CAACTATCTT 1380
 GAGCTGTGAC AGTCTGAGCG TCCCGCGGCG CCGCGAGCGC AGACGAGTGT TACTAGCTCT 1440
 CCGTGGAGTG CTAAGAAJAT CCTGAGACTC CTGGGTTTT TGTGTTGCTG TTGTTGTTTT 1500
 TAAAGAGGTG TGTGTGCTTA TAATTATATT TAATTATATT TGTCTGCCAC TTGAGAGTTT 1560
 TGGGCGGCTG AGGTTTTCATT TAAATTTTGT TCMAGAGATT GTTTCCACAA GTTGAGTTT 1620
 75 CAAACCCCTA TACTGATCTT CAACTAGACT GTTCTGAGTT GTTCCGAAA ACGCTTCT 1680
 CCAITTCCTG AAGTGTATT GATCAAGAAA ATGTGTCTCT GGGTGTGTTT TTTCACTCT 1740
 CTAAGAAATA AATCTGTGAA TCTGTAAAAA AAAAAAATA AAAAAAATA 1800

Seq ID NO: 8 Protein sequence
Protein Accession #: NP_071899

1 11 21 31 41 51
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 AERLRVQIMQ DHPHYKYRFR BRGVFLBGLA EPQAAALRGE GORVAMDGL 180
 LQPFQHFPA GPPLLPPIHG GHTDQCSLG APRLDGFLP TVTSPLEQV DHPAFAP 240
 85 HRCDSFANG YSYAGQSDTA GPPEPPAGIM HEPLEPRAG PSIKLLAPF SALRYVYGM 300

GSPAGGGGRG FQMOPQHQQH HQHQHPPPGP GQSPSPPEAL PCRDGTDPSQ PABELGEVDR 360
TEPEQYLKHFV CKXENGLPYQ GHDGVLNPLD SHGAISVVVS DASSAVVYCN YDGV

Seq ID NO: 9 DNA sequence		
Nucleic Acid Accession #: NM_018098		
Coding sequence: 112..2856		
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1	AAGCTTGGCG	CGCCGCGGCA GGAATGGCGG TATTGTGAG AGGAGTCGCG GTTGAAGAG 60
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	GAGAGATGTC CTCAGATTGA	AACAAGAGTG ATATTGGTTC AAGAAGCTGG AAAACAAGAA 300
15	GAACCTTATA AACCTCTTAA	GACTATTAAA ATATAGGAGT TCCGTGTTAT AAGATATAAA 360
	GAAGATGTCT CCGAAGAGC	GGATGABAAA GTTTATGA TAAGGACTAT 420
	AAAGTGGGCT CTGTAAGAAT	GGAGCTCAGT GAAGAATTG AAGTGTGGA TTCTYCGAA 480
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	TGCGCATTTT CAGTGCGCC	GTGTTATTGT ACAGATGAGA TGAACTTAGT ACTATGCTT 660
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	GGAGTATTTC GAAAGAGCTT	TAATTCAAAA GTTACACATT TGGTGGCAA TTGTACACAA 780
	GGAGAAATAT TCAGGSGTGC	TGTGAGTCTA GTTACTCCAA TTATGAMGC AGATATGATT 840
	TATAAGCTTT CGGAAAGCT	GATTAACGAT GATTTCTGAT CAGCTAGTGA TGACTTTGA 900
	AATGAATTTA AAGTCTCTCC	ATTTCAAGAT TGTATTTTAA GTTTCTGGG ATTTTCAGAT 960
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	GGAGATGAAA GATGCACTCA	CCTTGATGTT GAAGAGAATA TAGTAAAGA TTTCCCTTT 1080
	GAACCTTGGA AGAAACTTTA	TGTGTATGCT CAGAGATGCT TCTGGGAGT CATCTCAAA 1140
	GATGCCCGAG CTGCGAAGAC	TATGTATTTA TATGAAAAGG CAAATCTCCG TGAGCTCAAG 1200
	AAATCAGTGT CAATGCTTTC	TCTAAATACC CCTAACAGCA ATGCACAAAG AGTGTCTTA 1260
30	AAAGAAGCAC TTGCTCAGCT	TTCAAGAGAG ACAGAGGATG CACCATCTCC ACCCTGTAAG 1320
	CGCCCACTG CTGAGTCTTC	CTTTTCCATA GGTTCTGCTC TAGATATCTC CAAACAACC 1380
	GAGTGTAGCA TTAACATGAG	AGACACCCCA AGTCTTTGTA CTAAGTCTTC TAAAGAGTCC 1440
	ACTCGAGTTT CTCTAAGCA	GTCCAGCAGG TGGCAAGTGT CAAAGAGGCT TTATCAAACT 1500
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	CGATTACTTT TAAATGATCT	TAGAGAGCAT ACAGCTGATG AAATATCAGA CAAAGAGACT 1980
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	ACCCCTCTGG ACAGAGAGGA	ACAGATTAAT CTCTCTCTCT TGAATGATG TCTAGGTGAT 2220
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	CCAGCTCTCT TTAAGCATAT	TCACCTAATG CCTCTCTCTC AGATTAAGAA GTTATTGGAG 2340
	ATAAGAGAGA CAGAAGATTG	CCATAATGCT TTGCGCTTGC TTGTGAGGCC ACCAAGAGAG 2400
50	CGGCAAAATG TGCTACTGAG	TTTCGAGTAT ACATCAGATG AACTTCCAAA AGAAACCTGG 2460
	CTAAAGATGC TTGTGTGACA	TGTACTATAC ACCATTGTGA AAGCAGATGC TGAGATCTCT 2520
	ATTATACTGT CTGATCCAGA	ATCCTTTTGA GTAAATACAA AAGATATGGA CAGTATGAT 2580
	AGTAGAGCAT CAAAGCAAT	AAAAAGAGCT TCAAAAAGAG TTACAGAGGC ATCTCTCTTC 2640
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	CGAAGATGTC CTTCACGAAA	TGATATGATC GTTCTCTAGA CACATCATCA 2760
55	TAGCAGATTA TCCCTCTCC	CTCCCTTGTG AGCCTCTCTT CCTCTCTTGA AAGGAGAAGT 2820
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	AGAAATGATG GACAGCTCTA	TACTCAATA AGAAATGATC TAAATGATA CTGTAAATTA 2940
	GCATCTGTGT AAGCTTGAAA	GAAGATATAA TAAACATAAA CATGCTATT TGAATTTCT 3000
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65	TACCAAGCTC CTATGATGTA	AGTCTTGAGA TTTTATTTTG AAGATGATG ACCATGAGA 3420
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	TTTTGCAAAAT TGAGATAAGG	ACGAAAGATG TGAAGAACAT TGTATTATT GCCAAAACAA 3540
	GATGTTGTGA GCYTGTTCAG	AGGAGGTACG GTATATTAT GTATATTTTA TCACATGAGA 3600
	AACTCTTGT TATGTGATCA	AGTCTTGAGA TTTTATTTTG AAGATGATG CCATGTGAGA 3660
70	ATTGTGGTAA AGACTGTCTT	TACCCCTCAT GAAATATCT TGAAGTGGC ATCAGTTTGA 3720
	CTAATCTCTA GTGAATGCA	TAGATATGCG CATGTCCAAC TTTTATTTGT GGCTTATAA 3780
	TAAATGTAAA AATTCAGAA	TCAATTGCGG TGATATCTTT CACATAGGCC 3840
	TTTTTATGAT CAGTATGAA	GTTCATAGTA ACAAAAGCAT TTTTATTTCC 3900
	TATTTCTTTA GGAATGCTTA	CAAAATGTTT TCACTTAAT TCAAGTTTTC TGTTTTAATA 3960
75	GTAACTGAC TATAGATTGT	ATGCTATGCG ACTTCTGAG AGTATGAAT 4020
	GACTCTTTGC TAAATTTAAA	AAGCAATGTG ATTAGTANGA ACTTTGAAA TAAATAGCTA 4080
	AATCCCAAAA AAAAAAAA	AAAA

Seq ID NO: 10 Protein sequence		
Protein Accession #: Q9H8V3		
	1 21 31 41 51	
1	MAENSLVST	TQRLSLADGS IPDSEKTEIS KENLLIGSTG YVEEDHQIE TRVLVQAG 60
	QKDELTKALK	DIKSEHSLGK SVSEHSHLDS PEPEHVFVPL PQDQVPRDL YEACDKVGF 120
85	PVYLKCSGKG	ESLPLGFCRPL YCTG90MLVL CFTGPRKKEK LVRLVTLVSH MGVIRKIDEN 180

5 SKVTHLVANC TQGRKFRVAV SLOTPIMKPE WYKAWERNR EQQFYAAVDD PRNEFKVPVP 240
 QQCIPSPGLP ASDERKTNMBE MTEMQAGKYL PLGDERCHTL VVENHIVKDL PFESPKLYL 300
 VQENFWGSI QGDAAGNTPE YLYEVANPE LACKSVGLDL WPHENRNRH ELASTLAQLS 360
 EDTVSPFPF RKPSRAEHLI SIGSLDLSIN TRESSINYGD TPSCCTRESK GSTFVPSQS 420
 ARMQVAKELY QTESNYHML ATTILQVQPV LEESQQRGGP ILAPEIKTI PGSPIDPVD 480
 HTKIGDLEED LVMWDBSKS IODIFYLKYK DLVKTYPPVY NPFEMSKETI IKCKEQKPRF 540
 BFLATINQAR PRCQRLQVY LILPQRLPL SVALLADLK HTAFNDNPKR TPLERAGSI 600
 KEMTHINLED KRTEHQKOT FDUVYEDGC PANLSSHRS LQWQVETISL GENPCDRGQ 660
 VTLFLNDCL EIARKHRKI GTFRSPHQGT RPASLKLHI LMPLSQIKVY LDIRETECH 720
 10 NAFALLVRPP TEGANVLLSF QNTSEDELYS NMLNMLCRIV ANTKICADAE NLIYADPFS 780
 FEVNTFEDPS ELBAEALIS KRTKPTAF SPKFTKRAL BRALATSHGS VQDRSPSPND 840
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Seq ID NO: 11 DNA sequence

Nucleic Acid Accession #: XM_044166

Coding sequence: 1..1576

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 20 CTTTGTTC GCATGCCTA TCTAGTGCT ATCTGGAATA ATGGAAGAA ATGGGGGCTT 60
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 CAGGGGGGGC GAGGAGGGGG GAGGTGGGGG GGGCGGCGCC CCGCGCGCAG GACAGCGCCC 240
 CCGCGAGCGC GCGGGGGG GCGCGCGCGC GCGCGCGCGC GCGCGCGCGC GCGCGCGCGC 300
 25 GCGAGCGGAG AGCGCCGACG CCCCCACGCG CCCCCAAGGG GCGAGCGAGC CGAGCTCTGT 360
 GCCTCTCTAC AAAGGCGGCG AGCTGCGCTC GAAGGGCAGC AGCAACACCA CGAGTGTGT 420
 TCCGTGGTGC ACCTCGGAGC AGTGGGCGA GATCTGGGCG AGGCAAGGCT CGAGATTAAT 480
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 30 GTCTCTGCT CTGGCGCGCC AGGTACACAT CCGTGTCTAC GTGCGCTTAC GCGTGTGTG 720
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 80 AGAAACAAA AATACGAAA AAAAAAAA AAGCAGTCT TTATATATT AATATTCTAT 3360
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Seq ID NO: 12 Protein sequence

Protein Accession #: XP_044166

1 11 21 31 41 51
 1 | | | | |
 80 PCFAMPSIIV SOMERNRQVY GELGCTFGSA KDRGLEDER ALQLALDQLC LIGLSEPPAP 60
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 ALYBAELRL KGSSTFSCY NPTFSIVAS TVGQGVLLK NRGATFTI KTVRGEQPY 180
 85 FWTGTREVD ATAREIISA ASFEMIRAS RNKSGAANFV APALPGQVTI RRVKPYRVVG 240

LVVPGKGTAT KRIQQQNTY IITPSRDRP VFEITGAPGN VERASEEIST HIAVKTGKIL 300
 EYNNBNDFLA GSPDAIDDS YSDAWRVHQP GCKPLSTFRQ NSLQCIQECG YDSGPBAPRL 360
 QEGSQDFRG GYLFPAGQVG KQDVTRGVAF TSPFLAQGE NARTFVSFLS SASSESSISA 420
 KASQGPQAM RSPATSNQPE LMLPSRPFG EPLQGPQSKG RGSQSPVGG KDCQVFESE 480
 5 VTAALVPCQH MLFPCQCAVR ICERTDFECP VCHITATQAI RIFS

Seq ID NO: 13 DNA sequence

Nucleic Acid Accession #: Eos sequence

Coding sequence: 1..2982

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	GATACATGAT	ATTCGACGTT	GTGACACACA	CTGATATGTA	CTTTAAGGCT	ACTCCCTTCA	180
15	AAACGAAAGG	AAAAATGCA	AATCACTATA	GTAAAGAACT	TCATGAGCTC	AGGGCTGAAA	240
	CCTCAGAGAA	ATATATGCA	TTTGTACTCT	ATTGCGAATG	ACTGACGACT	TTTATAGAGT	300
	GAGATCATGT	TTCAATATGA	TAAGAAGAAG	ACTGTTCCCC	AGATACAAAC	TATAAGCAAT	360
	GCACTCTTAA	CTGGAGTCTT	GTCTCTAAGT	GAATTAJAAC	GCTCGAGAGT	CACAAJAACC	420
20	CTGCAAAACC	TAGTGTGCT	TTACTTTATA	ATGTGTGCTA	CAGCGAGAGC	CGAAAGACAA	480
	TTAAATTGTA	CATTCAAAAT	AAAACGTAAAT	AATACAATGA	ATGCAATGTC	TGTAATAGCT	540
	GCTTTGGAAA	GAGTAAAGAT	TCGACAATAT	GAACACTGCT	GCTGTTCTGT	CAGGATATCC	600
	TGCCCTTCCT	CCCCGAGA	GTGGGAAAG	CTTCAGTGTG	ACCTGACAGA	TCCCATGTTC	660
	TGTTCTCTGT	ACATCCACG	TGCCACACG	TTTCTTCTCA	GCAATCCAT	CCCATGTGTG	720
	CCTCGGCGCA	CTGTGCTTTC	CCAGGTCCCC	AAAGCTACCT	CTTTTGCTGA	GCTTCAGAT	780
25	TATTCACTGT	TGACCCACAA	TGTTCCCTCT	CCAAATAGGG	AGATTCAACC	CTTTTCAACC	840
	CAGCTCTCAG	CTCCCTATGC	TGTCAGCCCT	GCCATTGACA	TGCCCCCACT	CTTGGAAGCA	900
	ATCTCTCTGT	CTATCTCTCA	AAACCAATCT	TCCGACACTT	CAAGTCTCTT	GAAGAGCTCT	960
	TTTCTCTCTC	CCACCTGTTC	TGCCCGATGG	AAATGTCAACA	CTACCAAGGC	ACCTCTCTTC	1020
	CAGACAGACA	TGTTCAACAC	CAGAGATGAT	TCTGATCTTG	AGAACCAAGT	TTGTCCAGAT	1080
30	GGAGAGCTCT	TGTTCTTGGG	CAGCTCGGAG	CTCAATCTCG	CAGGAGAAAT	GATGACACAA	1140
	GTGAGGAGAG	CTGTCTATCT	CCGACCTCAG	ATGCTGGCTC	CTCTGGTCTA	AAAGTTGCTG	1200
	AAAGTAGTGG	ATGACATGGG	CCTACAGCTG	AACTTTTCAA	ACACAGCAAT	AAGTCTAACG	1260
	TGCCCTCTCT	TGCTCTGCTG	TGTGATCAGA	GTGAATGCCA	GTGATTTCAA	CACAACTACC	1320
35	TTTGTGGCCG	AAAGAGCTCC	AAATCTTCGA	GTTTCTCTCG	AAACCCAGAC	TCTGTGAGAC	1380
	AGTATTGCGA	CAATCTCTCA	TCTTCTCATG	CTGATGATTA	ATTTACACG	TCAATGATCT	1440
	GAGCTAGCTT	CCAGGTTTCA	GTTCATTTT	TTTGAAAGAC	CTGCTTTGTT	TCAGATCTCT	1500
	TGCCCTGAGA	ACCTCTCTCT	GATCAGCATC	GTCATATCAT	CAGATGTGAC	AAACCTAGCC	1560
	GTGAGAACT	TGACAGAGAA	GTGTACAGCT	ACATTTATGC	AGCTCAACCC	GAGCCAGCAT	1620
40	GAATTAACCA	TGATATGTTT	ATTGTGGCAG	TGTCGAGAAA	ATGTGCGCAG	AGAGCGAGCT	1680
	TCAGACAATG	GCTCTCTGTG	CAAGACAGAG	AGATTGAATG	AAACCATCTG	TACTCTTAGC	1740
	CATCTAACAA	GCTTGTGCGT	TCTGTCTGAC	CTATCTAGGA	CATCTGTGCT	GCTCTGCTAA	1800
	TGATAGGCT	TGAGCTCTCT	GTGATGATAT	GTTGTGGGAG	TTTCAATCA	TTTCTCTGTA	1860
	GTUACTCTTG	TAACTACAT	AGCTTTTGA	AGATATCGGA	GGGATATACC	TCTGAAATAC	1920
	CTCATCCAGC	TGTTGTCTGC	CTGTGCTCTG	GTGAACTGTG	TCTTCTCTCT	GAGACTCTTG	1980
45	ATTGCTCTGT	ATAAGATGCA	AGGCTCTGCG	ACTCTGAGCG	CTGTATTTCT	TGATATTTT	2040
	CTCTCTGTGT	CATTGACATG	GATGGGCTCA	GAGCATCTTC	ATTAATGACT	GCCCTCTTTC	2100
	AAAGTATTTA	ATACTTACAT	CCGAAATATC	ATCCTTAAAT	TCTGCAATGT	CGTGTGGGGG	2160
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	TGCTATGAGA	AAATCCCAAA	TGTTTACACG	GATGACTCTT	CTGAGATCAA	CAACAAATCA	2280
50	GTATTTCTCA	TTACCGTGCT	GGGATATTTC	TGTGTGATAT	TTTTCGAA	CTCTGACATG	2340
	TTCAATTGCG	TGCTGTGTTCA	GCTCTGTGGA	ATTAAAGAGA	AGAGAGCACT	GGGAGCCGAG	2400
	CGAAAACCCA	GTATTCAGAA	CTCCAGAGGT	ATGCTGGGCC	TTACATTTT	ACTGSGAATA	2460
	ACTTGGGGCT	TGTTCTCTTT	TGCTTGGGGA	CGAGTTAAGC	TGAGCTCTCT	GATCTCTGTT	2520
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55	AATGTCAGGA	AGCAATGGAG	CGGGTATCTT	TGTTGTGGA	AGTTACGCTC	GGCTGAAAT	2640
	TCTGATCGGA	GTAAATCTCC	TACTAATGTT	TTAAAGAGAG	AGACTGTAAA	CCAGAGAGGT	2700
	TCCAGCTCTT	CAATATCTCT	ACAGTCAGAC	AGTATCTCC	CTAATCTCAC	CAGACTCTCA	2760
	GTGATTAATG	ATTGCTCTCA	ACACCAAGAG	GGGATGAGAA	ATGCTCTCAC	AGAGAGGAAT	2820
	GGGGTCTCTT	TTAGTGTTC	GAATGAGATG	GTGTGCTCTC	AGGATTTTAC	TGGAAGAACG	2880
60	CACATGTTTA	ACGGAAGAGA	AGATTCCTGC	AATGGGAAGG	GCGATATGCG	TCTCAGAAGG	2940
	ACTTCAAAGC	GGGGAAGCTT	ACACTTTATT	GAGCAATATG	GA		

Seq ID NO: 14 Protein sequence

Protein Accession #: Eos sequence

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	NESTKTKITI	VKTPNAGVYK	PQKNTCHLS	LCNDSAPFG	EMFQYDKES	TPVQKNTLN	120
	GTPLVGLG	HEGSEILFET	FATLGRVET	MCATASAGST	LCNFTIKLN	NPMCAVIA	180
70	ALERVKIRAP	EMHCSSVRIP	CFSPSELEK	LQCLQDPDV	CLAHDPRFP	FESSQSIPV	240
	PRATVLSQVP	KATSAFEPD	YSYPVTHNPS	PIQSIQPSLF	QPSAIASSP	ADIMPQSGT	300
	ISSPMPTVTH	KATSPPVKAS	PSPSTVSLPA	NVMTSAPPV	QTDVMTSIS	SULRNLQW	360
	EEALLSGLE	PHLAGNNG	VERLLHPPD	KLAPLQRL	KWDDIGLGL	NFSMTTSLT	420
	SPSLALVNP	VNAGSNTT	FVQAPQANLQ	VSLSTQAPEN	SIQTTLES	LAENLPHMD	480
75	ELASRVQVIR	PETPALQDPP	SLNLSLSISY	VISSVANLT	VRLNRNTVY	TKRHNPQGO	540
	ELTRVCFVMD	LDRHGGRRGM	SDNGSCVDR	KLRKTEICET	HLTFSPVGLD	LSRVSPLAQ	600
	HWALTYITV	QGLSEILFET	VTLYTILAE	KLRDYSK	HLQCALLL	MLHFLDSWG	660
	IALLYMQGLG	ISVAFPLTFY	LVLSFTWML	EAPRNYLAL	KFVNITYIKY	ILKECFIDG	720
	VPAVVVTILL	TISPNDVGLG	SVKGFPGSG	DDPCVINNA	VFYITVQVY	CVIPLANVS	780
80	PIVVLQGLK	TKKSGGLQAG	RKSTIGQLS	LAGLTFPLGL	TRGAPFAPNG	PHVNTYILF	840
	ALRNTVQLGP	IPVTCVLA	VFKQWRSR	CCRLKRLER	GWDSKTATNG	LKEQVTNQVQ	900
	SSSNSLSDS	SNSTNTSTLL	VNNDCKSVHS	QGNNASTERN	GVSPSVQNGD	VCLSDFTGQ	960
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Seq ID NO: 15 DNA sequence

Nucleic Acid Accession #:		Eos sequence						
Coding sequence: 1..2904								
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		GATCTAGTAT	ATTCAGACTT	GTGACACCA	CTGATGTTTA	CTTTAGATCT	AGCTCTCTCA	180
		AACGAAACAG	AAAAACATTA	AATCACTATA	GTAATAAACCT	TCATATGCTT	AGGCGTCAAA	240
		CCCGACAGAA	ATATCTGCAA	TTTGTCTACT	ATTTCGAACT	ACTCAGAGTT	TTTTAAGAGT	300
10		GAGATCATGT	TTCAATATGA	TAAAGAAGAG	ACTGTTGCCA	GAATACCA	TATAAGAAAT	360
		GCACACTTAA	CTCTTAAGT	GAATTAAGA	CATTAATG	TACATCTCA		420
		ATAAACTGA	ATATATCAAT	GAATGCATGT	GCTGTAAATG	CTGCTTTGGA	AAAGTAATAG	480
		ATTGACACCA	TGGAACACTG	CTGCTGTCTT	GTACAGGATC	CTCCGCCCTT	CTCCCCAGAA	540
		GAGTGTGAAA	AGCTCTGAGT	AGACCTGGAG	GATCCCATTT	TGTGCTTGCC	TAACATATCA	600
15		CTCGCCGCTC	CAATGCTTCT	CTCCAGTGG	ATCCGATGAG	TGCTGTGCTT	CACGTGCTT	660
		TCCGACGTCC	CCAAAGCTAC	CTCTTTGTCT	GAGCCTCCAG	ATTATTACCT	TGTAACCCAC	720
		AATGTTCCTC	CTCCAAATGG	GGAGATTCAA	CCCCCTTCAC	CCGACGCTTC	AGCTCCCATTA	780
		CGTTCGAGCC	TGCGCATTTA	CATGCCCCA	CAGTCTTGAA	CGATCTCTTC	CCATATGCC	840
		TAACACCATG	CTCTGCTGCT	GTGAAGAAGT	CATTTCCTCT	TCCGACCTGT		900
20		CTCGCCCTGT	CGAATGTCAA	CACATCCAGC	GCACCTCTGT	TCGACAGAGA	CATGTCTAAC	960
		ACCGACAGTA	TTTCTGATCT	TGAAGACCAA	GTGTTGCGAG	TGGAAGAAGC	TCTGTCTCTT	1020
		GGCAGCTGTG	AGCTCAATCT	CGGACGAGAA	ATGATCAACC	AAGTACAGAG	ACTCTCTCAT	1080
		TCCGCCCTGT	ACATGCTGCT	CTCTGTGCTT	CAAGATGTC	TGAAGATGAT	GGATGCTATT	1140
		GGCTACAGC	TGAACCTTTC	AAACACGACT	ATAAGTCTAA	CTCCGCCCTT	TTTGCTCTCT	1200
25		CGCTGTATCA	GAGTGAATGC	CAGTATGTTT	ACACAACTA	CGTTTGTGCG	CCAGAGCCTT	1260
		CGAATCTTC	AGGCTCTCTT	GGAAACCCAA	CGTCTTGAGA	ACGATATTGG	CCAAATTAAT	1320
		CTTCTCTCAT	CGTGAATGAA	TATTTACDCA	GCTCTAGACA	TGAGACTGAC	TCCAGAGT	1380
		CAGTCAAAAT	TTTTGAAAC	ACCTGCTTGG	TTTCAGGATC	CTTCCCTGGA	GAACCTCTCT	1440
		CTGATCGCT	ACGTCAATCT	ATCGATGTTT	CGAAACCTGA	CGTTCAGAGAA	CTTCAGACAA	1500
30		ACGCTGACG	TCAACTTAAA	GCACATCAAC	CCGACCCAGG	ATGATGTAAAC	ATCGAGAGAT	1560
		GTATTTTGG	ACTTCTGAC	AAATGTTGCC	AGAGAGAGCT	GCTTCAGACA	TGCTCTCTCT	1620
		GTCAAGAGCA	GGAGATTTGA	TGAACCATCT	TGTACTCTTA	GCATCTTAAC	AAAGCTTGCG	1680
		GTCTCTGTG	ACCTATCTAG	GACATCTGTG	CTGCTGCTCT	AAATGATGCG	TCGTAGATTC	1740
		ATTACATATG	TGTTTGTGG	GCCTTATCTA	ATTCTCTGTT	CAGTCACTCT	TGTAAACATC	1800
35		ATACCTCTT	GAGGAATATG	CTCTTCAAAA	TCTCATCTCA	CGCTGTGCTCT	GTATAGAGAT	1860
		CGCTCTCTCT	TGCTGAACCT	GGTCTCTCTC	CTGAGCTCTG	GGATGTCTCT	GTATAGAGAT	1920
		CAAGCGCTCT	CGATCTCACT	GGCTGTATTT	CTCTCATTTT	TCTCTGTGCT	CTCATCTACA	1980
		TGATGTGCC	TAGAGACATT	TAGATATATC	CTGCGCTCTT	TCAAGTATAT	TATACCTATC	2040
40		ATGCCAAAT	ACATCTTAAA	ATTCTGCATT	GCTGGTTGGG	GGGTACAGC	TGTGTTGTGT	2100
		ACCATCATCC	TGACTATATC	CCGACATAAC	TATGGGCTTG	GATCCTATGG	GAATATCCCC	2160
		ATATGCTTAC	CGATGACTCT	CTCTGTGATC	ACACAACTAA	CGATATCTTA	CATTAAGTCA	2220
		TGCGGATATT	TTGCTCTCTT	ATTTCTCTCA	ACACTGACCA	GAATGATCTC		2280
		CAGCTCTGTC	GAATTAATAA	GAGAGACCAA	CGGACGCCCC	AGGAAATAAC	CAGTATTCAA	2340
		GACCTCAGGA	GTATGCTGTG	CTTTACATTT	TACTTGAGAA	TAATCTGGGG	CTTTGCTCTC	2400
45		TTTGCTGGG	GACGCTTAAA	CTGAGCTCTT	AGTATCTGT	TTCACATCTT	TATACACTTA	2460
		CAAGGATTTT	TCAATATCAT	CTTTTACTGT	CTGCTCAGAG	AAATATCTAG	GAGCAATGG	2520
		AGGGCTGATC	TTTGTGTGTG	AAAGTATACG	CGTGGCTGAA	ATTCTGACTG	GATTAATACT	2580
		GTACTATATG	GTTTAAAGAA	GCAGACTATTA	AACCAAGAGG	TGTCAGCTCT	TCCTAAATCT	2640
		TTACAGTCAA	CGATGAATCT	CATCAACTCT	ACACACATCT	TATGAGATA	TGATCTGCTA	2700
50		GTACACGCA	CGCGGAATGG	AAATGCTCTT	ACAGAGAGCA	ATGCGTCTCT	TTTATGTGTT	2760
		CAGAAATGAG	ATGTGTGCTT	TCACGATTTT	ACTGGAATAAC	AGCATATGTT	TAAAGAGAG	2820
		GRAGATTCTT	CGATGTGAAA	AGGCGGTATG	GCTCTCAGAA	GGACTCTCAA	CGCGGAGAGC	2880
		TTACACTTTA	TGAGCAAAAT	GTGA				

Seq ID NO: 16 Protein sequence

Protein Accession #: Eos sequence		Coding sequence: 1..2811						
		1	11	21	31	41	51	
60		MVFSEVQGH	VGRTEVLITL	KFPLVLIICL	RVVILVLSLE	DTMSSLSLPP	PDVTLSSLPS	60
		NETKRIKTI	VKTFNAGVQK	PQENICHLSS	ICNDTSAPFRG	EHMPQDKES	TVFQKHITN	120
		GTATVLSLE	ELNLTGKAT	LEKLTNPAAC	AVLAASLRVA	IRUPSCISLE	VYICPSSPS	180
		ELEKLQCLDQ	DPVLCADLP	RGSPFSSSGS	IPPVPRATVL	SQVFKATSPA	EPDFDSFVTH	240
		NVPSPIGIEI	PLQPQSPAP	ASSPAIDMPP	QESTISSPMP	QTHVSOTPPP	VKAFSPSPVT	300
65		SAPANWHTS	APPVQTQIVN	TSSIBOLNKG	VLMEKALSL	GLSEPLHAGE	MIHQVSELLL	360
		SPFMHMLA	QELVYVQET	GLQAFENST	ELTSPRLAL	AVHVSAPSE	TTTTFVQD	420
		ANLQVSELTQ	APENSIGTIT	LPSSMLNPLP	ADHMSLASRV	QNFVFETPAL	FQDPSLENLS	480
		LISVVISSEV	NILTVNRLTR	MTVTVLKHIN	PSQSLTVTRC	VPMDLRNNG	RGNSDNGCS	540
		VDRRRINETI	CCSMLTSGS	VLLDLSKSTV	LAQNMALIT	ITVIGCLSS	IFSLTATVY	600
		LAPEKIBDY	PEKILGLCA	ALLALNVPL	LSHSLALTM	QGLCEVAVF	LYEFLVLYG	660
70		WGLEAFIMY	LALVKVNTY	IRKYLLEPCT	VGVGVDAVVV	TIILTISDN	YGLSGYKFP	720
		NGSDPDCWI	NNNAVFYIT	VGVPCVLFLL	NVSMFIVVLV	QLCRICKKIQ	LQARQRTSY	780
		DLRSIAGLTF	LILGTNGFAP	PANGVQVVF	WLPALFPTTF	GGFTTPTFC	VASNRKRW	840
		RYLQCDLRL	LASDSEST	ATMGLKQHT	NOQVSSSNE	LQSSSNSTIS	TTLLVNDICS	900
		VHAGSNKRLS	TERNGVSFV	QNDGVLCHDP	TKQIMFWER	EDSCNGKRM	ALRRTSKRGS	960
75		LMPIDRM						

Seq ID NO: 17 DNA sequence

Nucleic Acid Accession #: Eos sequence									
Coding sequence: 1..2811									
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TTCAAGATAT	TCTTGTGCTT	CATTGTGCTT	CATGTGCTTC	TGTTAAGATC	CTCGAGAGAA				120
GATCTAGTAT	ATTCAGACTT	GTGACACCA	CTGATGTTTA	CTTTAGATCT	AGCTCTCTCA				180
GTTACTTAA	GCTTATCCCT	TTCAAGACAA	ACAGGCGTCA	AACCCAGAG	AAATATCTGC				240

AATTGTGCAT CTATTGCGA TGACTCAGCA TTTTITTAGG GTGAGATCAT GTTTCATAT 300
 GATAAAGAA GCACTGTTCC CCAGANTCAA CATATACGTA ATGGCACCTT AACTGGAGTC 360
 CTGTCTCTTA GTGATATAAA AGCTCCAGAG CTCACACAAA CCGTACGAA CCTAAGTGAG 420
 ACTTCTCTTA TAATATGTC TACAGCAGAG GGCACAAAGCA GATTAAATG TACATTCACA 480
 5 ATAAACTGA ATAATCAAT GAATGCATGT GCTGTATAG CTCGTTTGA AGAGATTAAG 540
 ATGACACAA TGGAAACCTC CTGCTTTTCT GTACAGATAC CCTGGCCCTC CTCGCCAGAA 600
 GAGTGTGAAA AGCTTCAGTG TGACATGAG GATCCCATG TGTGCTTTGC TGACATTCGA 660
 CTGGGCCAC CATTCTCTTC CAGCAATCC ATCCGAGTC TGTCTGGGT CATCTGCTCT 720
 TCCGAGTCC CCAAAGTAGT CTCTTTTGCT GAGCTCTCAG ATATTACCC TGTGACCCAC 780
 10 AATGTTCCCT CTCGANTAG GAGAGATTCAA CCCCCTTCAC CCAGCCCTTC AGCTGCCATA 840
 GCTTCAGCCG CTGACATGTA CATGCCCCA GAGTCTGAAA GAGTCTCTTC CCGTATGCC 900
 CAAAGCCGAT GAGATGTCG CACATCCAGC GCACTCTCTG TCCAGACAGA CATGTCCAG 960
 15 TCCGCCCTG GGAATGTCAA CACATCCAGC GCACTCTCTG TCCAGACAGA CATGTCCAG 1020
 ACCAGCAGTA TTCTGTATCT TGAGAACCAA GTGTGTACGA TGGAGAAGCG TCTGTCTGT 1080
 GCGAGCTGG AGCCTTAACCT CGACGAGGA ATGATCAACC ATGTGCTTGC TGTGCTCTGT 1140
 TCCGCCCTG ACATCTCTC CTTCTTGCT CAAGATGTC TGAATAGT GAGTCTCAT 1200
 GGCCTACGC TGAATCTTC AAACAGAGCT ATAGTCTCAA CTTCCCTCTG TTTGCTCTG 1260
 20 GCTGTATCA GAGTGAAGC CAGTATGTTT ACACACACTA CTTGTGGCG CCAGAACCTT 1320
 GCAATCTCT GAGTCTCTG GAAACCCCA GCTCTCGAGA CAGTATGTC CACATTCAT 1380
 CTCTCTGA CCGTATGAA TAATATACA GCTCATGACA TGGAGTAGC TCCGAGGT 1440
 CAGTCAATT TTTTGAAC ACCTGCTTGT TTTCAAGATC CTTCCCTGA GAACCTCTCT 1500
 CTGATCAGT ACCTCATAT ATCAGTGTTC GAAACCTGA CCGTACAGAA CTGACAGAA 1560
 AACGTACAG TCACATATA GCACTCAAC CCGACCAAG ATGATTAAC ATGAGAGAT 1620
 25 ATATTGGG ACTTGGGAG AATGTGTGCG AGAGGAGCT GGTACACAA TGGCTGCTCT 1680
 GTACACAGA GGAGATTGA TGAACCATC TGATCTGTA GCACTTAA AGCTTCCG 1740
 TGTCTGTG ACCATCTAG GACATCTGT GTGCTGCTC AATGATGCG TCTGACCTC 1800
 ATACATA TGAGTGTG CATTCTCA CAATTTCTGT CAGTACCT TGTAACTAC 1860
 ATAGCTTTG AAGAGTCC GAGGAGTAC CTTCCGAAA TCCATCA GCTGTGCT 1920
 30 GCTCTGCTT TGTCAACCT GGTCTCTCT CTGAGCTGT GATGTCTCT GTATAGATG 1980
 CAGGCTGCT GCACTCAGT GCTGTATTT CTTGATATT TTTCTTGT CTATCACTA 2040
 TGACGCTG TGAAGAGT CATAATGCT CTGCTCTG TGAAGAGT TATAACTAT 2100
 ATCCGAAAT ACATCCTAA ATTCGACT GTGCTGTGG GGTACACAG TGTGCTGTG 2160
 ACCATCACT TGACTATCT CCAGATTAAC TATGGGCTG GATCTATG GAAATCCCT 2220
 35 AATGTTTAC CGATGAGCT TCTCTGATC TCTCTGATC ACACACACT GATGATCTA CATTAAGCT 2280
 GTGAGAT TCTGTGCT ACATGCTCT CTGCTCTG TGTGCTCT TGTGCTCT 2340
 CAGCTCTGT GATTAATAA GAAGAGCAA CTGGAGGCC AGGAAACAA CAGTATCAA 2400
 GACTCAGGA GTATGCTG CTTACATT TTAAGTGAA TAACTGGG CTTGCTCTG 2460
 TTTGCTTGG GACAGATTA CGATGACTC ATGATCTCT TTTGCTCT TAACTACTA 2520
 40 CAGAGATT TGAGTCTG CTTCTCTG CTGCTCTG CTTCTCTG TAACTACTA 2580
 AGGCGTATC TTGTGTGTA AAGTATCG CTGCTGAAA ATTCGAAA TGTCTCTA 2640
 GAGGGAATG GGTCTCTTT TAGTGTCT AATGAGATG TGTGCTCTA GATTTCACT 2700
 GGAAGACAG ACNTGTTAA CAGAGAGGA GATCTCTCA ATTCGAAA CATTAGCT 2760
 CTCAGAGGA CTTCAAGCG GGAAGCTTA CTTTATGT AGCAATGTG A

Seq ID NO: 18 Protein sequence

Protein Accession #: Eos sequence

11 21 31 41 51
 NVFVRQGR VGRTEVLLT PKLFIIVICH HVLVTSLER DTNSSLSP PEVETSLMD 60
 VTEILLPSE TVKVPQNIC VLSIGDQSH FRGSEHMY DRETVPOQ HITMGLTGY 120
 50 LSLSELKRS LKRTQLSE TYFMKATAE AGSTLANCT IKLANTWRK AVIALSERK 180
 IRFMSICCS VRLPCSPSE ELEKIQDLQ DPVLCADHP RGPFFSSQS QVTVPRATV 240
 SQVPRATSA EPPDSEVTH HVSPFIEIG PLSQPSAP IASPAIDMP QSTLSEPM 300
 QTVRSTPP VQASPSPT GAFANVHTS APFVQDLYN TSSLLERQ VLQEKALGL 360
 55 GLEPNLAGS MINQVSLIK PFPMLAPLA QRLKVDDEI GLQLFNSTT ISLSPSLAL 420
 AVIHNASSP NITTFVQPD ANIQVSLST APENSIGTT LPSLNNLPL AHMELASRV 480
 QNFNFPAL PQDSELNLS LQVYLSISV ANLVFRLTA HVTYLLKLN PQDLVPRC 540
 VTNLGRNKS NGKMSKES VDEHRLST VLLLSRTSV LPQNMALTV 600
 60 ITYLGQLES IFSLVTLTY IAEPLIRDY PSKILQLCA ALLLNVLVL LDSNLYKLM 660
 QQLCISVAV LEYFLVSPF WHGLBAPMT LALVYVFTY IRKYLKFCI VGMGVAVTV 720
 TLTITSPDM VGLSGKRF KSGRDFPCM KNNVAVITY VQYVIFLL NVSPVIVLV 780
 QLCNTRKQ LQNCRTSLQ LLCTWRFAP FAWGPVNTV MYLFAINPL MYLFAINPL 840
 QGPIFIPYC VAKERIVQN RVLCCGKLK LAENSGNAT ERNGVSPVQ NGDVCIDMT 900
 GKQMFNEKE DSCNGKQMA LERTSKRSL HPFBQ

Seq ID NO: 19 DNA sequence

Nucleic Acid Accession #: Eos sequence

Coding sequence: 1..3045

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 TCCAGATAT TCTGTGTCAT CATTGATCT CATGTGCTC TGGTAACATC CTGTGAAGA 120
 GATCTGATA ATTCAGATT GATCAACGCA CTTGCTGAT TATCTGTGT CATCTTGGC 180
 75 CCTCTCTCCA ATGAGGTGTA AACACACAGC CTAATGATG TTACTTTAAG CTATCTCCCT 240
 TCAAGAGAAA CAGAAAAAAC TAAATACCT ATAGTAAAA CCTCAATGC TTAGCGTCT 300
 AAACCCAGCA GAAATATGCT CATTGTGCT TCTATTGTA ATGACTCAG ATTTTCTGA 360
 GTCGATATCA TCTTCTGATA TGTAAAGAA AGCACTGCT CCGCATAGA ACATATAGA 420
 AATGGCACCT TAATGTGAGT CTTGTCTCTA AGTGAATTA AACGCTCAGA GCTCAAGAA 480
 80 ACCCTCGAAA CCAATAGTGA GACTTACTTT ATATATGTG CTACAGACGA GCGCCAAAGC 540
 ACCTAAATAT GTACATCTAC AATTAACCTT ATAAATACA TGAATCAGT TCTGCGATA 600
 GCGCTCTGAT AATGATATA GATTGACCA ATGACACTC ATGCTGTCT TGTGGAGAT 660
 CCGTGCCTTT CTTCCCGAGA AGAGTGGGCA AAGCTCAGT GTGACCTGCA GATCCCATC 720
 GTCGTCTGT CTGACATCC ACOTGGGCCA CACTTTTCT CAGCCCAATC CATCCAGAGT 780
 85 GTCTCTCGG CAGTGTGCT TTTCCGCTCT CCGCAAGCTA CTTCTTTTC TATGCTCCA 840
 GATTATTCAC CTGTAACCA CAAATTTCC TCCCATAG GGGAGATCA ACCCTTTCA 900

	CCCCAGCCTT	CACGTCCTAT	AGCTTCCAGC	CCTGCGATTG	ACATGCCCCC	ACAGTCTGAA	960
	ACAGTCTCTT	CCGCTATGCG	GCAAACCCAT	GTCTCGGCGA	CCCGACCTCC	CTGGAAGCG	1020
	TCATTTTCTT	CTGACAGCTT	GGATGCGCCT	GGATATGCTA	ACGTACACAG	CGACCTCTCT	1080
5	GTCCAGACAG	ACATGCTGCA	CACCACGAGT	ATTTCCTGAT	TTGAGAACCA	AGTTGTGCG	1140
	ATGAGAGAGG	CTCTGCTCTT	GGGCGACCTG	GAGCCTAACC	TGGCAGAGAA	AATATCAAC	1200
	CAGATGCGAG	GAGCTCTGCA	TTCCGCGGCT	GAGATGCTCG	CCCCCTGAG	CTGAAAGTT	1260
	CTGAAGTAGT	ATGCGTCACT	TGGCTATGAG	CTGACTTTCT	CAAGACACAG	TATATATCTA	1320
	ACCTCCGCTT	CTTTGCTGCT	GGCTGTGATC	AGAGTGAATG	CCAGTAGTCT	CAACAACAT	1380
	ACCTTTGTGG	CCCAAGACCC	TGCAAAATCT	CAGGTTCTCT	TGGAAACCCA	ACGCTCTGAG	1440
10	ACACGATATG	GCACATATAC	TCTTCTCTTA	TGGCTGATGA	ATAATTTACG	ACGCTGAGC	1500
	ATGSHGCTAG	CTGACAGCTT	TGGCTGCAAT	TTTTTTGAAA	CACTCTCTCT	GTITTCAGAT	1560
	CGTTCCGCTG	AGACGCTCTC	TCTGATCAGC	TACGTCATAT	CATCGAGTGT	TGCAAACTGT	1620
	ACCGTCAGGA	ACTTGCACAG	AAAAGTGACA	GTCAATTAAA	AGACATCAAA	CCGAGGACGAG	1680
	GATGATGTAA	CAGTGAAGAT	TGATATTTGG	CACTTGGGCA	ATAAGTGGTG	CAAGAGAGCG	1740
15	TGTCACAGA	ATGCGTCACT	TGCAACAGAG	AGAGATGCTG	ATGAACCACT	CTGTACCTGT	1800
	AGGCATCTAA	CAGCTCTGCG	GGTCTTGCTG	GACCTATCTA	GGACATCTGT	CTGCTGCTGT	1860
	CAATATGATG	CTCTGACGTT	CATTACATAT	ATTGGTGTGG	GGCTTCTCAT	AATTTTCTGT	1920
	TCAGTGTACT	TGTATACCTA	CATGACTTTT	GAAGAATGCT	GGAGGATGAT	CCCTTCGAAA	1980
	ATCTCATCC	AGCTGTGTGG	TGCTGTGCTT	CTGCTGAAAC	GGCTCTCTCT	CCGTGAGACT	2040
20	TGGATTGCTC	TGTATAGATG	GCAAGGCCCT	TGCATCTCAG	TGGCTGTATT	TCTTCATTAT	2100
	TTTCTCTTGG	TCTCATTACG	ATGATATGGC	CTAGAAGCAT	TCCATATGTA	CGTGGCGCTT	2160
	CTCAAGATAT	TTAATFACTA	CATCCGAAAA	TACATCTCTA	AATCTCTGAT	TGTGCGTGT	2220
	GGGTATCAG	CTGTGCTTCT	GACATCATCT	CTGACTATAT	CTCTGATAAT	CTATGAGTAT	2280
25	GGATCTCTATG	GGAAATTOCC	CATGTGTTCA	GCGGATGACT	TCTGCTGGAT	CAACAACAT	2340
	GCAATATCTT	ACATTGACTGT	GUTGCGATAT	TTCTGTGTGA	TATTTTGTCT	GAACTGTGAG	2400
	AGTGTATCT	CTGCTCTGCT	TCAGCTCCGT	GAATTAATA	AGAGACAGCA	ACGTGAGACT	2460
	CGGCAAAAA	CGATATCTCA	AGACTCTAGC	AGTATCCCTG	GCGCTTACAT	TTTACTCGGA	2520
	ATAACTGTGG	GCTTTGCGCT	CTTTGCTGGG	GGACCAAGTA	ACGTGACCTT	CATGATATCT	2580
30	TTTGCGATCT	TTAATFACTT	ACAGGATTTT	TTCAATTGCA	TCTTTTACTG	TGTGCGCAAA	2640
	GGAAATGCTG	GAGCGGATAT	GAGCGGATAT	CTTTGTGTGG	GAAGATTAGC	GGCTGCTGAG	2700
	AATTTCTGAT	GGAGTAAAGC	TGCTACTAAT	GTGTTAAAGA	AGCAGACGCT	AAACCAAGGA	2760
	GTGTCCAGCT	CTTCAAAATC	CTTACAGTCA	AGCAGTAACCT	CCACTAACTC	CACACACACT	2820
	CTAGTGAATA	ATGATGTGCT	AGTACACCGA	ACGGGGAATG	GAAATGCTTC	TACAGAGAGC	2880
35	AATAGGCTGT	CTTTTGTGCT	TGCAAGATGCA	GATGTGTGCT	TTTACAGTAT	CACCTAGAA	2940
	CAGGCAATTT	CTTACAGAAA	GGAGATTTCC	TGCAATGGGA	AAAGCCGATAT	GGCTCTCAGA	3000
	AGGACTTCAA	AGCGCGGAAG	CTTACACTTT	ATTAGGCAAA	TGTGA		

Seq ID NO: 20 Protein sequence:

Protein Accession #: Eos sequence

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	1	11	21	31	41	51	
	MYPSVQGGH	VQRTSEVLT	KFIPVLVIL	IVVLVLSLE	DTNSSLSP	PAKLSVPSFA	60
	PSSEVETTS	LDVLTSLP	ENETKTRIT	IVKTFNASGV	KPQRICNL	SICNDSPFR	120
45	GEIMFYDKE	STVPQGHIT	NOTLTVGLSI	SELKREBLNK	LTLQTSFTY	IMCATBAQS	180
	TLNCTPTIKL	NFMBAACAI	ALLERKVERP	MEKCCSEVRI	PCPSPEELG	KIACDILQPI	240
	VCLADHPRP	PFSQSPV	PIVATVLSQV	PKATSFASRP	DYSPFTVSP	SPFGITQELS	300
	PQPEALIAS	PAIDMPQSE	TISSPMPQTH	VSGTPEPVKA	SFSPSTVAP	NNVNTSAPL	360
	VQDTIVNTS	ISDLNVLQV	MERALSGLSI	EPNLAGEHIN	QVERILLASPP	DMPLADTSP	420
50	LRVDDIQLQ	LAFSFTTISL	TFSLALAVI	RVAASFTTT	TPVAGDAM	QVLETOAPE	480
	HEICTITLS	ELMLNPMQ	NELASRQFH	FETPALPDQ	PSLEHLSLS	YVSSSVANL	540
	TVRLTRNVT	VTLHIMPQ	DELTVRCVP	DLGRNGRGG	WSDNGCSVRD	RLNMTICTC	600
	SHLSPGVLL	DLRSFVPLA	QPMALTTFTT	IGCGLSIFL	SVLVTYIAP	KEIRHIDPSK	660
	ILIGLCAALL	LLBLVFLLES	WIALRQDGL	CTSVAPFLY	FLVSTWNG	LEAPFWLAL	720
55	VEVNTIEK	VILKCTVGS	GVPAVVVTH	LTISSPDMVL	GSYKFPNGS	PDPFCINNN	780
	AVPYITVVY	FCVILPLAS	MFIVVLQCL	RINKKQLGA	ORSTSIQDL	SIAGLTFLIG	840
	ITWGAFAPPA	GFVNTFNTL	PAIPLNTLQ	FIFIPKCVAR	ENRVKQRRY	LCQGLRIAS	900
	NEDWETATN	GLAKCTVNG	VSSSNGELQ	SGNSTSTLT	LPHNDCVIA	SGNGWASTER	960
	NEVSPVQNG	DVCLADPTK	QNFNKEKDS	CNGKRMALR	RTSKGRSLHF	IDOM	

Seq ID NO: 21 DNA sequence

Nucleic Acid Accession #: HM_005756.1

Coding sequence: 37..3117

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	1	11	21	31	41	51	
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	CTCGGGGTCA	GGATGGTTTT	CTCTGTGAGG	CAGTGTGGCC	ATGTTGGCAG	AACCTGAGAA	120
	GTTTTACTGA	GTTTCAAGAT	ATTCTCTGTC	ACATTATTTC	TTCAATGCTT	TGTGGTAAAC	180
	TCCTGTGAGG	AAAGTACTGA	TAACTCTGAT	TGTGTACACG	GACCTGCTAA	ATTATCTGTT	240
70	GTGATCTTG	CCCTCTCTCT	CATGAGCTT	GAAACAACCA	GCGCTCAATG	TTTACTTACT	300
	AGCTTACTCC	CTTCAAGAAG	AACAGAAARA	ACTAAATACA	CTATAGTAAA	AACTCTCAAT	360
	GCTTCAGCGG	TCAACACCCA	GAGAAATATC	TGCAATTTGT	CATCTATTGT	CATGAGTCTGA	420
	GCAATTTTTA	GAGATCTTCA	CAGTCTTTCA	TAATGTAAGT	AAAGCACTGT	TCCCCAGAT	480
	CACACATATA	CGAATGCGAC	CTTAACTGGA	CTCTCTCTCT	TAAGTGAATT	AAAGCGCTCA	540
	GAGCTCAACA	AAACCTCTGA	AACTCTAAGT	GAGACTTACT	TTATATGTGT	TGCTACAGCA	600
75	GAGGCGCCAA	GACATATAAA	TGTGATCACT	ACATAATAAC	TGAATATATC	AATGATATGA	660
	TGTCTGTGTA	TAGAGAGATA	AGAGATTCAG	CATGCAACCA	CTGTGCTGCT	CTGTGCTGCT	720
	TCGTGTGAGA	TACCTGTCCC	TTCTCTCCCA	GAAAGATGTG	GAAAGCTTCA	GTTGTAGCTGT	780
	AGGATATCCA	TGTCTGTCTT	TGCTGACCAT	CCAGTGTGGC	CACCAATTTT	TTCCAGCCAA	840
	TCCATCCGAG	TGTTGTGCTG	GGCCACTGTG	CTTCTCCAGG	TCCCCAAAGC	TACCTCTTTT	900
80	CTGACGCTAG	CGATATCTCT	ACTCTGACAC	CAGATGTTCT	CTCTCTCAAT	AGGGAGATT	960
	CACACCTCTC	CCGCCCGGCG	TTCAAGCTCC	ATAGCTTCTC	GCGCTCGCAT	TGACATGCTT	1020
	CCACAGCTCT	AAACCTCTCT	TTCCCTCTAT	CCCCAAACCC	ATGTCTCCGG	CCGCCCACTT	1080
	CTGTGGAAGG	CTCATATTTC	CTCTGCCACC	TGCTGTGCC	TGCGATATGT	CACCACTACC	1140
	AGCCGCTCTC	CTGTCGACGA	AGACATCTCT	AGACACCTCT	GATATCTCTG	CTTGTGAGAC	1200
85	CAGTGTCTTC	AGATGAGAAA	GGCTCTGTCT	TTGGCGAGCC	TGAGAGCTTA	CTCTGACAGA	1260

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GAAATGATCA ACCAAGTCAG GAGACTTCCTT CATTCCCGCG CTGACATGCT GGCOCCTCTG 1320
 GCTCAAGAAT GTCTAAAGAT AGTGGGTATAC ATGTGGCTAC AGCTGAACTT TCAACAAAGC 1380
 ACTATAGATC TAATCTAGCT TCTCTCTGTA TCGAGATGAA TGGCAATATG TGGCAATATG 1440
 TCAACACACA CTAACTTTGT GGCOCNAGAC CCTGCAAATC TCAGCTGTTT TCTGGAAGAC 1500
 CAAGCTCCTG AGAACAGTAT TGGCAACATC ACTCTTCCTT CATGCTGTAT GAATAATTAT 1560
 CAGACTCATG ACATRGAGAT AGCTTCGAGT GTCTGATCTA ATTTTITGAA AACACTGCTG 1620
 TTTTTCGAGT CCGTATATCT GGAAGATGAG TCTGTATACCT GCTAGCTCAT ATCTGAGAT 1680
 GTTGCAAACC TGACCTGCGG GAACCTTGACA AGAAAGAGTGA CAGTCACATC AAAGACACAT 1740
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 GTCTGCTGCTG CTCAAATGAT GGCCTTGAGG TTCAITACAT ATATTGTGTG TGGGCTTTCA 1980
 TCAATTTTTC TGTGCTGAC TCTGTAAAC TACATAGCTT TGTAAAAGAT CCGGAGGGAT 2040
 TACCTCTCEA AAATCTCAT CTGAGTGTGT GTGCTCTGCT TCTGCTGAA CTGTGCTCTC 2100
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 TTTTACTGAG GATATATCTG GGCCTCTTCC TCTTCTCTCT GGGAGCCAGT TAACCTGACC 2640
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 TCTACAGAGA GGAATGGGTT CTTCTTTAGT GTCTGAGATG GAGATGTGTG CTTCTACATG 3000
 TTTACTGAAA AAGACACAT GTTATACAGC AAGAGAGAT CTCTCAATG GAGAGAGCT 3060
 ATGCTCTCA GAGGACTCT NAAGCGGGA AGCTTACAT TTATTAGACA AATGTGATCT 3120
 CTTTCTCEA AAATCAAGC ATGATGCTTG ACAGTGTGAA ATGTCGAATT TTACCTTTTA 3180
 CACATGTAGA GATGTATGAA AATCAACCTA TTTTATTTCT GGACACATCT GGGAGAGAT 3240
 AAGCAATTA GGGCGATGA TTATTTATC AAGAGAAC CAGAGATCA CACATGTT 3300
 TTTAGAGATT TTTTATCTT TTTCTTAT AAGAGAGAT TGTGTAAGCA TTTTAAACA 3360
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 TGTGTAGTT TATGTGTTT GTATATGCT TAAATCTGA TAACATGAG TGACCAATG 3540
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 TGTGAGATC ATGTTTGTIT TGTCTCACTG GATAATCTAG AAATCTCTG CTGTTCCGCT 3660
 AAATCTTAAA GCTCTTTTGT GAGATGATAT AGATGTGAA ATACGAAAC CACTAGTAAA 3720
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 GTGACGACC GTTACAGCA CAAACAGCAT CCAATATGAA TACCANTCCC CTGACGCCAT 3960
 CCGAGTACT CAGATTTAG AATCTCAC AGATATTTTA GATTTTACC TTGSCACAG 4020
 AGAGGGATGA ACTGTCACTC AGACCATGTG TCAGGAAAT TGTGAAGTA GATGAGGTAC 4080
 ATACACTGCC GCTTCTCAA TCCCCAGAGC CTTTAGAGAC AGGAGAGTG ACTAGATTC 4140
 CTTCTCTTAA AAGGTACAT ATATATGAA AAAATACATA TTGCGTCTT TTAAGAGCA 4200
 ACTGAGTT ACTATGTGA TGTATATGAC TGTACACTC TGCCCTACC AGGCTATPAA 4260
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 TATACAGGT CTATCTCTT TCCCTCTAC ATCTCTGTA GCGATGCTC AATGACATC 4440
 TATTAGGAA CATTCAAAAC CCGTITTAGT TAAGTCTTTC ACTAAGTTC TCTTGAGT 4500
 ATTTCAAGT AATGTGGAAT CTCAGACTAA CAGATAGTAA AATACACAT TCTGTAGT 4560
 GCACTGTCT TTTGCAATAT TTTCTTTCTG ATTTATTTAA TTTTCTGTA TTTATATGTT 4620
 AATCAAAA AGTTAAAT CANTGAATA AATTGCGAT TAGA

Seq ID NO: 22 Protein sequence
Protein Accession #: NP_05747.1

1 11 21 31 41 51
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 MVSFVKQGH VQTEBVLIT PKFLPVLICL HVLVATSLER DTHSSLSPP PAKLSVVSFA 60
 PSSREVTTS LQVTLGLLL SHETGVKQK NICHLSGICH DSAPFGEIM FQDRESTRV 120
 QKQILITVIT TQVLSERLK RSLRANTLIT LSTYFIMCA TBAQSTLAC TFFILANTM 180
 NACAVLALE RVKIRPSEHC CCSVRIPCPS SPERLEKIQC DIQDPIVCLA DHPGPPFSS 240
 SQSLFVPERA TVLSQVFEAT FSAPEQVETG VTRNVSPBIG EIQPLSPQPS APIASBPAD 300
 MPQSGTSSS PMQCHVSGT PEPVNASPSS PTVSAPRVN TSPAFQDT IWTASISDL 360
 ENQVLQETA LRLGLEPVL AGSLVWVSR LRESFDMLA FLAQLRLKVV DLGIQIQLNS 420
 NITLISLSPS LALAVIRVNA SSFNTTTTVA QDANLQVSL ETQAFENSIG TITLSSPLS 480
 NLPAIDMELA SHQVNFPEF PALFQDPSLE NLGLSYVIS GSVANLVN ITRNVITLTK 540
 RINFSQDST VQVFWFSLR HGRSRSDSH CSQVDERLK ITTICSHSLT SPVSLLELR 600
 TSVPLQDMA LFTTITGCG LSLFPLSVTL VTYIAFKIR RYDPSKILQ LCAALLIHL 660
 VFLQDSIAL YDQGLISIV AVPLHYFLVL BPTMGLSEAF HWYLAVKVP NYTIRKYLK 720
 FCIVHGVGFA VVHTIHLIS PMNYGLSGYV KTRNVSPBIG CWINSAVEY ITTIVGVCI 780
 FLLAVSHRIV VLQGVGSLR KQGLAKRKT FQVAGVRNR RQWRVLAQCC KRLAENSMD SKTATNGKL 840
 VYTRVLAFIF NLTQFPFPI FQVAGVRNR RQWRVLAQCC KRLAENSMD SKTATNGKL 900
 FVLTQGVSSS SMLSGSSHS NSTTLLVNN DCSVHAGSN NASTERGVUS FSVQNGDVL 960
 HDPTCKQIMF NEKEDSCNCK GRMALERTSK RGLSLFIDQM

Seq ID NO: 23 DNA sequence
Nucleic Acid Accession #: NM_001565.1
Coding sequence: 67..363

1 11 21 31 41 51
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 AGACACAGTA ATCAAACTGC GATTCTGATT TGCCTGCTTA TCTTTCTGAC TCTAAGTGGC 120
 ATTCAGAGAG AGCTCATCTT TGTATACCTA CCGTCTACCT CACTCAGCAT TAGTAATCAA 180
 CCGTTTAATC CAAAGTCTTT AGAAAACTCT GAAATATTC CTGACAGCCA ATTTTCTCCA 240
 CGTGTGTGAG TCAATGCTAC AATGAAAAAG AAGGCTGAGA AGAGATGTCT GAATCCAGAA 300
 TCGAGAGCCA TCAAGATATT ACTGANAACA GTTPAGCAAG AATATCTTAA AGATATCTCT 360
 TAAGAACGTA CAAAGAGATA ATCGAGGAGT TGCTTCCBAG GATGAGCAGC ACAGAGAGCT 420
 CCTCTCCCAT CACTTCCCTA CATGGAGTAT ATGTCAAGCC ATAAATTGTC TTAGTTTGCA 480
 GTTACACTAA AAGGTGACCA ATGATGGTCA CCAATCAGC TGCTACTACT CCTGTAGGAA 540
 GGTTAATGTT CATCACTCTA AGCTATCTAG TAATAACTCT ACCTTGACAC TATAATGTAA 600
 GCTCTACATA GCTGTGGGA TGTCTTCTGA GAAATGTCTA CCGTCTCAA TATTTCCTC 660
 ACCTTCCCCA TCTTCCAGG GTACTAAGGA ATCTTCTCG TTGCGGTTT ACTCAGAATT 720
 TCGAATCTC AATAACTAA AAGGTATGCA ATCAATCTG CTTTATAAG ATGCTCTTT 780
 ACTTCAGGA CTTCCAGCT CATCTCCCA AGGGGCCCA ATCTTCTCAG TGACTATCTT 840
 CATACATCT CAAATCTCTA ATCGAGGAGT GAAATGTCTA CCGTCTCAA TATTTCCTC 900
 CTTATTTAAT GAAGACGCT ACAAGTATA AGTCTTAGT GTATATATT CCTATATTG 960
 TTTCACTGTA CATGAAATA CATGTAATA AGTACTATG ATCAATGAT ACACAGAAAA 1020
 TTTTAAAAAT ACAGATAGAT ATATGCTCTG CATGTATCAT AGATAAATG TCGTGAATGG 1080
 TTTTCAATA AATATGAGGT ACTCTCCGG AATATTAAG

Seq ID NO: 24 Protein sequence

Protein Accession #: NP_00556.1

25

1 11 21 31 41 51
 MNGTALLIC LIFLTLGSIQ GVPLSRVTRC TCGISRNQPV 60
 EIIATMKKK EKRLANPESK AINHLKAVS KEMSKRSP

Seq ID NO: 25 DNA sequence

Nucleic Acid Accession #: XM_030559

Coding sequence: 1...119

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1 11 21 31 41 51
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 AGCAAGTTT GAGGATTT TCGCTGGAA GATCAACAA GATCAACAA TCGAAATTT 120
 GAGGAGTTT ATGGAATT ACTCAACTGT CAAAGATGCC CCAATGTGA COTTGTGTA 180
 GGCTATCGAG ACATCAATGG AGACTACTTA CCTATAATA ATGATGATA TTATCACAAA 240
 GCTGTTTCAA CGCCCAATCC ACTGCTTAGG ATATTATTAC AAAGAAGAGA AGAGACGAG 300
 TACAGTGCTT TACAGTGCTT CACTCATATG AGAGAGAGA ATGTTTAA CACGTTATG 360
 CCGTCTGACA ACCATAGAAA AAACCCACAT ATAGTCATTA GTATGCCCCA AGACTTTGA 420
 CCGTGTGCTT CTATTATAGA COTGATATT CTCCAGAAA CGCATGTAG GGTACGTCT 480
 TACAAATAG CAGCAGGAGA ACCCTTAGGA TTCTCATGCC GGAATGCTC CATGTTTCA 540
 GTACACACAT ATGCTCTAGA AAGGTTTCCA GGGATCTTGA TATCCAGCT TCGTCCAGA 600
 GGTCTGCTC AAGATACAGG ACTATTAGCT GTTAATGTAGA AAGTTTAGA AGTTAATGGC 660
 ATAGAAGTTT CAGGGAAGAG CCTTGATCAA GTAACAGACA TGAATGATCC AATAGAGCCT 720
 AACTCATCA TACAGTAGAG ACCGCGCAAC CAGAGGAATA ATGTTTGGG GATACATGC 780
 ACTCTGCGA GTTCCGCTGA CACTCATATG AAGAGCTTCT TGCTCACC ACAGCAATT 840
 GAACAGCTC TTGAGCCAGA GGTATGAGAC AGCGAAGAG ATGACATTAT CATTGAAGAC 900
 AATGAGTGC CACAGCAGAT TCCAAAGGCT GTTCTTAATA CTGAGAGCCT GAGGTGCTTA 960
 ACACAGATG AGCTAAGCTT TGAGTCTGGA CAGAAATGCT TTATCTCCTT TAATGAGTG 1020
 AGCTTAGCG CCAATGCAAG CACTCAAAK AGCAATTG ACACATGTC TCCAGATCAA 1080
 AACTCTTAG AAGAGATGG AACAATATA ACATTATG

Seq ID NO: 26 Protein sequence

Protein Accession #: XP_030559

55
 60

1 11 21 31 41 51
 MNRSHHAG GCLCTGVKVK SPFGAEFRP FLERSKPKV EEPYGLQHV IKIPNVDLV 60
 GYADIHGDL PINDDNFYHK AVSTANFLLR IFIQKREED YSAFTDTLI KGGVLRNL 120
 RPDHRRKPH IVISMPQDR PVSSIIDVDI LPETHRRVL YKOTERPLG FYIRDGSSVR 180
 VTIHGLEKVP GTFISRLVG GLAGSTDLA VDEYLEVNG IYVSGSLQK VDTMHANGR 240
 NLIITVBNM QBNVFERH TSGSGGGSTG HLLGTTPQI EYSEFDEED SEEDIIIED 300
 NVQVQIPKA VNTESLESL TQIELSPESG QNGFIPNEV SLAAIASEN TEFTHAVDQ 360
 KULEEDOTII TL

Seq ID NO: 27 DNA sequence

Nucleic Acid Accession #: NM_003667.1

Coding sequence: 1...2651

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1 11 21 31 41 51
 ATGGACACCT CCGCGCTCGG TTGCTCTCTG TCCTTGCGCT TGCTGCTGCA GCTGGGAGC 60
 GGGGGCAGCT CTCCAGAGTC TGTGTGTGTG CTGAGGGGCT GCCCCACACA CTGTCTATGC 120
 GAGCCGACAG AGACTATCTT GCTCCAGGTT GACTCTCTCT ACCTGGGCT CTGAGAGCT 180
 CTTCCAGACC TCAGGTCTCT CACTCTCTAC CTAGACCTCA GTATGAAACA CATGAGTCA 240
 CTGCTCCGGA ATCCCTCTGC CAGTCTCCGC TCTCTGGAG AGTTAGTCT TGGGGGAAC 300
 GCTCTGACAT ACATCTCCAA GGGAGCATTC ACTGGGCTTT CAGGTCTTAA AGTTCTTATG 360
 CTGCAATA ATGCTCTAG ACAGATACCT ACAGAGGCTC TCGCAATT TTGAGAGAT 420
 CAATCCCTGC CTCTGATGTC TAACCAATC AGCTATGTC CCCCAGCTC TTTCAGTGC 480
 CCGCATTCCT TGAGGCACT GTGCTGTGAT GACAATGGT TAACAGAAAT CCGCTCCAG 540
 GCTTTTAGAA GTTTATCGGC ATCTGAGACC ATGACTTGT CCGTGACAA ATACACACAC 600
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 AGAATCACT CCGTGGGAAA GAAATGCTTT GATGGGCTCC ACAGCTAGA GACTTAGAT 720
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 GAATCATAT TCTATACAA TCCATCCAAA TTGTGTGGG GATCTGCTTT TCACATATA 840
 CTTGACATA GTTCTAGAG TCTATAGGCT ACTGACAAA TACTGAATT TCGATATA 900
 ACTGAACTG CAAACTGGA GAGTCTGACT TTAATCGAG CACAGATCTC ATCTCTCTC 960

	CAAAACGCTC	GCAATCAGTT	ACCTAATCTC	CAAGTGTGAG	ATCTGTCTTA	CAACCTATTA	1020
	GAGATTATAC	CCAGTTTTC	ATGTCGCCAA	ANGCTTCAGA	AAATGAACT	AAGACATATT	1080
	GAAATCTAGC	AAATTAAGT	TGACACTTTC	CAAGCTGTTC	TGAGCTCTGC	ATCCGCTAAT	1140
5	TGCTGTGGA	ACAAATATG	TATATATTGC	CCCAATGCTT	TTTCCATTCT	GCCATCTCTA	1200
	ATAAAGCTGG	ACCTATGTC	CAACCTCTCT	TGCTCTTTTC	CTATAACTGG	GTTCATGTTG	1260
	TTAACTGACT	TAAATATTA	AGGAATATCT	GCTTACAGAA	GCTTGATATC	ATCTGAAATC	1320
	TTTCCAGAAC	TCAAGGTAT	AGAAATGCTT	TATGCTATAC	AGTCTGTGCG	ATTGTGAGTG	1380
	TGTGAGAATG	CCGTAAGAG	TTCTAATGAA	TGGAATAAAG	GTGACACAG	CAATGATAGC	1440
	GACCTTCATA	AGAAAGATG	TGGAATGTTT	CAGGCTCAAG	ATGACAGTGA	CCTTGAAGAT	1500
10	TTCTTGCTTG	ACTTTGAGGA	AGACCTGAAA	GGCTTCGATT	CAGTGCAGTG	TTCACCTCTC	1560
	CCAGGCGCCT	TCAAAACCTG	TGAACACTCT	CTTGATGCTT	GGCTGATCAG	AATGAGATG	1620
	TGACACATAG	CAAGTGTGAC	ACTATCTATG	AGACTCTTGG	TGACTCTAAC	AGTTTTCAGA	1680
	TGCTCTCTGT	ACATTTCGCC	CATTAAACTG	TAAATGTGGG	TCATGCGAGC	AGTGAACATG	1740
	CTCAGGGGAG	TGCTCTGAGT	CGTGTGCTGT	GGTGTGAGAT	CGTTCACTAT	TGGCAGCTTC	1800
15	GACGACAGTG	GTGCTCATG	GGGAAATGGA	GTGTGTATCC	AGTGCATGTC	TTTTTGTGTC	1860
	ATTTTTCCTT	CAGATATGCA	TGTTTCTCTG	CTACTCTCTG	CAGCCCTGGA	GCGTGGGTGT	1920
	TCTGTGAAT	ATTTCGCAA	ATTGTAAGC	AAAGCTCCAT	TTTCTAGCCT	GAAATGATAT	1980
	ATTTGTGCT	GTGCCCTGCT	GGCCTTGACG	ATGGCGGCGG	TTCGCTGCTG	GGGTGGGAGC	2040
	AAGTATGCGG	CTCTCCCTCT	TGCTGCTTTG	GGGACGCGCG	CACATGGGTA	2100	
20	TACATGGTGG	CTCTGACTCT	GCTCAATCTC	CTTCTCTCTC	TCATGATGAC	CATTGCTTAC	2160
	ACCAAGCTCT	ACTCGAATT	GGACAGGGGA	GACCTGGAGA	ATATTGGGGA	CTCTCTCTAC	2220
	GTAAACACAA	TGCTCGTGT	GCTCTCTCAC	AAGTCGATCC	TAAACTGCC	TGTGCTCTTC	2280
	TGTCTCTCT	AAACTCTGCA	TTATATCTGC	CGAGAAATAT	TAGTCTTTCA	2340	
	CTTCTCTCT	TAGTCTGACT	TCTCGATGTT	CTCAATCCCC	TCTCTACAT	CTTGTTCAAT	2400
25	CCTCATTCTA	AGGAGGATCT	GGTGGAGCTG	AGAAAGCAAA	CCTAAGTCTG	GACAAGATGA	2460
	AAACACCCAA	CTGTGATGCT	AATTAACTCT	GATGATGTGG	AAAAGAGCTC	CTTGACTCTA	2520
	ACTCAAGCTC	TGATTAACCTT	TGACAGCTCC	ATGACCTGCT	TGCTGAGCTC	2580	
	GTGCACTAC	CACTTATCTC	AGTACTGAG	AGCTGCCATC	TTTCTCTGTG	GGCATTGTG	2640

Seq ID NO: 28 Protein sequence
Protein Accession #: NP_003658.1

	1	11	21	31	41	51	
35	MTSRRLVQL	SLPVLQLAT	QSSPSRSGVL	LRCQPTHCHC	PDGMRLLRV	DCRDLGLSEL	60
	PSNLVSFTVS	LDLSNNHIG	LLNPLFLNRI	FLEELRLAG	ALTYTPKAP	TGLYSLKVLN	120
	LQNNQLRVF	TALQNLRLS	QSLRLDNHII	SVYVPCFSP	LHSLRLHMLD	DNALTEIPVQ	180
	APRSLGALQA	MTLALAKIHH	IPOYAFNLIS	SULVILALSH	RHSELKJPCF	DGLHSLDLTD	240
40	LAYNNLDEF	TAJTLTSLH	ELUHTNPIG	FLRSPFQHL	RELATITLHG	ASQITFPEQL	300
	TGIANLEST	LTGAQISLSP	QTVCKQLNPL	QVLDSLNYLL	EDLSPFVQC	KLIKIDIRNL	360
	EYIEIKVDFT	QQLLSLRNLN	LANNKIAIHH	PNAFSTPLSL	IKDLNSLLSL	SSPFIITGLIG	420
	LHLLKIKTNH	ASQLISLSSH	PFELKYLDP	HAGCCAPV	CGENATIKSQ	WIKGNSDSD	480
	DLIKEDMNP	QKQILDLAD	FLIDYEDLK	AJNEVQCSPE	PGPKFPCBIL	LDGMLIRIG	540
	WTIAVLATCT	NALYTSVFR	SPLYISPIKL	LIGVIAAVNM	LTGVSSAVLA	GVDAPTFGSP	600
45	ARHGAWNEH	VCGHVIPLS	IPASSSEVFL	LTUALLSGF	SVKYSKFRET	KAPFSSSLVK	660
	ILLCALLAAT	MANVPLGGG	KIQAQSHCLP	LPVSPCTGQ	YNNALLLNS	LCKLAKTIAY	720
	TLVYCELEKI	DLNLTWCSH	VKGLIADLT	NCLILPCPVA	LPFSLIMLT	FISPSVIKPI	780
	LLVVVPLPAC	LMPLYLILFN	PHFKEDLVSL	RQZTIVMTR	KHPSLMSINS	DVVEKQSCDS	840
	TQALVTFPSS	SITYDLPSS	VPSPAYPVE	SCHLSVAPV	PCL		

Seq ID NO: 29 DNA sequence
Nucleic Acid Accession #: NM_002497.1
Coding sequence: 135..1472

Coding sequence: 135..1472						
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55	GGCAGAGTA	GGGCTGGGG	GTCACTGCTG	CTGGGGGCTC	TCTCATCCA	GGTCCCTGGA
	GTCTCTGCTG	CTGGAGGCTC	CCCACTTGCG	GGGCACCTCT	CGACAGGAC	CGCACTCTGC
	GGCACTGCGC	GCACTGCTCT	TCCCGGCTGT	AGACATATG	AGTGTGATCT	ACCAATGCTCA
60	CAGGCTCTCA	CGGCGGCTGC	CAGAGATCC	GGAGGAAGAG	TGATGGCAG	ATATTAGTTT
	GGAAAGACT	TGACTATGCG	TCCATGACAG	AACTGAGAGA	ACAGATGCTG	GTCTTCTGAG
	TGATTCTGCT	TGTAGTACGT	AGCAATCCAA	ACATGCTGTG	TGATATATAT	CGGATATAT
	ACCGAGACAA	TACAGACCTG	TGCTATGTAA	TGGATATATG	TGAGGAGGCG	GACTCTGACTA
65	GTGTAAATAC	AAAGGGAACG	AACTACTAGA	TGAGAGTTT	GTCTCTGAG	
	TGATGACTCA	GTTAGCTCTG	GGCTCTGAAG	AGTGCCACAG	AJZAAGATGAT	GGTGTGCATA
	CGGTATATCT	TGAGGATCTT	AAAGCTGCTG	ATGTTCTCTG	GGATGCGCAG	CGAAAGGCTA
	ACCTGTGAGA	CTTGTGATCT	GCTAGATAT	TAAACCATGA	CAGCAGTTT	GCAAAACATG
	TTTGTGGCAC	ACCTTATTAC	ATGTCTCCTG	ACCAAAATGA	TGCAATGCTC	TACAATGAGA
	AATGATATCT	CTGTGCTATG	GGCTGCTTGC	TGATATGATT	ATGTGCATTA	ATGCTCTCAT
70	TTACAGCTCT	GGATGAGTGA	AAAGCTGCTG	GGATGAGTGA	AGTAGACGAA	ATCTATGATA
	TTCCATACCG	TACTCTGAT	GAATGGAATG	AAATTAATTA	GAGGATGTTA	AACTTAAGAG
	ATTACCATCG	ACCTCTTGTT	GAGAAATAT	TGAGGAACCC	TTTATAGACA	GATTGTGTTG
	CACAGACGCA	AGAAAGAAAT	CTTAGAGBAA	GAGGSGAACA	ATTAGAGAGG	CCAGAAAGAT
	CCGAGAGATC	GGCTGCTGTA	TGATGAGCG	TGAATCTGCA	GGAAATTCAG	TTACAGAGAG
	GAGAGCGAGC	TCTCAAGACA	AGAGAAGAAA	GATTGGAGCA	GAAAGACAG	GAAGCTTTGT
75	TTCTGAGAG	ACTAGCAGAG	GACAAACTGG	CTAGAGCAGCA	AAATCTTGTG	AGAGACTAGA
	GCTCTCTAAA	GGAGCGSAG	TTCTCTTCTC	TGCAAGTAA	TCCAGAGCTT	CTTAATCTCT
	CATCTCTGAT	GAGCTGCTTA	TGATGAGCT	TGCTGTGAGA	AGTAAAGGCA	ACATATGACA
	GGATGAGAAA	TTGATAGAGT	CAGCTCCACAT	CTAAGTCCAA	GTGCAAGGAC	CTAGAGAAAL
	GGCTTACGCG	TGCCCATGCT	CGGGCTCAG	CCGCTGAGA	TATTAGAGAA	AATTACACAC
80	TGAAAGAGAG	ACAGATCTTG	AGCATGGCTT	AGCGAGTAG	AGAGACACAG	AGCTGTATAC
	AGGATATAT	GGATGAGAG	AAATCTCAT	GAATTATCCA	TGCTGATGAT	TGAAATCTT
	GGCCCCATGA	GCATGCTCT	TCTGTATAGT	ACACATAGAT	TGTGGAATT	GGTTTATGCT
	TTCTTCAGCA	TGATGATCT	AAATATGTCA	CATTAAATTT	TTCTTCTCTC	TTTATAGACG
85	ATATTATAAA	AGATATACTT	TTCTGTGTGG	GCCTTTAATC	CTGTGTGTG	TACTAGTAG
	GACATAGAGA	TGTGATCTC	TAAATCTGG	GAGAAAAAT	AAATATTAGA	AAAAATATTT

	TATGCAAGAA	GAGTAGCACT	CACTGAATAG	TTTAAATGA	CTGAGTGGA	TGCTTACAAT	1860
	TGCTATGCT	AGATTAAAT	TTTAAATCTG	AGATTTTTAA	TGTTTTITAG	CTTAGAAAC	1920
	CCAGTTAGT	GCAATTGGT	CATTAATACC	ATGAATCTCT	GCTATAAAT	ATTCATGCG	1980
	TCGTGATCT	AATCTGTA	GCTTTGGA	ATTCATCAC	TGTAGTATT	GTATTCTTT	2040
5	TTTTTTTCT	TATGCAAGAA	TATGAGCTCT	CTGTCATTA	CCTACTTCT	TCCGACATA	2100
	TAAAGAATT	CTTCAGTTA					
	Seq ID NO: 30 Protein sequence						
	Protein Accession #: NP_02488.1						
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	MPSRADYEV	LYTITGSGS	ROKIRKESD	GKILVWKEED	VQSMTEERKQ	ELFWSVNLVR	60
	ELKHFNIVY	YDIRIDRNT	TLIVIMEYCS	GDCLISVLEF	GTKRSEVLR	SPVLRVQTGL	120
	TLALKECHIR	SDGGHTVLR	LKPSANVFLD	GKQVIGVIFD	GLARILNAR	SFKRTFVPTG	180
	LYTHSPQHR	MSNKGSDT	ELGLAYLCL	ALMPFFVQSL	QIAGLKRIE	OHAFRIFPTY	240
15	SDLENIITR	MLNLYDHRP	EVEETLENPL	YADVADSRD	TTGTGATCT	GHETGACCA	300
	PKVLEKLE	LTQLRERRAL	KARBERLEKQ	ELGVFLREI	ADRIELKAR	LNLYNLSLE	360
	RKFLSLANP	ELNLNPSVI	KKVHPSGES	KENIKESMS	ESQLTSKSK	KDLKRLHMA	420
	QLRAQALSDI	ESRYLQSKRQ	ILGHR				
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	Nucleic Acid Accession #: NN_020242						
	Coding sequence: 72..429						
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	GTCTAACCA	CCAGTAATG	ANGGTGATCG	ATTTGCGAGG	ATATATACGA	GGAGCTCTCT	180
	TCGAGAAGA	TCGTGGTCA	CTGATGAGAA	CAGCAATGTA	TGCTTATCTG	TGCTGTCTCTC	240
30	CACAGATCTC	CGGTGCACT	CCAGACCTGA	CTGCAATGAC	TTCAATCTGT	ATCATGTTGC	300
	AGATGTGAA	ACCACTCAG	ATCTCTATG	TGCAACATGT	CTGAAAGAGC	TGTGGGATCT	360
	TGCGATGAG	GTTTATATG	GTACCACTCT	TGCATATATG	CACATCTCTG	CCAGCTAGAC	420
	ATTACTACT	ATGGGACAT	CTGATCTGA	TAAATTTTCT	CATAACCTGA	GAGGAGTAT	480
	CCCAAGAGT	TTTGATATT	TGTTTTCCTT	ATATGATCTT	GAAGAAGTAT	GGGCTGAGC	540
35	TGGAAGAGT	TTCTCTTGA	ATGTCTCTT	TATTTAGAACT	CAGACAGAC	AGATATATGA	600
	TCYACTGAC	TCGTGATGG	CTGGAGCTTA	TATGCAAGAG	GAAGCTCTCT	AGAGCTCTCT	660
	TGTTGTGGT	GGGTGGGAG	AGGTGGTAC	CAAGCTACTG	GAGGCTCATG	AGGTGCTGTG	720
	TGGAAGATG	AGGATAGAC	GTGTGCACT	ACATCAATAG	ACATAGAGAT	TGCTGATATG	780
40	TCATCTGCT	TTGAGCTGC	ATCTGATCT	ATGAGAGAAA	ATAAAGAGTA	CGTGAAGTCT	840
	ACCGACTCC	CTACTACAC	TGGTGATTT	AGGAGAGCA	AGGAGAGCA	GGHETGACCA	900
45	TCGAGAGGG	ATGAGATTA	AGGAAGCGG	TAAACAATAT	CGATCATATG	CGTCCCTGGC	960
	CCAGGTATT	AGGAGCTTA	TCGATCTGA	TATGAGAAA	CAGGACATGT	TTTGTCAATG	1020
	AGAGTCGAA	CTTACTCTT	TACTAGAGC	TGCTCTTGG	GGTAAATGCA	AAAAGCACTG	1080
	AATTGCAAT	GTTTATCTG	GATCCAGGTG	ATTTGCGAG	ACCTCTATCA	AGCTCTCTCT	1140
45	TGCTCAAGA	GCGAGCTGA	TTAAACAACA	GCGATAGTA	CCCAAGAGAA	CCCAAGAGAA	1200
	TGTGACGCG	CTCCAGCTG	AGTGAAGAG	CGTCAAGAA	CACCTGGGCG	AGCTCTGCTC	1260
	AGGACAGCA	CCACAGGAA	GCTTCTGAC	CAGGACAGAA	AGHAGATCA	ACTATATGTA	1320
	GTATTTCCG	GAAGCAATG	TATTTCTTAA	ACCTCTATCA	CGAGUAAAG	AGCTCTCTCT	1380
50	AGAAAAGTT	ACCAATTAG	AGAGCTTAC	CTCCAAAGAG	GAATAATAT	TTCTATCTAA	1440
	TAAATGATT	GTGAATTC	GAGAGGATC	AAHTAATAG	TGTGAAAGAG	TCCCAAGAA	1500
	ATCCCGGGA	GTTTCTTCG	CTGAGGAGCA	GATGTCCTGT	CTTCTCAGAT	TAGAGATATA	1560
	GATTCAACT	CTGCGAGAC	AAATAGAGCA	ATCTGAGAT	CTGATGATG	AGAGTATGTA	1620
	AAATCAATC	CTCAGGGAG	AGAATAGAG	ATCAGATTGA	TTAGAGCGTG	TGGAAGAGAG	1680
55	TCAGAAATG	GATGCCGCA	CCATTGCGA	ATCGAAGAAA	GCTTTCTCTG	AAATCAAGTG	1740
	CTGAGGAAA	ATGACAAA	ATCAGCAAGG	ATTTTCACTT	AGGCTTCTGA	AAAGAGATG	1800
	TTTGTGCA	AAACATGAA	AGTTAAAGC	CAACTCTCTG	AGAGCTCTCT	AGAGCTCTCT	1860
	TAAATCAAG	CAGAAATATG	AGGAATTACA	AGAACTTCT	AGGAAAGAGC	AGCTAGATT	1920
	GGAATCGAG	CTGAGAGCT	TGGCTCTCT	GAAGCTTAAT	CTTGAAAGAC	TTTTGAAAGC	1980
60	ACCAAGAGC	TGCAAGCGC	AGGAAGTTT	TGAGATTAAT	AAATATCTTG	GTGAAACACT	2040
	TAAATGATA	ACTACACCA	CCAGAGGCTA	ATATGATCT	AGAGCTCTCT	AGCTCTCTCT	2100
	AGGCTTAAA	ATGGAAGCT	TGGCTCTCT	ATACATCAG	AAATCTTAGA	TATTAGATTA	2160
	TCATATTA	ATGAGCCAG	TTCCTCTCT	GATAGATAGA	CACGCTTTG	AGGCCATCT	2220
	TGAGAGCTT	AGAACAGTC	AGGAACAAAT	GAGTGTCTTT	CGAGCCMAAT	CTGAGTACG	2280
	AGAGCTAAA	AACTTAAGC	TTGACAGCA	CTGATGCTG	AGCTCTCTCT	AGCTCTCTCT	2340
65	ATATCGAGT	ATGGAAGCT	TGGCTCTCT	TGATTTAGG	AGGAAAGAGC	AGAGCTCTCT	2400
	CTCAGATTG	ATATCTCTG	AAAAGCACT	TGAGAGACT	CAACTATAAA	ATGACTTTCT	2460
	GAAGAAGTG	GTATCATGAC	TGGAGTAGT	CTGCTTACTT	GTGAGAGAGG	AGCTTTCTCT	2520
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70	TGAAGAGCT	ATGATAGT	AGATAGATC	AGATATAGT	AGGTTAGAAA	ACCAAGAAAG	2640
	CTGTGAGAG	AAAGCTGCC	TACAGATTC	CTATGACAG	TTACAGAGAT	TAAATGAATT	2700
	TGAGATTGAC	CAACTTCAA	GAACACTCCA	AAACTCTAAA	AGAGAAATAT	AAATCTGATG	2760
	ATCTGATCTG	AAATATTGA	TGAGGCTCTT	CTGAGCTGAG	AGAGCTCTCT	AGAGCTCTCT	2820
	ATCATATGAG	ATGATAGCT	AGAGAGCTGA	CGAGTCTTAA	GNATCTCTTA	AGTTCTCTTA	2880
	CGCTGTAGCT	CCAGGAAAC	AGAAAGAGAC	GGCCATAGT	GACGACAGCA	TGTCANAAAT	2940
75	ACAGAACTA	GAAGAGAGCT	TGCTTGCTAC	TGAAAGAGT	ATGATGCTCT	TGGAAAGAGT	3000
	TAGAGATTCT	GATAGAAAG	TTTATGCTAG	CACTGAGAG	AGAGCTCTCT	AGCTCTCTCT	3060
	ATCTCTCTCT	GATATAGAG	AAACTAAGA	CACCTGTAAA	CAGACTGTA	AGGCACTATA	3120
	TTGCAATAC	AACTCTGCT	TGGTTGACAG	AGAGAGAGGC	AGAGTGTGTA	TACAGAGACA	3180
	GGAGTGGAT	ATTCTGATC	TGAAGAAGAG	CTTTAGAGCT	AGGAATCTTT	CTGAGAGCAT	3240
	AGAGAGGAT	ATGCTCTGTG	TCATGCTACT	CTGATCTGCG	CAGAGAGAGC	TACAGAGACA	3300
80	GGAGGCCCTG	ATTGAGCAAC	GCTATACGAA	CTGTAAACCA	AGAAAGAGG	AGTATGAACA	3360
	GAAGAGGAT	GAATATACT	TTCAATAGAG	CAGACATGAA	CAGACTGTA	AGGCACTATA	3420
	TGAGATGCC	CAGATTCCTA	AGACACAC	AGAGCTCTCT	AGAGCTCTCT	TGGAACACTG	3480
	GGAAACGCA	GAACAGAGA	TAGAGATGAG				
85							

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GTAATGGAGT GTGGAATAT TGATCTTAAT AGTTGGCTTA AAAGAGAAAA ATCCATTGAT 1860
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 AGCTTAATGA ATTTTGGGAT TCGAAACCAA ATGCAACACG ATCAACACAG TATGTGTTAA 2040
 GATTCACAGG TTGGCAACAG TAATTAATAT CCACCAAGAG CAATCAAGA TATGTCTCTG 2100
 TCCAGAGAGA ATGGGAATAT TAAGTCAAGG ATAAAGCCCA AAGGTATGAT TTGTGTCTTA 2160
 GGATGATATT TGTGTATATG GAGTACACGG AAAACACAT TTACACAGAT AATTATGAGT 2220
 ATTTCTAAAT TACATGCCAT AATTGATCCT AATCATGAAA TGAUATTCG CATAATTCOA 2280
 GAGAAAGATC TCAAGATGAT GTTAAAGTGT TOTTAAAAA GGGACCCAAA ACAGAGAGTA 2340
 TCCATTCTGG AGCTCTGGCG TCATCCTGAT GTTCAATTC AAMCTATCC AGTTAAACCA 2400
 ATGGCCAGG AGEDYRNATG GAGTCAAGAA TATGTCTTGA CACACTGTG TGGTGTGAT 2460
 TCCCTTAATC CAAATTTGAA AGCTGTCAAA ACTTTATATG AACACTATG TGGTGTGAA 2520
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Seq ID NO: 34 Protein sequence:

Protein Accession #: AAH0633.1

1 11 21 31 41 51
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 MESEDLGORE IDIKINFKVE DTDELSIAK ISADTIDRSQ TVNQIMQAM 60
 NPEDHLSLL KLEKSNVPLS DALINKLIGR YSQATIALPF DKYQNSFSA RIQVRFAELK 120
 AIQEPDADAR YEQMARANCK KPAFVHISA QFELSGNVK KSRQLQKAV ERGAVPLEML 180
 EIALRNINLQ KQGLISEBEK NIGLASTVLT AQESVGSILG HLQNMNSDC SRQGTIARF 240
 LYKRNPPD AGEDYRNATG GAGTCAAGAA TATGTCTTGA CACACTGTG TGGTGTGAT 300
 TERSERDLV VPGSKPSGND SCERLHLKVS QNSHFKEPLV SDKSESLII TDSITLNRKT 360
 ESSLAKLES TKVEYEPFVP ESNQKQWQSK RKSEICINQNP AASSHHQPV ELARKVNTFQ 420
 RHTTFEDPVE GVSKQSPDIE TSKMPDPSI KCTPSNTLD DYMSCFRITV VMDDFPPACQ 480
 LFTYQGPLC PQQKQJLTA TPLQNLVLA SSANCIPIV KRLTSLIQ IGSSESRVPL 540
 QVLEKKQIY AIKYNVLESA DNQTLDSYRN EYATLKLQQL HSDKILRLD YEITDQYTN 600
 VMEQGNIDIN SMILKKKSID PWRKSKYWRN KLEAVHTIQ HGVISEDLKP ANFLVDGNML 660
 KLIDFGLIAG QPQDSTSVRK DSGQTVRYN PPEAKIDMS SKENKSKSK LEVKEQDWEL 720
 GCILYLYNG ETPQKJLQ ILSLALIDH NHEISFPDIP EKLQDVFLSC CLDEBPKRI 780
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Seq ID NO: 35 DNA sequence

Nucleic Acid Accession #: NM_005823.2

Coding sequence: 85..1953

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 TGTGGAACCC GATCTCTGCT GATCTCTCTG TCTCTCTCTG TCGACCTCGG ATGGGTGACG 180
 CCTCGAGGA CCTGCTGCTG AGAGACAGGG CAGAGAGGCTG CACCCTTGGA CGAGTCTCTC 240
 GCCAACCCAC CTAACATTTT CAGCTCTCTC CTCTGCGAAC TCTGTGGCTT CCGTGTGTGG 300
 GAGTGTTCCT GCTCTGAGAC GAGGCTGTTC CCGGAGCTCG CTCTGGCTCT GGACAGAGAA 360
 AATGTACAC TCTCAACAGA GAGCTGTGCG TTTCTGTGCT ACCGCTCTT TGAAGCTCCC 420
 GAGACTCTGG AGCGCTCTCC ATTGTAGCTC TGCTATTTCC TCAACCCAGA TCGTCTTCTG 480
 GGGCCCAAGG CTTGACAACG TTTCTTCTCT CGCATACAGA AGGCAATGTG GGACTCTCTC 540
 CCGAGGGGGG CTCCGAGGCG ACAGCGCTCT CTGCTTGGCG CTCTGGCTCT CTGGGTGTG 600
 CCGGGGCTC TCTTGAGGA GGTCTAPFVG CCGACTCTGG GAGCTCTGCG TTGCGACCTC 660
 CTTGGGGGCT TTTGGGCGGA GTGCTGCTAC CCGGGTGTG GAGTCTGCGC 720
 GGACCCCTGG ACCAGAGCCA GCGAGAGGCA GCGAGGGGCG CTCTGCGAGG CCGGGGAGCC 780
 CCTACGCGC CCGGCTCGAC ATGCTCTCTC CTGCGACAFA AGCTCTGGG GGGCTGTG 840
 CCTCTCTGG CAGCAACAT CATTCTGCGA TTCCGCGAGG CGATCTGGC CTGCGTACCG 900
 CACGCTCTCT CTGGGAGCCC ATCTCTGCGG CAGCTGTGAC GGACACTCTT CCGGCGCGCG 960
 TTCCGCGGGG AGTGTGAGAA GACACCTGTG CTTCTAGAGA AGAGGGCCG CAGAGATAGC 1020
 GAGAGCTCTA TCTCTACAA GAATGTGGAG CCGTCTGCTG GCGCTCTGCT GCGCTCTG 1080
 GCGACTAGA TGAACCCCTT GACGCCCTAC CCTCTCACT ACAGACAGT GAGCTCTCTA 1140
 AAGCATAAAC TGAATGAGCT CTACCCACAA GOTTACCCCG AGTCTGTGAT CCAGACTCTG 1200
 GAGTACTCTT TCTTCANAGT GAGGCTCTGAG GACATCTAGA ATGTGAATGT GAGCTCTCTT 1260
 AGCTACTGAT TGAATGTGAC AAAGGCGCAG AATGTAGCTG TGAAGTGTG 1320
 ACCCTGATGT ACCCTTTTGT GAGGCGAAGG GCGCAGCTAG ACAAGACAC CTTAGACACC 1380
 CTGACCCGCT TCTACTGGCG GTACCTGTGC TCTCTCAGCG CCGAGAGGCT GAGCTCTCTG 1440
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 TGTGAGCTCT TCTATCCAAA GCGCCGCTCT CTCTTGACA ACATAGAGG GTCCGATAC 1560
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 CAGCAGAAATG TGAATCATGA CTTGGCCAGC TCTATGAAGC TCGCGACGGA TCGGCTCTGT 1680
 CCGTGTGAGT TGGTGTGAGT GCGAGAACTT CTGGAGCCCC ACCTGTGAGG CTTGAGAGCG 1740
 GAGAGCGCG ACCCTCTGAG GCGCCGCTCT CTCTTGACA ACATAGAGG GTCCGATAC 1800
 ACTCTGAGC AGTCCGCGT ACCTGAGCTG CCGAAGCGCT ACCTGTCTCT AGACTCTGAG 1860
 CTGCGAAGAG CCGTCTGGGG GAGCGCGCTG CTTCTAGAGC CTGAGACTGT TCTCAGCTCT 1920
 CTGCGAGCTG TCTTAGCTCT CACCTGTGCG TTAGGSGCCC ACTGCTCTG TCGGCCAGC 1980
 CTTCTGGGG ATCCGCTCT GCGCGAGAGC AGGCAACGGT GATCTCTGCT CACCCCAAG 2040
 AGACTGTGG CTAAGTAAAC GGGACATGCG CCGCTGACAG CAGCT

Seq ID NO: 36 Protein sequence:

Protein Accession #: NP_005814.1

1 11 21 31 41 51
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 MALPTARELL GCGTTPALGS LLFLFLSILG VQPSRTIAGE TQGEAAPIDG VIANPPHIS 60
 LEPQILLGPP CAESVGLSTE RVRELAVALA QKNVLSTEG LKRLAMRLES PPELDLALP 120
 DLLFLFNFDA FSGQCATFRP FSRITANAGV LLPRGAPERG RLLPAAALCN GVRGSLLEA 180
 DVRAALGLAC DLQRFVAERS BEVLLFLNVS CPQFLIDQD EAABAALQGG GPPTVPESTM 240
 SVFTMDNARS LPLVLQDPII RSTPQGVNLS WQKRSSEDSQ WQKPTILIA PFRVREVT 300
 ACPGSGKARE IDESLIPTYK HELSACVADA LLATQMDRVN AIPPTFRLD VLKIKLEDELY 360

PQGYPSVVIQ HLGLVPLEMS PEDIRKNVNT SLETLKALLE VNKGRHMSQ VATLIDRFVK 420
 GRQILDDDTL DTLTAFYFVG LCLSPSEELS SVFESSIMAV RPQDLDTDFE ROLIDVLYPKA 480
 ELAPRNRHS EYFVKYISPL GEDLSEBLKA LSGQNVSEBL ATPEHLRDLA VLPJTVARVQ 540
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 PCLLGGPVPVL TVIALLLAST LA

Seq ID NO: 37 DNA sequence
 Nucleic Acid Accession #: NM_013404.1

Coding sequence: 89..1975

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	GCTCCCTCTC	CTGGGATCTA	CACAGACCAT	GGCCTTGGAA	GGGCTGACCC	CCTGTGTGTC	120
	CTGTGGGAGC	GGCGCTGCGA	GGTCTCTGTT	CTGCGCTCTC	AGGCTCGGAT	GGGTGCTATC	180
15	CTGCGAGGAG	AGACAGAGAC	GGGCTGAGAG	CGGCTGGGAG	GGGCTGGGAG	GGGCTGGGAG	240
	AAGCCCTCAT	ACCATTTCTA	GGCTCTCCCC	TGSCCAACTC	CTGTGCTCTC	CGTGTGCGGA	300
	GGTGTCCGCG	CTGAGCAGCG	AGCGTGTGCG	GCGCTGTGGT	GTGGCGCTGG	CACAGAGGAA	360
	TGTCAAGCTC	TCACAGAGAG	AGCTGCGGTC	TCTGCGCTAC	CGGCTCTCTG	AGGCCCGGGA	420
	GGACCTGTCG	GGCTCCAGAT	TGAGCTGCTC	GTATATCTCT	AAGCCGAGAT	GGTTCCTGGG	480
20	GGCCCAAGCC	TGCACCGGTT	TCTTCTCCCG	CATCAAGAG	GCCATATGGG	ACCTGCTCCC	540
	GAGGGGGGCT	CCGAGAGCAG	AGCGGCTGCT	GCGTGGGCTC	CTGGCGCTCT	GGGTTGTGGG	600
	GGGTTCTCTG	CTGAGCAGAG	CTATATGTGCG	GGCTCTGGGA	GGGCTGCTCT	GGAGCTCTGC	660
	TGGCGGCTTT	GTGCGCAAGT	CGGCGGAGTT	CGTCTACCC	CGGCTGTGTA	GCTGCTCGGG	720
	ACCCCTGGAC	CAGACACGAG	AGGAGGCGAG	CAGGGCGGCT	CTGACGGGCG	GGGAGCCCCC	780
25	CTACGCGCCC	CCGTGACAT	GGTCTGTCTC	CAGATATGAC	GCTCTCGGGG	GCGCTCTGCG	840
	GGTCTGGGCG	CAGCCATCTA	TGCGGAGCAT	CTGCGAGGCG	ATGTTGGGCG	CTGTGCGGCA	900
	AGGCTCTCTC	GGGCTGGGAT	CTGCGAGGCG	ACATCTCTCT	GGGCGGCTT	GGGCGGCTT	960
	CCGCGCGGAA	GTGAGAGAGA	CAGGCTGTCT	TTACGAGCAG	AAGGCCCGCG	AGATAGAGGA	1020
	GAGCTCATCT	TTCTACAGA	AGTGGAGAGT	GGAGGCTGCG	GTGATGCGCG	CCCTGCTGCG	1080
	CACCCAGAGG	GAGCGGTGTA	AGGATCTGCT	CTTACCTACT	GAGCAGCTCG	ACGTTCTAAA	1140
	CTATTAAGCT	GATGTGAGCT	AGCCACAGAG	TCTGTGATCG	AGCATCTGCG	AGCATCTGCG	1200
	CTACTCTTCT	CTCAAGATGA	GGCTCGAGGA	CATTGCGAG	TGGAATGTGA	GCTCTCCCTGA	1260
	GACCTTGAAG	CTTTCTGTCT	AAGTGCAGAA	AGGCGACGAA	ATGATCTCTC	AGGCTCTCTG	1320
	GGGCGGCTCT	CTACAGGTCG	CGACCTGTAT	CGACCTGCTT	GTGAGGGGAA	GGGCGGCTCT	1380
35	AGGCAAGAGT	ACCTTGAAGT	CTTCTGAGCT	GGTCTCTCTC	GGGCTCTCTC	GGGCTCTCTC	1440
	CCCGAGGAGG	CTGAGCTCTC	TGCGCCCGAG	CAGCATCTGCG	GGGCTGAGCG	CCGAGGCTCT	1500
	GGACACGTGT	CCGACAGAGC	AGCTGTGAGT	CTCTATCTCC	AAGGCCCGCG	TGCTCTTCTA	1560
	GAGCATGAAC	GGGTCCGAAT	ACTTGTGAGA	GATCAGCTCT	TTCTCTGGTG	GGGCGGCTCT	1620
	GGGAGTCTT	AGGCGGCTCT	CTGAGCTCTC	TTGAGGATCT	GACTTGTGTA	CTTCTCTAGA	1680
40	CTGCGAGGCG	GATGCGCTCT	TGCGCTTGAC	TGTGGCTGAG	GTGACGAATC	TTCTGGGAGC	1740
	CCAGCTGGAG	GGCTGTGAGG	CGAGAGAGCG	CGACCGCGCG	GTGCGGAGCT	GGATCTCTAC	1800
	GAGCGAGGCG	GAGGACCTCT	ACAGCTCTCT	CGGCGGCTCT	CAGGCGGCGA	TCCCGGAGCG	1860
	CTACTCTGCT	CTGAGCTCTC	GCGTCTGAGA	GAGCCTCTCT	GGAGCGCGCT	GCTCTCTAGG	1920
	ACCTGAGACT	GTCTCTACCG	TCTTGGCACT	GCTCTGAGCG	TCCAGCTCTG	CCTGAGGCGC	1980
45	CCACTCCCTT	GCTGGCGGCG	GGCTCTGCTG	GGATCCCGCG	CTGAGCAGGA	GAGGAGCGAG	2040
	GGATCCCGCG	TTCCAGCCCA	AGGAGACTCG	GGCTCATGTA	AGGAGACAT	GGCCCTCTGA	2100
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Seq ID NO: 38 Protein sequence

Protein Accession #: NP_037536.1

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	FRQLGLDFCA	EYSELGTEV	RELAVALAQK	NKVLSTGLRL	CLANRLSEPP	EDDLADPLDL	120
55	LLFLNDFDAS	GPQACTRFFS	RITKANVDLL	PRGAPERQRL	LPALALCNWG	RGSLLESDAV	180
	RLAGGLACLD	PRFVFAESAE	VLLFLRLVSC	GLFLQDQGEA	ARALAQGGP	PGYGFSTMSY	240
	SPDALRGRL	PVLGQPTIRS	IPGLIVAAHE	GRERDPFWR	QBERTILPR	PRFLVRETC	300
	PGSLRELEID	ESLITPTGSE	LELCVDAAL	ATGQDQVAF	PTFTDQLV	KEKRLDLYQL	360
60	GYPSVLIQHL	GYLFLKMSFE	DIRKNVNTSL	ETLAKALLEV	EKGHMSFPAP	RRPLPQVATL	420
	IDRVKRGSGD	LDKDTLDTLT	AFYTPVLCSE	SEELSESVPE	SSIAWRPQD	LPTCDPRLHD	480
	VLYKARLARF	QNHGSETEY	KIGSLGQAP	DELKRLALQSG	NHVELATPM	KLATDAPL	540
	TVARVQLDGL	PIREVLGCAE	RELPFVNDL	RQKQDLDLT	GLSLQGLHFM	GYLVLDLSVQ	600
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Seq ID NO: 39 DNA sequence

Nucleic Acid Accession #: NM_001508.1

Coding sequence: 1..1362

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	CCGAGATTTC	AGGTGGCCAC	CTGATACAA	ATCACCTCTA	TTCTGTGTGA	CTGATATATC	120
	TGTGTGATGG	GGCTCTGGGG	GACAGAGTTC	ACCATATGCG	CTCCAGAGGT	GCTGCGAAGG	180
	AAAGGATATC	TGCGAGAGCA	GGTGAAGAGC	CACATGTGTA	GTTTGTGCTG	CTGAGCATTC	240
	TGTGTGTCTC	TCATGCGCAT	GCCCATGGAG	TTCTACAGCA	TCATCTGGAA	TCCCTGAGCC	300
75	AGTCCAGACT	ACACCTGTCT	CTGCAAGTCT	CACACTTCTC	TCTTGAGAGC	CTGATCATCT	360
	GCTACGCTGCG	TGCAAGTGCT	GAGCTCGAGC	TTTGAAGGCT	ACATGCGCAT	CTGTACACCC	420
	TTCAGGTACA	AGGCTGTCTC	GGGACTCTTC	CAGGTGAGAG	TGCTGATGCG	CTCTCTCTCG	480
	CTCACTCTCG	CCCTGTGGGC	AGCTCCGCTT	CTGTTGCGCA	TGGSTACTGA	GTACCCCTGG	540
	GTGAACTGTC	CCAGGACCGG	GGGTCTCACT	TGCAACCGCT	CCAGGACCGG	CCACACGAGG	600
80	CAGCCCGAGA	CTCTCAATAT	GTTCATCTCT	ACCAACCTCT	CCAGGCGGCT	GACAGCTTTC	660
	GAGTGCAGCA	CTCTGTGCTC	CTCTGTGCTC	TACTCTGTG	TTCTGCTCTC	GTAGCTATCT	720
	ATGTCTCGGA	ACATGATCGA	GGTCTGAGCT	AAAGGCGGGA	AGGGCTGCTC	GGGCGGGGCG	780
	AGCGCGCTCT	CGAGCTAGAG	GAGTGTCCGAG	AGGAGAGAGA	CAGGAGACCG	CAGAGAGCAG	840
	ACCATCATCT	TCTCTAGGCT	GATTTGTGTC	ACGATTAAGC	TATCTGTGAT	GCCGACAGAG	900
85	ATTGCGAGGA	TCATGTGCTG	GGGCAACCTC	ACGAGGAGCT	GAGGAGGCTC	CTACTTCGCG	960

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GGGTACATGA TCTCTCTCCC CTCTCCGGAG AAGTTTTTCT ACCTCAGCTC GGTATCATCAAC 1020
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TGGCCGCTVT CCGTACAGCA CCGAACACAG GAGAGAGGCT TGGCGTACA TGGCGCTCTC 1140
ACCAACGACA GCGCGCCCTT TGTGACGGCG CGGTGTCTCT TCGGTTCCCG GCGCGAGTCC 1200
TCTGCAAGGA GAAGTCAAGAA GATTTTCTTA AGCACTTTTC AGAGCGAGGC CGAGGCCGAC 1260
TCTAAGTCCC AGTCACTGAG TCTGAGTACA CTAGAGGCCA ACTCAGGGGC GAAGACGACC 1320
AATTCTGCTG CAGAGATGCG TTTTCAGGAG CATGAAAGTT GA
  
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Seq ID NO: 40 Protein sequence
Protein Accession #: NP_001499.1

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MASPSLPGSD CSQIIDSHSV PEFVATWIK ITLILVLLII FVWGILLGNSV TIRVTQVLQK 60
KQVYIQRVTD RMVSLACSDI LVFLIGNMNE FYSIINPLT TSYTLACKRL RFLPEACRY 120
ATLILVLLII PERVILCSIP PRVAVSOPC QVILLIGVPI VTSLVALALH LFMATSTYPL 180
VNVISHRGLLT CHRSTZRIHE QPETSNMBCI TNLSSRWTFV QSFIFGAFVV YLVVLKSLVAF 240
KCMNMQVLMV KSQKSLAGG TRFPQLRKSE SEESRTARQY TIIFRLIIV TLAVCMHPMQ 300
IRIRHAAAKP KIDWTRBYFR ATMILLPFSE TPFFLSVIN FLUTVSSQG FRREVQVVLG 360
CHLSLQAHIN EKGLRIVARS TTDIALFPQR PLLFASRRGS SARSTKIFL STTQSEARQY 420
SLSGSLSLSS LEWNSGAKPA HSAARNGFQR REV
  
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Seq ID NO: 41 DNA sequence
Nucleic Acid Accession #: NM_022358

25
 30
 35
 40
 45

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Coding sequence: 65..1057
1 11 21 31 41 51
GGAGCGCGGG GTCCGGGACAC AGGAGACGAG TTGGGACCGC GGGGGGTACC GGGCGCGGGG 60
CGCATCGTGG AGGCGCGGAC TGGCGCGGGC CGGGCTGTCT CTGTGCACCC TGTTGTAACT 120
GCTGTGTGGC GCTGTGTCTCT TCGAGCGGCT CGAGTCCGAG GCGAAAGGCG GCGCGGACGG 180
ACTACTGTGC GACTCTCTCC GAGGAGATTC GCGTCTCGCG CGAGAGACTA TGGAGCTTCT 240
CGCGAGATTC GAGCGCGTGG CGCTCCAGGC TGAGCGCCAC CGCGCGCGCC GCGAGTGGAA 300
GTCTCCCGCGC TCTCTTACTT TGGCATCAAC GGTATCACT ACATCGGTT ACGGCCACAGC 360
CGCGCGGGTT AGGACTTCGG GCAAGGTCTT CTGATCTTTC TACGGCTCTC TGGGCACTCC 420
CTGAGAGGCT GTACATCTCT AGAGCTGCTC GAGCGGCTCT GCGCGGCTCT TGGCGGCTCT 480
CTCTTGTGCT GCGAAGTCTC GCGTGGGCTT GCGGTGGAGC TGCGTGTCCA CGAGAAACT 540
GGTGTGTGGC GGGCTGTGAG CGTGTGCGCC CACCTGTGGC CTGGGGGCGC TGCGTCTTCT 600
GCAGCTTGAG GCGTGGACCT TCTCTCAAGC CTACTACTAC TGCTTCATCA CCTTCACAC 660
CATGTGCTCT GCGACTGTGC TGGCTGTGCT GAGCGCGGAG GCGTCTCGCA GGAAGCTCTC 720
CTACGTGGAC TTACGTTCTC TCTACATCTT CCGTGGGCTC AGGTTATTG GCGCTTCTCT 780
CAACCTGTGT GTCTGTGGCT TCTGTGTGCG CAGCGCGCAC TGGCGCGGAG CGCGTGTGCG 840
CGCGCGGACG CGCGCGCGCC CGGGGGGCGC GAGAGAGGCT GCGCTCTGCG TGCGCGCGCC 900
CGCGCGCGCC TCGTGTGCT TGTGTGTGCG CTCTTCCACG GTGACGACG TGGAGAGGCT 960
CGCGCGCGCC AAGCTGTGCT TTTGCGCGCC CTCGAGCGCC GGGGTGTGCG GTGGCGGACA 1020
GGTCTCCAGG CCGTGGCGCC GGTGGAAGTC CATCTGACAA CCGCACCGAG CGCGAGGATGT 1080
AATGTGGAAT GGAAGGGTCT GCGTTTCACT ATCAGGGCAC CTTCCCGGCG GATTGGAAG 1140
GGAGGAGGGG CCGTGTGAGG GTCTTCTGCG AGCGAGATT TTTCAATTAT GCTCTGTGCT 1200
AAGTGCCTCT CTTCTCTTCC AAAAATATAT TACAGTCACA CCATAAAAAA AAAAAAAA 1260
AAAAAAA AAAA AAAA AAAA
  
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Seq ID NO: 42 Protein sequence
Protein Accession #: NP_071753

50
 55
 60

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1 11 21 31 41 51
MRPSPVBAAG LVLTLCYLL VAAVFDALB SEAESGRQLR LVQKQALRR KFGFSAEDYR 60
ELERIALQAE MRAAGRWQRF PQSPFYFAIT ITTIQYGBAA PGDSBKVFC MYALLGIFL 120
TLVFFQSJGS ELNAVVRLL LAACKCLGLR MTCVSTRELV VAGLLACAT LALGAVAFSP 180
FQMTFPIAY YCFITLTI QVDPVVALGS GMLGRLPVP VAPFVILLI GLYVIGFNL 240
LVVLEFLVAS ADMFERAAP PSRPFPQAGE SRGLWLPERP ARSUGBSVFP CHVHLKERCA 300
RNLGFSFSPS SPGVVRGGQA PRPGARWKSII
  
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Seq ID NO: 43 DNA sequence
Nucleic Acid Accession #: NM_000869.1

65
 70
 75
 80
 85

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Coding sequence: 220..1656
1 11 21 31 41 51
GGAAACATGA TCCAGCTGAA GCACTGATT CAGGAAAACT TGGCAGTCTC CCAACTTGG 60
TGGCCGAGGG AATGTAGAGC TCGACGCTCA GAGAGTGTGA CCAATGGCCA CAGAGAGGAG 120
GCTGGCTVGG ACTTAGAGTT GCGAGAGGCG AGAGCTGTGA AAGCTCGCTA TCGTCTGTG 180
TGAGCTCTG GAGCACTGCA TATGTTTGA AAGCTCGCTA TCGTCTGTG GGTCCAGAG 240
GGCTCTGTG CTTGTCTCTT CCGCCACATC TCGGACAGG GAGAGACGAG GAGAGACGA 300
ACACACACCA GCGCGCTCTT GCTGAGGCTG TCGAGATTAC TTTTGACCA TACAGAGAG 360
GCTGTGCGCC GCGGAGGCTG GCTGAGGCTG TCGAGATTAC TTTTGACCA TACAGAGAG 420
TATGCACTC TGAAGTGA TGAAGAAGT CAGGTGTCTA CCACTTACT CAGTACCGG 480
CAGTACTGGA CTGATGATT TCTCCAGTGG AACCTTGAG ACTTTGACAA CATCACGAG 540
TGTTCATCTC CCAAGACAG CACTGTGGTC GCGACATTC TATCATATGA GTTCGTGAT 600
GTGGGAAAT CCGCAATAT CCGTGTGCT TATCATATGA GTTCGTGAT 660
TACAGACCTC TCGAGTGTG GACTGCTGT AGGCTGACAA TCTACAACT CCGCTTGAT 720
GTCAGAACT GCTGCTGAC CTTACCAAGT TGGTGTGACA CCACTACAGA CATCAACTC 780
TCTTGTGAGC GCTTGCAGA AAGGTGAAA TCGGACATCA GTGTCTTAT GAGCAGAGGA 840
GAGTGTGAGT TGTGAGGCT GCTGAGTGA TTTTGGAGCT TACAGTATCA AGAGCTATC 900
TACTATGAGC AAGATGAGT CTATGTGGTC ATCCGCGCGC GCGCCCTCTT CTATGTGCT 960
AGACCTGACT TGGCAGGAT CTTCTCTGAT GTCATGACCA TGTGTGGCTT CTACTCTGCC 1020
CCCAACATG GCGAGAGGAT TCTTCTCAG ATTAGACATC TCTTGGGCTA TGTGTGCTCT 1080
CTGATCATG TTTTGCAC GCTGAGGCGC ACTGACAGC GAGCTGCTT CATGTGTC 1140
TACTTGTGTC TGTGACAGC TCTGTGTGTT ATAAAGTTGG CCGAGAACAT CTTACTTGTG 1200
  
```

CGCGCTGTGTC ACAGACAGAA CCTGCACGAC CCGCTGTGTC CTTCGTCTGG TCACCTGTGT 1260
 CTGGAGAGAA CACTTCCCTG AGGAGACACT CACTCTCCCA GAGGCCCCA 1320
 GCCACCTGCC AGGCCACCAA GACTGATGAC TGCTCAGCCA TGGGAAACCA CTGCAGCCAC 1380
 ATGGGAGGAC CCGCAGACTT CGAGAAGACG CGAGGGGACA GATGTATGCC TCCCCCACA 1440
 CCTCGGAGAG CTTGCTGGCG GTGTGTGTGG CTGCTCAGAG AGCTGATCTC CATCGGCGAA 1500
 TTCTGTGAAA AGAGGAGACT GTGAGCCGAG ACTGCTCTGG ACTGCTCTGG CATGTCCAT 1560
 GTCTGTGACA AGCTGTATAT GCACATTAT CTGCTACGGG TGCTGGGCTA CAGCATCAAC 1620
 CTGTATTGCT TCTGTGTCAT CTGGCAGTAC GCTTGTAGTG GTACAGCCCA GTGAGGAGAG 1680
 GGGTACAGCT CTGTGTAGGT GGGGACAGAG GATTCTTCTT TAGGCCCTCT AGGACCCAGG 1740
 GAATATCCAG TACGATGACT GTGAGGAGCT AGATGTCCCT GCGCTCTTC CATGTCCAT 1800
 TCACTCTCAG CAATCAACAG CAAAGCTCTG ACCCTTCCAC CAJAAACTGG GTTGTCAAG 1860
 CCGTTACACC CTGTGCCAC CCGCCAGCAG TCACCATGGC TTTAAATCAT GCTCTCTTAG 1920
 ATCAGGAGAA CTTGCGGACG TCCCTAGTCT CACTCTAGGT GTGAGATCTT CCGCATGTAT 1980
 CCTCACTGA ATAGAGAGCT GTGAGATCTT GCTCTCTGCT CACAACTGCT GTTGTAGGT 2040
 GAAGGCAAAA CCAACTCTCT ACTACACAGG CCGTATAACT CTGTACGAGG CTTCTCTAAC 2100
 CCGTAGTGTG TTTTTTTCTT TCACTCACT TGTGCGACCT TCCTGTAGCA TCATCCCCC 2160
 ATCAGATGAT GGGATGTGGA AGAATAAAT GCAGTGAAC CC

Seq ID NO: 44 Protein sequence
 Protein Accession #: NP_00860.1

1 11 21 31 41 51
 MLMLVQALL ALLLEPLLQ GEARRSRNT RPALLRLSDY LINTNRKGR PVEDWRKPT 60
 VSDIVVIAI LVNDEKQVL TTYIWRQYR TOSFLWNPE DFDNITGLI PTDSINVDI 120
 LINEPVDVK SPIHPIVYR HQSRVQRYR LGVPTACSLD ITNPFVPMV CSLTFYRWA 180
 TIGDINISL ELRFRVSDR EYVPSGQIE ALGLVLFRE FENGSRITLY FQWFWIER 240
 RPLVIVVSL LPSIPLMVD YGYPPLPNS GSRVSKITL LIGYSEVLII VSLTLPAT 300
 GTPLIGVYF VCHALVLSL AETPIFVRL HKQDLQPPV AHLRHVLER IAMLCLRE 360
 STSRKPPATG QATKDDCSA NMHCBSKGG PQDFPEQPRD RCFSPFPRPE ASLVAGLL 420
 ELSEIRFLE KHEISREVAR EMLRVGSVL KILPFIYLA VLAYSTFLN LNSIQYA 480

Seq ID NO: 45 DNA sequence
 Nucleic Acid Accession #: NM_015507
 Coding sequence: 241..1392

1 11 21 31 41 51
 CCGCAGAGA GCTCTGCCCA GCTTACGCCG CGCGCCCCA CGCCCTCCCC AGGCCCGGAG 60
 CGCCTCTGCC GCGGTGCTGT GCTCTCCCTC CACAGCTGCA GGGACAGCAC CCGGTAACTG 120
 CGAGTGGAGC GGAGGACCGG AGCGCGCTGG GAGAGAGGAG GCGCGCGCTT AGCTGCTACG 180
 CGCTCGCGCG GCGCGCTCTC CGAGGGGGCG TCAGAGAGAG GAGAGAGAGC CCGTGCAGAA 240
 AAGCTCTGCT GCTCTCCCTC GCTCTCCCTC GCTCTCCCTC GCTCTCCCTC AGCTGTTTCT 300
 GGGAAACCGG CCGAGTCAAG GATCAACGGG TTGTAGCATC CGGCACGTCA CCGCTGGGTC 360
 TGTCACTATG GAATCAACT GCGCTCTGTC TACGGCTGCA GAGAAACAG CAAAGGAGTC 420
 TGTGAAGCTA CATGCGAAC TGAATGTAG TTGTGTAGT GCTGTGGACC AAACAARATG 480
 AGATGCTTTC CAGGATACAC CGGAAACCT TCGNCTCAG ATGTGATGA GTGTGAGT 540
 AAACCCCGCG CATGCAACA CAGATGTGTG AATACACAG GAGCTACAA GTGCTTTGCG 600
 CTCAGTGCGC ACATGCTCAT CCGCATGCTC ACCTGTGTA ACCTATGAG ATGTGCAT 660
 ATAACTGCTC AGTACAGCTG TGAGACAGCA GAGAAAGCGC CACATGCGCT GTTGCATGCC 720
 TCGAGCTCC CCGTCCGCC AAATGAGAG GACTGTGAG ATATTAGTA ATGTGCTCT 780
 GGTAAAGTCA TCTGTCCCTA CAATCGAAGA TGTGTGAACA CATTGTGAAG CTACTACTG 840
 AAATGTGACA TTGGTTTGGT ATCGCAATAT ATCAGTGACT GATATGACTG TATGATATA 900
 AATGAATGTA CTATGGTAG CCGTGTGAG AGGCACATG CCAATGCTT CATACACAA 960
 GGGTCTGA ATGTGTAAAG CAAAGCGGGA TATAAAGCCA ATGAGCTGT GTTGTCTGCT 1020
 ATCCCTGAAA ATTCTGTGAA GGAAGTCTCT AGAGCACTG GTACATCAAA AGACAGACT 1080
 AAGAGTTCG TGCTTCACAA AAACAGCATG AAAGAGAGG CAATAATAAA AATGTTTACC 1140
 CCGAAGACCA CCGAGCTGCT TACCTCTAG GTGAGCTTGC AGAGTCTTCA CTATAGAGAG 1200
 ATAGTTTCCA GAGCGCGGAA CTCTCATGGA GGTAAAAAAG GGAATGAGA GAAATGTAAA 1260
 GAGGGGCTCG AGGATGAGAA AAGAGAAAGG AAAGCCCTGA AGATGACAT AGAGGAGGGA 1320
 AGCCTCGGAG GAGTATGTGT TTTCCTTAG GTTAATGAGC CAGTGAAAT CCGCTGAAT 1380
 CTGTGTGATA GAGACTGAAA GACTCCBAA CTGAGACATA AGAATTAAA TATCTCGT 1440
 GACTCGAGCT TCAATCATGG GATCTGTGAC TGGAAACAGG ATAGAGAAGA TGATTTTGAC 1500
 TGGAACTCTG CTGATCGAGA TAATGCTATT GCGTCTCTATA TGGCAGTTCC GCGCTTGCGA 1560
 GGTGCACAGA AAGACATGCG CCGATTGAAA CTCTCTCTACT CTGAGCTGCA ACCCCAGAGC 1620
 AACTCTGT TTCTCTTGA TACCGCTCTA GCGGAGAGCA AAGTCCGAAA ACTTGAGT 1680
 TTGTGAAA ACAATACAAA TCGCTCTGCA TGGGAGAGA CACAGAGTGA GATGAAAG 1740
 TGGAGACAG GGAATAATCA OTTGTATCAA GAGACTGAG CTACCAAAAG CATCATTTT 1800
 GTGAGAGAC GTGCGAGGG CATTACAGCT ACCATGTCAG GATGAGGCT CTGCTGTGT 1860
 TCGAGCTAT GAGAGAGAG CACTCTACT CTGAGACT GAGTGTACT GATCTTAT 1920
 TTGACTTTGT ATGTGAGTCT CTTGTGTTT TTGATATTC ATCATAGAGC CTCTGGGACT 1980
 TTAGAATTAC TAGTCAGAAA ATTGTAAATG ACCACAGAAA ATATTATGT AAGATGCTT 2040
 TCTGTATATA GATAGCCAAA TATTGCTTT ACCAGATATA TCAGTATCT TCTCGCTA 2100
 TTCTGTATCT TTCTCAGT ATATATATA ATATGAAAT GTGATTTAT CTTCCCTCT 2160
 CAGTATATCT GATTGTATA AGTAAGTTGA TGAGCTTCT CTACACAT TCTGAGAAA 2220
 TAGAAAAAAA AGCACAGAGA AATGTTTAC TGTGTGACT TATGATACT TCTGGAAGA 2280
 TATGACTCA AGATAGACT TTTCCTTACT TCGCTCTACT TAGGCAACT 2340
 TGTATATTA ATCTCTTGT ATATATAATA TCCAAATCAT CAAAAAAA AAAAAA 2400

Seq ID NO: 46 Protein sequence
 Protein Accession #: NP_056322

1 11 21 31 41 51
 MFLPHELALP LLEHSHVAGF GNAASABHGG LLASARQGV CHYTQKLACC YGHRNSKGV 60
 SEATCRDCKP RGVNHNHNC KCPVYRTRG CQJUNHSCG FRCVQJURYV NTRHYRFGC 120
 LSGHMDHAP TCRVSRCTAM INCQVSTGCT ERSQCLCPB SGLRLAPNR DCLDIDECAS 180
 GRVICPYNRR CVNTFGSYVC KCHIGPELQV ISGRYDCDII NECTMDSRCT SHANCFNTQ 240

GSFKCKCKQG YKNGLRCSA IPENSVKEVL RAPGTIKDRI KKLIAHKSHM KKKAKIKQVT 300
 PEPTTPTPK VNLQPNRYEE IVSHNGSNIS GKKNSEIRKX BOLDEKREER KALANDIEBR 360
 SLKQDVFPFK VNLQSPGLI LVQRKALTSR LKHRELATIV DCDFHWICD WQDRBDDPT 420
 NHPADENMAI QTYWAPALA GHSIDIGRLK LLLPLQAPQS NFCLLPDRLV ADKVGKRLAV 480
 FVNSNNALA WERTTSDEKH WKTGKILQLY GTDATKSIIF EAERGRKGTQ ELIADVVLVLV 540
 SGLCPDLSLLS VDD

Seq ID NO: 47 DNA sequence
 Nucleic Acid Accession #: NM_005046
 Coding sequence: 16..777

1 11 21 31 41 51
 | | | | |
 GGATTTCGGG GCTCCATGGC AGATCCCTT CTCTCGCCCC TGCAGATCT ACTGCTATCC 60
 TTAGCTCTGG AAATCCGAGC AGAAGAGAGC CAGGCTGACA AGATTATTGA TGGGCGCCCA 120
 TGTGCAAGAG GCTCCGACA ATGCGCGGCT GCGCTCTCTA GTGGGATCT GCTCCACTGC 180
 CGAGGCTCTC TGCTCAATGA GCGCTGGGTG CTCACCTGCC CCGCACTGCA GATGAATGAG 240
 TACACCGTCC ACTCTGGGAG TGATACCGCT GGGGACAGGA GAGCTCAGAG GATCAAGGCC 300
 TCGAAGTCAT TCGGCAACCC GCGCTACTCT ACACAGACCC ATGTTAATGA CCTCATGCTC 360
 GTGAAGCTCA ATAGCAGCG CAGCTCTCTA TCACTGTGTA AGAAGATCAG GCTTCCCTCC 420
 CCTGTGAAC CCCCTGGAAC CACTCTGACT GTCTCCGGCT GGGGCACTAC CACAGAGCCA 480
 GATGTGACTT TTCCCTCTGA CCTCATGTC GTGATGTCA AGCTCATCTC CCCCAGAGAC 540
 TGCAGCAAGG TTTACAGAGA CTACTGGAAA AATTCCATCG TTGTGCTGCT CATCCCGAAC 600
 TCCAGAJAA AACTCTGACA TGTGTGCTCA GGGGACCTCT TGTGTGTCAG AGGTACCTGG 660
 CAAAGTCTGG TGTCTGGGG AACTTTCCTT TGGGGCCAAC CCAATGACCC AGGATCTTAC 720
 ACTCAAGTGT GAGGTTCCTC CAACTGGATA AATGACACCA TGAJAJAGCA TCGCTAACGC 780
 CACACTGAGT TAAATTAAGT TGTCTCTCTA ACAGAAATGT CACAGAGATG AGGACACCCA 840
 TGAACCTATA TGAATCTATT GACTTACTCT TTCTCTAAG ATATATTAT ACCTCATGCC 900
 CTCTGTATA ACCATCAATA TTGTGTAAGA CCTAAACCA AACACAATA AGAACACAA 960
 AACCTCTAA

Seq ID NO: 48 Protein sequence
 Protein Accession #: NP_005037

1 11 21 31 41 51
 | | | | |
 MARSLLPLQ ILLSLALELT AGREAQGDKI IDGAPCARGS HPWQVALLSG NQICCGVLV 60
 NERWLVFAK CDSNYSYVHL GSDTLADGRA QRIKASKSFR HPQYSTQTRV NDMLVKLNS 120
 QARLSHWVK VRLPSRCEPT GTTCTVSWG TTFBPDVTFP SDLMCVDKL LSPQDCTRVY 180
 KDLLESNMLC AGIPDSKINA CNGDSGGPLV CRSLQLSLVS WGTFFCQWPH DRGVTYQVCK 240
 FFWEDHTKH EIR

Seq ID NO: 49 DNA sequence
 Nucleic Acid Accession #: NM_003466.1
 Coding sequence: 11..1363

1 11 21 31 41 51
 | | | | |
 GAATTGGGGG ATGGCTACA ACTCTACATG ATCTGGCCAT GAGGGGGCTGA ACCAGCTGGG 60
 AGGGGCTTTT GTGATGAGCA GACCTCTGGC GGAATGTGTC GCGCAGGCCA TGTAGAGCTT 120
 GGCCACACAG GTGTGAAGCC CCTGGACATC CTCTGCGCAG CTCGCGCTCA GCAATGTGTT 180
 GTTGAGCAAG ATCTCTGGCA GGTACTAGCA GACTGCGCAG ATCGGCGCTG GATGTATAG 240
 GGCTCTGAG CCCAAGTGTG CACGCCCA GGTGTGZG AGATGTGZG ACTCAAAACC 300
 CGAGAACCTC ACCATGTGTT CTGGGAGAT CCGAGACCGG CTCTGGCTG AGGGGTCTG 360
 TGACATGAC ACTGTGCCCA GTGTGAGCT CATTAAATGA ATCAACCGA CCAAGTGTG 420
 GCAACATTC AACCTTCTTA TGGACAGCTG GTGGCCACG AAGTCCCTTA GTCCGGAC 480
 CAGCTGATC CCGCTGATC CTGTACTCT CCGAGATCA CCGAGTGGG ATTCCTGG 540
 CTCCACTAC TCCATCAATG GCTCTCTGGG CATCGCTCAG CCTGGCAGCG ACAGAGAGGA 600
 AATGGATGAC AGTATACAGG ATAGCTGCCG ACTAAGCATT GACTCAGAGA GCGACGACG 660
 CGAGACCCA AMCACTCTC CAGACATGCT CTTCAGCAG CACACACTG AGCCCTCGA 720
 GTGCCATTTT GAGCGGCACG ACTACCCAGA GCGCTATGCC TCCGCCACCC ACACAAAG 780
 CGACACGGGC CTCTACCGG TGGCTTGTCT CAACAGCAC CTGAGCAGC GAGAGGCCAC 840
 CTCCACCCCT TCCACACGCG CACTGGGGG CAACTCTCTG ACTACACAGA CTTACCCGTT 900
 GTGCTGATC CTTGCTCTC AAGCAGAGA ACCCGGAGG TGTCAATCTC TGTCAATCTC 960
 TAGCTCCACC CTTCTCTCTT TATCAGCTC CGCCTTTTGG GATCTCGAGC AAGTCCGCTC 1020
 CGGGGTCCCG CCTTCAATG CTTTCCCA TGTCTGCTCT GTGTACGGCG AGTTCAACGG 1080
 CCAGGCGCTC CTCTCAGGCG GAGAGATGTT GGGGCGCAG CTGCGCGAT ACCCAACCA 1140
 CATCCCGACC ACAGACAGG CGAGTATGCT CTCTCTCTCC ATGACAGCA TGTGTGAG 1200
 AAGTGAATC TGTGCAATG CCTATGGCCA CACCCCTTAC TCTCTTACA GGGAGGCTG 1260
 GAGCTCCCC AACCTCAGCT TCGTAGTTC CCAATATTAT TACAOTCCA CATCAGGCC 1320
 GAGTGACCG CCAACACTG CACGCGCTT TGACCATCTG TAGTGAAGC TT

Seq ID NO: 50 Protein sequence
 Protein Accession #: NP_003457

1 11 21 31 41 51
 | | | | |
 MHNISIRSGH GGLNQLGZAF VNGRLPEVV NQRIVDLAHQ GVRPCDISRG LRVSHGCVSK 60
 ILGRYETGS IGRVIGSGK PKVATPKVVE KIGDTRKRP TNFAWEIRDR LLAEDVCND 120
 TVPSEISNR IIRTKVQVFP NLRPSSWAT KSLSPGHTLL PSVAVTPPS PQSDLGST 180
 SINGLILQF PHSRSGED EDQSCULEI DQSSSSQPR KILDTAFSG HHLEPLPCP 240
 ERQHYPEAVA SPSTHKRGG LYPLLLNST LDDGKATLP SIFPLGRNL THQTPVPVAD 300
 PHSFAIKQE TPVSSSSST PSSLSGAPL DLQVQGVGF PPAAPFAHS VYQPTQNAL 360
 LSGRNVGVT LQTHWPIET SQGSSVAGS LAGHWAGSY SNAYHTPTP SYTSWAPRP 420
 NBSLESPYI YSTSRKPAF TTTATFIDL

Seq ID NO: 51 DNA sequence
 Nucleic Acid Accession #: NM_013952
 Coding sequence: 161..1352

	1	11	21	31	41	51	
	TCGAGAAGGA	GGAGAGACAC	GGGGCCGAGG	GCACCCCTCCG	GGCGGGGGCGG	ACCCAAAGCAG	60
	TGAGGGCCCTG	CAGCCGGGCGG	GCCAGGGGAGC	GGGAGGGGCGC	GGCGCGGGACG	TACGGGAGGA	120
5	AGCCCGGAGC	CCTCGGGGCGG	CTGGGAGGCA	CTCCCGGGGG	ATGCGCTCAC	ACTCCATCAG	180
	ATCTGGGCAT	GGAGGGCTGGA	ACCAAGTGGG	AGGGGCGTTT	GTGAATGGCA	GACCTCTGCC	240
	GGAGATGCTT	CGGAGACGAG	GGCCACGCGG	GGTGTAGAGC	CTCTGCGCAT	CTCTGCGCAT	300
	CTCTGCGCAG	CTCGCGCTCA	GCCAATGGCT	GCTCAGCAAG	ATCCTTGGCA	GGTACTACGA	360
	GACTGTGAGC	ATCCGGCGCTG	GAGTGAATGG	GGGCTCCAAAG	CCCAAGGTGG	CCACCCCCCA	420
10	GGGTGTGGAG	AGAGTATGGG	ACTACAAAGG	CCGAAAGCCCT	ACCATGTTTG	CTCGGGAGAT	480
	CCGAGAGGCG	CTCTGCTGAT	AGGCGCTCTG	TGGAGATGAC	ACTCTGGCCA	GTGTGAGCTC	540
	CATTATATGA	ATCATCCGGA	CCAAAGTGGCA	GCAACCAATTC	AACTCTCCCTA	TGGAGAGCTG	600
	CGTGGCGACC	AGTCCCTCTGA	GTCGCGGACA	CAGCGTGAATC	CCGAGCTCAG	CTGTAACTCC	660
	CCCGAGTCTA	CCCACTATGG	ATTCCGTGGG	CTCACTACTAC	TGCAATCAATG	GGCTCTGTGG	720
15	CATCTCATCC	CTGAGAGGCG	GGAGAGCCCA	CTTGACCCCT	TCCAGACAGG	CAGCTGGGCG	780
	ACTAGACATT	GAGTCAACAG	AGAGGACGAG	GGAGCCCGCA	AAGCACTCTT	GCACGTGGAG	840
	CTTCAGCCAG	CACCACTCTG	AGCGCGTGG	GTGGCCATT	GAGCGGCGAG	ACTACCCAGA	900
	GGCCTATAGC	TCCCGCCAGC	ACACAAAGG	CGAGCAGGCG	CTTACACCGG	TGCCCTTGCT	960
	CAACGACAC	CTGAGAGGCG	GGAGAGCCCA	CTTGACCCCT	TCCAGACAGG	CAGCTGGGCG	1020
	CAACCTCTCG	ACTACACAGA	CTTACCCCGT	GGTGGCAGCT	CCGCGCTTTT	GGATCTGCG	1080
	CAAGTGGCTG	CCGGGGTCCC	GCCCTTCAAT	GCTTTTCCCC	ATGTGCTGCT	CGTGTACGGG	1140
	CAGTTTACGG	GGCAGGCGCT	CTCTCTCAGG	CGAGAGATGG	TGGGGCCACG	CTCTCCCGGA	1200
	TACCCATCC	ACATCTCCAG	CAGCGTGAAG	GGCAGCTATG	CTCTCTCTGG	CATCCAGGCG	1260
	ATGTGTGCG	GAGTGAATA	CTCTGGCAAT	GCTCATGGCC	ACACCCCTCA	CTCTCTCTAC	1320
25	AGCGAGGCT	GGGCTTCCG	CAACTCCAG	TTGCTGAGTT	CCCAATATTA	TTACAGTTCC	1380
	ACATCAAGCG	GGAGTGCACC	GCCCAAGCACT	GCAACGGCGT	TTCACCATCT	GTAGTTGGCA	1440
	TGGGAGAGT	G					

Seq ID NO: 52 Protein sequence
Protein Accession #: NP_039246

	1	11	21	31	41	51	
	MPHNSIRGSH	GGGLGLOGAF	VNRRPLPEVV	RQRIVDLAHQ	GVRPCDISRQ	LRVSHGCVSK	60
	ILRYVETDS	IRPVOVLCSS	REUTATKVVV	KIDGTRKQHP	TFWFEIRHPI	LAGVDFGND	120
35	TVPSVSEIR	LITVTFQFPR	NLRFDECTAT	KSLSPHQTLI	PSSAVTPPES	POSDSLGRT	180
	SINGLGLIAQ	PGSDKRHMD	SDQSSCLSI	DSQSSSGPR	KHURTAFSPQ	HLSELEPCFP	240
	SRNGHYPERYA	SPRHTKGQD	LYPLPLNLT	LDGKATLTP	SNTPLEGNLS	THQTPVVAW	300
	PPFWLCSEKSA	PSRRSHRSH	CAGCGQERH	ARPSQGERH	WFRKQTFHP	TSPDARJAM	360
40	PLPLRQAHQ	SVNLTAMHFA	TPFTPTTARP	GASPTPAC			

Seq ID NO: 53 DNA sequence
Nucleic Acid Accession #: NM_012427

Coding sequence: 43..924

	1	11	21	31	41	51	
	CTTGTGGTTC	CTCTCTACTT	GGGGAATACA	GGTCAGGGG	CCATGGCTAC	AGCAAGAGCC	60
	CCCTGGAGAT	GGGTGCTCTG	TGCTCTGTAC	ACAGCCCTGC	TTCTCGGGGT	CACAGAGCAT	120
	GTCTTGCCCA	ACAATGATGT	TTCTCTGTAC	ACACCCCTCA	ACACCGTGCC	CTCTGGGAGT	180
	AGTCAGAGAC	TGGAGCTGTG	GGCCGGGGAA	GACCCCGGT	GGAGATGAGC	CACAGACGCG	240
50	ATCATCATAG	GATCTGAGTT	CGATATGTC	ACCCAGAGCT	GGAGCGCGCG	CGTCTTGCTA	300
	AGGCCCAACC	AGCTCTACTG	CGGGGGGGTG	TTGGTGATC	CACAGTGGCT	GCTCAAGGCC	360
	GGCCACTGCA	GGAGAAAGT	TTTCAGAGTC	CGTCTGGGCG	ACTACTCCCT	GTACACAGTT	420
	TATGATCTGG	GGACGAGAT	CTTCTAGGGG	GTGAAATCCA	TCCGCCAGCC	TGGCTACTCC	480
	CACCTTGCC	ACTCTAAGCA	CTTCAAGCTC	ATCAAACTGA	ACAGAGAGAT	TGCTCCACT	540
55	AAGATGTCTA	GACCCATCAA	CGTCTCTCT	CATTGTCCCT	CTGCTGGGAG	AAAGTGCTTG	600
	GTGTCTGGCT	GGGGGACAC	CAGAGACCCC	CAAGTGCATC	TCCCTAAGGT	CTCTCAAGTC	660
	TGGATATCA	GGCTCTAAG	TAGAAAGAG	TCCAGAGATG	CTTACCCGAG	ACAGATAGT	720
	GACACCATGT	TCCTGGCGGG	TGACAAAGCA	GTTAGAGACT	CTCTCGAGGG	TGATTTCTGG	780
	GGGCTGTGG	TCGCAATGG	CTCCCTGCA	GGACTCTGT	CTGGGGAGGA	TTACCTTTGT	840
60	GGCCGGCCCA	ACAGACCGGG	TGTCATACAG	AACTCTGCA	AGTTACACCA	GTGATCTGAG	900
	GAATCATCC	AGAGCATCT	CTGAGCATCT	CGAGAGTCA	GACACCGGCG	ACTCCACAT	960
	GCTCAGACCA	CAGCCCTGAC	ACTCTTTTCA	GACCTCTATT	CCTTCCAGGA	GATGTTCAGA	1020
	ATGTTTCATC	CTCAGCCGCC	TGACCCCATG	TCTCTGGAG	TGAGGGTCTG	CTTCCGCCAC	1080
65	ATTGGGCTGA	CGTGTGTCT	CTAGTTGAA	CTGGGAGCA	ATTCTCAAAA	CTGTCCAGGG	1140
	CGGGGGTCTG	GTCTCAATC	CTCTGGGCA	CTTCTATCT	CAGTCTGAG	GGCTCAAGCT	1200
	TCTCTGCAGC	TCTGACCCAA	ATTATGTCCC	AGAAATAAAC	TGAGAGTGG	AAAAAATAA	

Seq ID NO: 54 Protein sequence
Protein Accession #: NP_036559

	1	11	21	31	41	51	
	VLATAPRPM	VLALITALL	LVETERVLAN	NOVSCHEPNS	TVPSGNSQDL	GAGAGEDARS	60
	DOSSRIING	SDCDHETPM	QALLLEPQ	LYCGAVLVHF	QWLLTAHCR	KKVFVRLGR	120
75	YSLSPVYESG	QQMFGVKSI	PHFGYSHPGH	SDMLMLIKLN	RLRPTKIDVR	PIHVSHCPIS	180
	AGTKCLVSGM	GTTRSPQVHF	PKVLQCLNIS	VLSQKRCEDA	YPRQIDOTHF	CADKAGNRDS	240
	QQDGGGIVPV	CHSLGQLVLS	WDQYPCARPR	RGVYTNLNC	FFRMIGSTIT	ANS	

Seq ID NO: 55 DNA sequence
Nucleic Acid Accession #: NM_002214

Coding sequence: 681..2990

	1	11	21	31	41	51	
	CCGAGAGCGG	CTCCGCGCTG	TTGCTGGCAT	CCGAGAGCTC	CTCCCTTGCC	AGCCAGAGCG	60
	CTCCGAGCTT	CTCTCTCCGC	CTGCTCTCCG	AGACCGGCTC	GCAAGCTGTC	ACTATATGG	120
85	GTGCGCTCTC	CTGCGCACT	GTGGAGCA	CTGCGCTGAT	TGATGGSCCA	CAGACTTTTT	180

	TCGCCCTGCAC	CTCGCCGCGCG	TACCCTCCCA	CAGATCCAGC	ATCACCCAGT	GAATGTACAT	240
	TADGGTGGTT	TCGCCCCGAG	CTTCGGGCTT	TGTTTGGGTT	TGATTTGGTT	TGGCTCTCG	360
	CTAGCTGAT	TTACCCGAC	GAGCCGCGAG	CGCGTGGMA	GAAGAAAGT	CTCTTCTCT	480
5	TGTCGCCGAG	GAGCTGCGCG	AGCCCTTGCA	GAGCCCTCTC	TCCAGTCGCG	CGCGCGGCTG	600
	TGGCCGTGCA	AGGAGGTGCT	TCTCGCGGAG	ACCGCGGGAC	CGCGCGTGCG	GAGCGCGGAG	720
	GGCCGTAGGG	GGCCTGAGAT	GGCGAGCGGT	GCGCCGGGCC	GCTTACTCTG	ACCGCTTGCT	840
	CGGAGCGCG	GGTGATGCT	GCTGAGCTG	CGGAAAGCT	CTCTAGCGAT	CTCGAGCTA	960
	GGCCCGGAG	TGCCCGGAGA	GGCCGAGGCC	GGGTCCGGAA	GGGAGCGAG	GGCGGGGCG	1080
	GGGCGCGGCT	GTTTTGCAAT	ATGTGGGCGT	CGGCCCTGCG	TTTTTTTACG	GCTGCATTGT	1200
10	TCGTGCTGCA	AAAGACCCG	CGAGGTGCGG	CTGTGTTGCT	CTGGGCGAGC	TGGGTGTTT	1320
	CACCTTTGT	TTCAGCGAG	CGATGAGATG	TGCTACTCTG	TGCTACTCTG	ATATGCTAT	1440
	CCTGTGCGAG	GTGCTTTGCG	CTGGGTCCAG	AAATGTGATG	GTGTGTTCAA	GAGGATTTCA	1560
	TTTACAGTGG	ATCAAGAAGT	GAACTGTGTG	ATATTGTTTC	CAATTAAATA	AGCAAGGCT	1680
15	GCTCAGTTGA	TGATATGAA	TACCCATCTG	TGCATGTTAT	AATACCCACT	GAATAATGAA	1800
	TTAATACGAT	GAGAGACCTA	CTATCGAGCT	CTATCGAGCT	GCTTCAGGAT	CTCGAGCTA	1920
	ATTTTATGCT	GAAAGTTAGT	CCTCTGAGAA	AATATCTGTG	TGACTTTTAT	TATCTGTGTG	2040
	ATGTCTCCAGC	ATCAATGCAC	AAATAATATG	AAAAATTAAT	TCCGTTTGGG	AAAGATTTAT	2160
20	CTCAJAAAT	GGCATTTTTC	TCCCGTAGCT	TGTGTTGTGG	ATTGTGGTCA	TACGTTGATAT	2280
	AAACAGTTT	ACCATACAT	AGCATCCAC	CGGAAAGAT	TGATATCAAT	TGCGTGTACT	2400
	ACAATTTAGA	CTGATGCGCT	CCCCATGAT	ACATTCATGT	GCTGTCTTGG	ACAGAGAACT	2520
	TCAGTGAAT	TGAGAAAGCA	GTTCATAGAC	AGAGATCTCT	TGGAAACATA	GATACACCG	2640
	AAGAGGTTT	TGAGCGCATG	CTTCAGGAGG	CTGTCTGTGA	AAGTCATATC	GGAATGGGAA	2760
25	AAGAGCTTA	AAGATTTGCT	CTGTGTATGA	CGATGTGAGC	GCTCTCCTCT	GCTCTGTGTA	2880
	CGAAATTTGC	AGGCTATGTT	GTGCCCAATG	ACGGAAGCTG	TCATCTGAAA	ACACAAGCTCT	3000
	ACGTCAATCT	GACACATCAT	GAACACCCCT	CAGTGGGCCA	ACTTTTCAGG	AAATTAATAG	3120
	ACCAAGCACT	TAATGTCACT	TTTGACATCT	AGGAAAGACA	ATTCTCATGG	TATAGGATAT	3240
	TTCTACGCT	CTTTCAGGCG	ACATTTCTGT	GTGAATATGA	CTCAACATGA	CTCAACATGA	3360
30	ATAATTTGGT	AGGTGAGGCG	TATCAAGAAG	TCATTTTCAG	AGTGAAGATT	CAGGTGGAAA	3480
	ACCAAGTACA	AGGCATCTAT	TTTAAACATTA	CGCCACTCTG	TCCAGATGGG	TCCAGAAAGG	3600
	CAGGATCATGA	AGGATGCGGA	ACGCTGATCA	CGAATGATGA	AGTCTCTTTC	AAATGTACAG	3720
	TTACATATGA	AAATATTTAT	CTTCCAGGAG	GAJAAACATA	TCGATATATG	AAATCATTTG	3840
	GTTTTAAATG	AACGCTATAA	ATTCAATATC	ACGAAAGACT	CAGCTGTGAG	TGTAGGAGCA	3960
35	ACAGAGGACC	TAAAGGAAAG	TGTGTAGATG	AAACTTTTCT	AGATTCCAGG	TGTTTCCAGT	4080
	GTATGAGAGA	TAAATGTGAT	TTTGAATGAG	ATCTGATGCT	TGAGTACAGT	TGCTACAGT	4200
	ACAGAGGACA	CGGTTATGCT	CGGTTATGCT	GAGTTTGTGG	GAGTTTGTGG	TGTTTATGCT	4320
	ACAAATATTA	GCTTGGAAAA	TGTATGTGAA	AATACTGTGA	AAGGATGAGC	TTTTTCTGTC	4440
	CATATCACCA	TGGAATATCT	TGTGCTGGCG	GTAGAGAGCT	TGAGACAGCG	AGATGCCAAT	4560
40	GCTTCAGTGG	CAAAAGCTCT	GATCATGCTC	AGTCCCTCTC	AGGACAGGCG	CAGCATGTG	4680
	TCATTTCAA	GGGCGAATG	TGCAATGAAA	GAGGCACTGG	TGTGTGTGGA	AGGTTGAGT	4800
	CGACCGATCC	CAGGAGCATC	GGCGGCTTCT	GTGAAACTGT	CGCCACCTGT	TATACAGCT	4920
	CGAAGGAAA	CTGAATGTT	ATGCAATGCT	TTCAACCTCA	CAATTGTGCT	CAGGCTATAT	5040
	TGATCATG	CAAAAGCTCT	GCTTCTCTCA	TGAGACATCA	CATCTATGCT	GATCAAGCT	5160
45	CAGATGTTT	CTCAGGCCA	AGCTCATGTA	GAATATTTT	CATCATTTTC	ATAGTTTAT	5280
	TCTTGATTGG	GTTCCTTAAA	GTCTGTATCA	TTAGACAGGT	GATACATCAA	TGGAATAGTA	5400
	ATAAAATTA	GTCTCTTCA	GATTACAGAG	TGTGACCTTG	AAAAAGAGAT	AGGTTGATCT	5520
	TGCAAGTTT	TGCAAGTTT	CGATCTCACT	ACGCTGTGTA	GAGCTCTGTA	GAATATATTA	5640
	TGGATATCAG	CAAAATTAAT	GCTCATGAAA	CTTTCAAGTG	CAGCTCTTAA	AAAAAGATT	5760
50	TTAAACACTT	AATGGGAAC	TGGAATTTT	ATAATGCT	CTTAAAGATT	ATAATTTTAA	5880
	AAGTCAGGG	AGGAGACAAA	TGCTTCAGGG	TATGCCAGT	TGCTGTTGAT	ACATCTGAC	6000
	GAGAGCTAC	AAATCTCT	ATCATGAT	GACTCATAT	GCTGTGACT	TTTTCAGAGA	6120
	AAATGTGTC	TTACTACTGT	TTGAGACTAG	TGTCGTTGTA	GCACTTTTAC	GTAAATATTA	6240
	ACTTATTTAG	ATCAGCATAG	AATGTAGATC	CTCTGAGAG	CAGCTGATAC	ACTTTTACAG	6360
55	TACCTGTTAT	TCCAGCATCT	CCGAGACAGA	ACATGCTCT	GAGAGATGCT	AGCATTTGTT	6480
	CATCAATG	GTACATGAT	CCCTGCAGCT	GACATGTGAG	GAJAAANATA	ATCTCGAGAG	6600
	TATATCTTAA	GTTTCCCAA	CAGTCAACA	GTTGTTGTT	GAATAGACA	GAACAGTAGT	6720
	ATGATATAAT	ATTGCTGTT	TGACTCTTC	AGAGATGTA	GACATCAAC	CTTAATCTTA	6840
	AAGATATAT	CTGTTTAAA	GTGTGTAGT	TATGCAATG	GCTTTTAGG	TTGCTTTTAT	6960
60	TTTTCAGAGT	GATATCAAT	TCCAGCATCT	CTCTCTCTT	GCTTTTAGG	TTTGTTTTCT	7080
	TTTTTACAG	ATAAGTTAT	GTATGTCA	GATGACTGGA	TAAATTAAGT	GCTAATGTAT	7200
	TACTGCCATA	AAAAATTAAT	AATACATG	CACCTTTATCA	GAATCATAGT	TTTAAAGCT	7320
	GAATGTTAA						

Seq ID NO: 56 Protein sequence

Protein Accession #: NP_02205

1	11	21	31	41	51	
1	1	1	1	1	1	
65	1	1	1	1	1	60
	1	1	1	1	1	120
70	1	1	1	1	1	180
	1	1	1	1	1	240
	1	1	1	1	1	300
	1	1	1	1	1	360
75	1	1	1	1	1	420
	1	1	1	1	1	480
	1	1	1	1	1	540
	1	1	1	1	1	600
80	1	1	1	1	1	660
	1	1	1	1	1	720

Seq ID NO: 57 DNA sequence

Nucleic Acid Accession #: NM_001719

Coding sequence: 123..1418

85	1	11	21	31	41	51
1	1	1	1	1	1	1

GGGCGCAGCG GGGCGGCTCT GCAGCAAGTG ACCGACGGCC GGGAGCGCGG CTTGCCCCCT 60
 CTGCCACCTG GGGGGCTGCG GGGCCGGAGC GCGAGGCGCC GGTAGGCGGT AGAGCGGGGG 120
 GATGACAGGT GGGCTCACTG GAGCTGTGGG GCGCGACAG CTTCTGTGGG CTTCTGGGAC 180
 CCGCTTTTCT GCTGGCGCTC GCGCTGGCGG ACTTCAGCCT GGACAAAGAG GTGCACTGGA 240
 GCTTTCATG CCGGCGACTC GCGCGCGGCG AGCGCGGGGA GATGCGAGCG GAGATCTCTT 300
 CCAATTGGGG CCGGCGCCAC GCGCCCGGCC GCGACCTCCA GCGCAGACAC AACTCTGGCT 360
 CCAATTCTAT GCTGAGAGCTG TACAAAGCCA TGGCGGTGGA GGGGGCGCGC GGGCCCGGGG 420
 GCGAGGGCTT TCTCTACACC TACAAGGCGG TCTTTCAGTAC CAGAGCGCCC CCGCTGGGCA 480
 GCGCTGAGGA TACTATTTCT CTCTCCAGAG CGACACAGGT CATGAGAGCT GTACAGGCT 540
 TGGACATGA CAGGAATGTC TTCCACCCAG GTTACACCCA TGGAGAGTCT CGATTGTGAT 600
 TTCTCAAGAT CCGAGAAAGG GAGGCTGTCA CCGCAGCCGA ATTCCGATCT TACAAGGACT 660
 ACATTCGGGA ACCTCTGACG AATGAGAGCT TCGGAGTCAG CATTATATAG GTCTCTCAGG 720
 AGCACTTGGG CAGGAATATG CTTCTCTTCT CGACACAGGT CCGTCCAGCT TGGGCTCTGG 780
 AGGAGGCTCT GCGGCTTTT GACATCAAGC CACACAGGCA CCACTGTGTG GTCACTCCG 840
 GGCACACCTT GGGCCTCCAG CTTCTGGTGG AGACCTCTGA TGGGCAGAGC ATCAACCCCA 900
 AGTTGGCGGG CTGATGTTGG GCGCACGGGG CCGGACACAA GCGGCCCTCT ATGTGGGCTT 960
 TCTTCAAGCG CAGGATGCTG CACTTCCGCA GCACTCGGCT CACGGGAGCG AAGACGGCG 1020
 CCGGACACCG CTCCAGAGCG CCGCAAGAAC AGGAGCGCCT GCGGATGGCC AAGCTGGGAG 1080
 AGAACAGCAG CAGGACACAG AGGCAAGCCT GTAAGAGCA GAGCTGTAT GTGAGCTTCT 1140
 GAGACTTGGG CTGGCGAGAC TGGATCATGG GCGCTGAAGG CTAGCGCCGC TACTACTGTG 1200
 AGGGGAGTGG TGGCTCTTGC CTGACACTCT AGATGAGGCG CACGACACAG GCGATCTGGG 1260
 AGAGCTGTGT CCACTTCTAT AACCCGAA GGGTGGCCAA GCGCTGCTGT GCGCCGAGC 1320
 AGCTCAATGG CATCTCGGCT CTCTACTTGT ATGACAGCTC CAGCTGTCT CTGAAGAAAT 1380
 AGCAGAACAT GTGGTGTCCG GCGTGTGGCT GCGACTAGCT CTTCCAGAAA TGTAGACACT 1440
 TGGGCGAGG GTTCTCTTGT ATCTTCTATT CCGTCTCTGT CCGCGAGAGC ACAGACACAA 1500
 CTGCGCTTTG TGAAGACCTC CCGTCCCTAT CCGCAACTTT AAGGTGTGTA GAGTATTAGG 1560
 AAACATGAGC AGCATATGGC TTTTGTACAG TTTTTCAGTG GAGCATCCA ATGAACAGA 1620
 TCTCATAGCG CTGACAGGCA AAACCTAGCA GAGAAAGAAA AGCAAGCATA ATGAAGAAAT 1680
 GCGCGGCGAG AGCTATGGCT GCGAATGTCG AGCATATGCA GCGACTCTTT CTAGAGCTT 1740
 TTATGATGCG TTACGAGCCA GCGCACCCAG CCGTGTGAGG AAGCGGGGCT GCGAAGGGGT 1800
 GGGCAGATTG GTGTCTATGG GAAAGGAAAA TTGACCGGGA AGTTCTGTGA ATAAATGTCA 1860
 CAATAAAGCG AATGAATG

Seq ID NO: 58 Protein sequence

Protein Accession #: NP_001710

1 11 21 31 41 51
 | | | | |
 MHVRSIRAAA PHSFVALMAP LFLRLSALAD FSLDNEVHSS FHRRLRSQS RREHQRILLS 60
 ILILHRPRFP HLOQEDIRNAP MPMLDLYNAP AVBGGGGGQG QGSPYPPYKAF PSTQPPPLAS 120
 LQDSHFILTA DMWSPVNLV HDKREFFPLK YHREPRFDL SKIFPEBAYT AAFPIFYED 180
 IERHFHNFPT RIFSPVGLAS HLGRESLPLF LQDSTWJASG BSMLEVDITA FSHVNVNPR 240
 IBLILQLSVSE TLDOGSINFK LAGLIGRBRG QNKQPPKPAV FRATSVHFRS IRSTGQKRS 300
 QMRKTFIKQI EALRMAVFAE HSSSDQRQAC KGHLELYVSR DLWGQDWIIA PEGYAAAYCE 360
 GCAPIFLNRY HMAITHRAIVP TLVHFINFPT VFKPCCAFTQ LMAISLVLYD DSSNWLKSY 420
 RRVVFRAGCC H

Seq ID NO: 59 DNA sequence

Nucleic Acid Accession #: NM_002821

Coding sequence: 150..3362

1 11 21 31 41 51
 | | | | |
 AACTCCCGCC TGGGACGCC TCGGGGTTCG GCTCCGGCTG TGGCTCTGCT TGGGGCGCCC 60
 GGGCTCGGTT GGGTCCGGCT CTTGTGCGCG GCGCGGAGCA GTCTCGGCCC GCGCTGTGGC 120
 CCTCAGCTCC TTTTCTGAG CCGCGCGCGA TGGAGGTGTC GCGGGGATCC CCGGCGAGAC 180
 CCGCGCGGTT GCGCTGCTCT AGGCTCTGCT TCGTCCGACT TCGTGGGCGT ACCGACAGAC 240
 CCAATTGTTT CAGAACAGAG CGTCTCTCTC AGATATGACT CCGAGGCTCG GCGGCGCTCG 300
 TCTGCTGTGA GTTGTAGGCT CCGGCGCGCG TACATGTGTA CTGGCTGCTC GATGGCGCCC 360
 CTGCTCCAGA CAGCGAAGCG CTTTTCGCC AGGGCAGCAG CACTGAGCTT GAGCATGTGG 420
 ACCGCTGCTG GGACTCTGGC ACCTTCCAGT GTGTGGCTGG GATATATGTC ACTGGAGAGG 480
 AAGGCTGAG TCCACAGCG TCTTCAAGC TCAATGTGAT TGAAGCAGAT CCGTGTGCTC 540
 TGAAGCATCC AGGCTCGGAA CGTGAGATCT AGCCACAGAC CAGAGTCACA CTTGTTTGCC 600
 ACATTAATGG GCGACCTTCG CCGCACTAAC AATGTGTCG AGATGGGACC CCGCTTGTCT 660
 ATGGTCAAGG CAGACGACA GTGCGCGGCA TCTTCAAGC TCAATGTGAT TCGGCTGAG 720
 GTCTGTGCA GTTATGCTGT TATCTCTGCT GCGCCACAGC TCGTTTTGGC CAGGCTTGCA 780
 GCGAGCAGAA CTTACCTTGT AGCATTTGCT ATGAAAGCTT TCGCAGGGTG GTCTGTGACG 840
 CCGAGAGAGT GATATGAGCG AGATATGAGG AGGCTATGTT CATTGTGCGG TTTTCAGCGC 900
 AGCCACCCCG GCGAGAGAG GCGCTGCTGA AGATGAGAGC TCGATCACT ACCTGAGCT 960
 GCGCCGCCCA CCGTCCGACA GCGACAGTGT TTGCCAGAGG GTCTCTGCTG CTTGACGAGG 1020
 TCGCGCCAGC CAATGCGAGG ATCTACGCTC GATTGTGCGA GGGGCGAGGG GCGCCACCCA 1080
 TCTATCTTGA AGGACACATT CACTATGACG AGATTGAGAG GTGCGGCTTA TTTGAGGACT 1140
 GGGTFTTAC AGCTGTGAGC GCGCTGCGGA AGCTATGCTG TCGTCTGAG GGTGTGAGG 1200
 AGCCAGAGCT GTGTGTGGAG CAGCGGGGAG TCGCGCTGCC CACCCATGCG AGGATCTACC 1260
 AGAAGGCGCA CCGTCTGGTG TTGGCCAAAT TTGCTGAAGG TGTGTCTGTT GTCTACACT 1320
 GCGCGCGCGC CAACTTGCTT GTTCAAGGGA GAGGAGTGT CAATCTCAT GTGGCACTG 1380
 TCGCTCTCTG GCGAGAGAG GTTCTGTGTA AGATGAGAG TCGATCACT ACCGCTGACT 1440
 TGGATTGCTCT GACCCAGGCC ACACCAAAAC CTCAGCTTGT CTGTGACAGA AACTGAGATG 1500
 TCACTCAGA GAGCTCACGG TTGAGGCTGT TCAAGATGTC GAGCTTGGCG ATCAACATCG 1560
 TGGAGTGTA TGAATGAGCA TGTATCGGTT ATATTGAGAG CAGCCGAGCC GCGACATGCG 1620
 AGCCGACAGC CAGCTGAGC GAGCTGAGAA TGTGTGAGTA CACACAGCA CCGGAGCCAG 1680
 AGCAGTGCAT GAGTGTGACG AAGGAGGCCA GCGTCCGCTT TTCAGCCACA GCGGAGAGGA 1740
 AGCCCACTAT TAAGTGGDAA GCGGCAGATG GGAGCAGCTT CCGAGAGTGG GTGACAGAGA 1800
 AGCTCGGAGC CAGCTCATTT GCGGCGGCTA CTCGAGATGA CCGTGGACAG TACATCTGCA 1860
 TTGCTCCGCA GCGAGAGAG GCGCGAGATC GTGCCATGTT CAGCTCATGT GTGAGCATTT 1920
 TTATCACTCT CAATGTGAAA CCGAGAGGTA GAGCTGTGTA CAGAGCGCAC ACAGCCCTAC 1980
 TGCATGTGCA GCGCCAGGGG GACCCCAAGC CGCTCATTTA GTGGAAAGCG AAGAGCCGCA 2040

TCCCTGGAGCC CACCAGCTG GGACCCAGGA TGCATCATTT CCAGAAATGGC TCCCTGGTGA 2100
 TCCATGACGT GGCCTCTGAG GACTCAGCCG GCTACACCTG CATTCGAGGC AACGCTGCA 2160
 ACATCAAGCA CAGAGATGAG CCCTCTATGT TGTGGACAG TCCCTGGCCG GAGGAGTCGG 2220
 AGGGCCCTGG CAGCCCTCCC GGCCTACAGA TGATCCAGAC CATTTGGTGT TCGTGGGTGT 2280
 CCCTGTGGCG CTACATGATT GCGTATCTGG GCGCTARGTT CTACTCGAG AAGCGCTGCA 2340
 AAGCCAGAGG GCTGCAAGAG CAGCCCCAGG GCGAGAGGCC AGAGATGGA TCCCTCAAG 2400
 GAGGCTCTTT GAGGCTCTCG CAGGCTCTAG CAGAGATCCA GAGGAAATGT GCTTTGACCA 2460
 CTTTGGGCTC GGCCGCCCGG GCCACCAACA AAGGCCACAG CACAAGTAT AGATATGCA 2520
 TCCCAAGGTC TAACTCTGAG CCATACACCA CCGTGGGAAA GAGTGAATTT GGGGAGGTTG 2580
 GCTTGGCAAA GCTCAGGCG TGAGAGAGAG GAGTGGCAGA GAGCTTGSTA CTTTGTGGA 2640
 GCTTCGACG CAGAGATGAG CAGCCACAGC TGATCTTCGG GAGGAGATTG AGATATGCA 2700
 GGAAGCTGAA CCAAGCCACG GTGGTGGGCG TCCCTGGGCT GTCCCGGAG CTGAGGCCCC 2760
 ACTACATGCT GCTGGAATAT GTGATCTGCG GGAAGCTCAA GAGTCTCTGT AGGATATTCGA 2820
 AGAGCAGAGA TGAATAATTT AAGTCAAGAC CCGTCAAGCC CAGCTTGSTA CTTTGTGGA 2880
 GCGCCAGCT AGCCTCGAG ATGAGACACT TTGCCACAAA CCGCTTTGTG CATAGAGACT 2940
 TGGCTGGCGT TAACTGCTCT GTGACTGCC AGAGAACAGT GAGGTGTCTC GCGCTGGCCG 3000
 TCAGCAGAGA TGTGTACAC AGTGAAGTACT ACACACTCGG CCAGGCGCTG GTGCCGCTGC 3060
 GCTGATGTC CCGGAGGCC ATCTGGAGG GTAATCTCTC TACCAAGCT GATTTCTGG 3120
 CTTTGGTGT GCTATATGCG GAGATTTTGA CAGTGGAGA GATGCCCAAT GTTGGCAGG 3180
 CAGATGATGA AGTACTGSCA GATTTCAGG CTGGGAAGCG TAGACTTCTC CAGCCGAGG 3240
 GCTGCCCTTC CAAATCTTAT CGGCTGATCG AGGCTGCTGT GGCCCTCAGC CCGAAGGACC 3300
 GGCCCTCTCT CAGTGAATAT GCGAGCCGCC TGGAGACAGC CACCTCGGAC AGCAAGCCT 3360
 GAGGAGGAG CCCTCTCGAG ATGCTCTGGG CAGGCGAGGA CATCTCTAGA GGAAGACTCA 3420
 CAGCATGATG GCGCAAGATC CTCTCTCTCT GGGCCCTGAG GTGCCTAGT GCAACAGCTA 3480
 TTGCTAGGT CTGAGCAGGG CCGTGGCTTT CTCTCTCTTC CTACCCCTCA TCCTTTGGGA 3540
 GCTGACTCTG GACCAACTAG GGCACATGAG GCTTTGAGC TGGGCACTG TCCCTGGCCG 3600
 CTCTCTCTCT ATCAGGAGCA GTTGTGGTGG CAGAGTAAAC CCAATTTCTC GCGCTTCAAC 3660
 TTCTCCCTTT GACCGGCTCC AACCTTGCCA CTCACTTCCG AACTTTGCT GGGGAGGCT 3720
 AGGCTTGGGA TGAGCTGGGT TTGTGGGGAG TCCCTAATTA TTCTCAAGT CTGGGACAC 3780
 AGGATATG AGTCTCTGCT CCGTCTGGCC ACTGGGCGC AGGAGAGCA ATTATAGAG 3840
 ACACAGCAAG TGAATCTTCC CAATCTGGG CTTGTGACA CTGACAGGA CCGAGTCTT 3900
 CCCCACCTTT CTCTCTTTC CTCACTTAA GTGCTGGCA GATGAAGAG TTTTCAAGG 3960
 CTTTGGACCA TATATTAACC GCGCTTTTGT TATGACAC CAGGCGCTTT TATATTAAT 4020
 TCCAGCTG GGTGGTGG CATGAGAGT AGGGTGGCG CCGGAGATG AGAGAGGTTG 4080
 GCGATCTTA CCCCACACT TAAATTTGT GTTTTGTGT TTGTTTGT 4140
 TGTTTTGT TTATACATCG CTGCTCTCAA TAAATAGCC TTTTITA

Seq ID NO: 60 Protein sequence
Protein Accession #: NP_002812

1 11 21 31 41 51
 MGAARSPAR PERLPGLSVL LLLPLGGTQT AIVFIRKQPS QALQRRAL LRCVEAPGP 60
 VHYVWLLDGA PVQDTEREFA GQSSLSPFAW DRLQSGSTFQ CVARDVTGE EARSANASFN 120
 IHWLEGPVV LKHPASEARI QPQVOTVLRC HLDGHPRTY QWFRDGPLS DGGSNITVSS 180
 KERMLTLRA QPSESLBLCG CAGSAPGDC SGNFTLEIA DESVARVLA PQDVVARYE 240
 EAMFRCQSEA QPSESLGLF EDSTITNRS EPPLSRATV FANGSLLTQ VRPNMAGIYR 300
 CIGQGQGRFP ILEBATLHA EIEDMLPFE RVFTAGSEER VTCLPPEGLP EPSVMWEHAG 360
 VRLPETHRVY QKHGHELVAN IAESDAGVYT CHANLNAQR RQWNIIVAT VPSMLKJPGQ 420
 SLGSEKRPY LCLLQATPK PTVYVTRNQ LIEEDSRFE FKNLTLEMS VEPYDNIWR 480
 CWSSTPAGSI EAQARQVULE KIKPTPPPOF QQCFMFDEEA TPFCSATGRE KPTIMEBRAD 540
 GSSLPEWVTD NAGTLHFARV TRDQANRYTC IASNGPQOI RAHVQLIVAV FITPEVEPER 600
 TTVYGHRTAL LQCAQADPK FLIQKGRDR ILDPTELGR NHIPQNSIV LHDVAPEDSG 660
 RTYCIAGNSC NIKHTEARLY VYSGVPSBS EDGSPFFYK MGTGLSGV ANAVATIAVL 720
 GWNFYCKDRC KAKRLQKPE GKEPEMECLH GBLQNGQPS AETGEVALT SLGSPAPATN 780
 KRHSSTDNR PFRSLQPIIT TLOGSEBEV FLAKAQOLEH GVATLVLVVK SLQTKDEQQQ 840
 LDPSRELSMF GELHAWNVLR LGLCREARF HMYVLEVDL GELQPLRIS KSRIDKLRGQ 900
 FLSTQKRVLF CTVALQWHEI LBNHVFVHD LAARBLVGA QNVKYSALG LSTQYMSY 960
 YHFRQANVLF RMGSEPAILE QDFTSKSDVH APOVLAWEVF TIGIEMHGGQ ADDEVLADLQ 1020
 AGKARLPQPE GCPSLKRLYM QRCWALSPK RPSFEIASA LGDSTVDSRP

Seq ID NO: 61 DNA sequence
Nucleic Acid Accession #: NM_006103
Coding sequence: 29..406

1 11 21 31 41 51
 CACCTGACAC CGCCCGGGGC ATAGACACAT GCTCTCTTGT CGCTCAGGCC GCTAGACGCG 60
 GGCCCTCTCT CTGACGCTGC GCTCTGTGGG CTACACCTA GTTCACAGCA CAGAGAGACA 120
 GAGACCTGCG GAGTCCGCGC AGCTCAGAGT CTGACGCGCG GCGTGTGCCA CTTCTCGCCT 180
 TCTCTGCCA AATGATAAGG AGGGTCTCTG CCCCCAGGTG AACATTAAC TTTCCAGACT 240
 CGGCTCTGT CTGAGACAGT CCGCAGGTGA CAGCAGGTGT CCGTGCAGGA TGAATKTCGT 300
 CCGCATGCG TGGGCGGAG TGTCTCTGCT GCTCTCCACT TGTGAGGCT CAGCCACCA 360
 CAGCTCTGAG AGTGAAGAGA GAAATGTTCT GCTGCGCCTC GCACTGTGGT CCAGCCACC 420
 TGCCTCCGCC TTTTGGGA CTCTGTATTC CTTCTTGGCG TGACCAAGC TTTCCCTTT 480
 CCAACCAAT AAGTAAACCA CTTTCAAGCA AAAAAAAAAA AAAA

Seq ID NO: 62 Protein sequence
Protein Accession #: NP_006094

1 11 21 31 41 51
 MPACRLGLPLA AALLLSLLF GPTLVSGTGA ERTGVCPQLQ ADQNTQECV SDSECADNLK 60
 CCSAGCATFC LILFNDKEGS CPQVNIHFQ LGLCRDQCV DSQCPCQMKC CRNGCGRVSC 120
 VTNF

Seq ID NO: 63 DNA sequence

Nucleic Acid Accession #: NM_001203

Coding sequence: 274..1782

	1	11	21	31	41	51	
5	CUCGCGGCGC	GGAGTGGCGG	GGGCGTGGCG	GGAGCGGGCG	AGTGCGGAGA	CGGCGGCGCT	60
	GAGGACCGCG	GAGCGGCGCG	CCTCAGCGCG	GGGTGGAGTT	CAGCGTATCT	TTTCTAGATT	120
	GTGAAGAGAA	AGGAGATGAT	TTTCATGCGT	TGTTGATAAA	GTTTCAGACT	CTGCGTGATT	180
	CATAACCATT	TGGCTCTGAG	CTATGACAGG	AGAGGAAACA	AAAGATTAAA	CTTACAGGCC	240
	TGCCATTAGT	GAGAGAGCAA	CTTCTGTTAT	ACACATGCTT	TGGGAAGTGC	AGGAAAATTA	300
10	AAATGTGGCA	TGGTGGGAGT	AGTAAGCGCC	CGACCGCCGC	TCCGAAAGGT	360	
	TTCGCTTGTA	AATGACACCA	CAATTGTCCA	GRAGACTCAG	TCAACAATAT	TTCGACGACA	420
	GAGCGATTAT	GTTTCAAGAT	GATAGAGAGG	GATGACTCTG	GTTTGCGCTG	GCTCATCTCT	480
	GCGTGGCTAG	GACAGAGAGG	CTCAGATTAT	CACTGTGGGG	ACACTTCCAT	TCTTCATGAA	540
	AGAGATGCTA	TTGAAAGCTG	CACAGAAAGG	AGCAATGTGA	ATAAGATGAT	ACACCTCTCA	600
15	CTGCGTCCAT	TGAAAAACAG	AGATTTTGTT	GATGACCTTA	TACACACAGG	GCGTTTACTT	660
	ATATCTGTGA	CTGTCTGTAG	TTTGCTGTGT	GTCTTATCA	TATTATTGTT	TAACTTCGGG	720
	TATAAAGAGC	AGAGAACACG	ACCTCGATAC	AGCATTTGGT	TAGAACAGGA	TGAAACTTAC	780
	ATTCTCTGTT	GAGATCTCGT	GAGGAGCTTA	ATTGCGCAT	CTCAGAGCTG	AGGAAAGTGA	840
20	TCAGGCGCTC	CTCTGCTGGT	CAGAAAGGAT	ATAGCTAAGC	AGATTTCAGT	GGTGAACAGC	900
	ATTGGAAGAG	GCGCTATATG	GGAAGTTTGG	ATGGGAAAGT	GGCGTTGGCA	AAAGGTAGCT	960
	GTGGAAGTGT	TCTTACACAG	AGAGAGAGCC	AGCTGTTCGA	GAGAGACAGA	AATATATGAC	1020
	ACAGTGTGTA	TGGGCTGTGA	AAACATTTTG	GTGAGAGAAA	CTGCGAGTAT	CAAGAGGACA	1080
	GGGTCTGTGA	CCGACTTGTA	CTTAATCACA	GACTATCATG	AAATATGTTT	CGTTTATGAT	1140
25	TATCTGAAGT	CCACCAACCT	AGAAGCTAAA	TCAATGCTGA	AGTTAGCTTA	CTCTCTCTCT	1200
	AGTGCGTTAT	GTGATTATCA	CACGAAATCT	TTAATGATCT	AGGCGAAGCC	AGCAATGTCC	1260
	CATCGAGATC	TGAAAGTAGT	AAACATTTTG	GTGAGAGAAA	CTGCGAGTAT	CAAGAGGACA	1320
	GRACCTGGCC	TGGCTAGTTA	ATTATTAGTG	GATACAAATG	AAATTGACAT	ACCACTTAAC	1380
	ACTCGAGTTG	GCACCTAAGC	CTATATGCGT	CCAGAGATGT	TGAGCAGAGG	CTTGACACAGA	1440
30	AACTCACTCC	AGTTCTAAGT	CATGGCTGAC	ATGTATAGTT	TGGCGCTTAT	CTTTTGGGAG	1500
	GTCTCTGAGA	GATGCTGTGA	AGGAGGTATA	GTGGAAGAT	ACCACTCTCT	TATATCATAC	1560
	CTAGTGCCCA	GTGACCCCTC	TTATGAGGAC	ATGAGGGAGA	TTGTGTGCAT	CAGAAGTTTA	1620
	CGCCCTCTAG	TCCCAAAATG	GTGGAGAGCT	GATAGGTGTC	TAAAGCCAGT	GGGAAAACCT	1680
	ATGACAGAGT	CTGGCGGCGC	CAGCTCTGCA	TCGAGGCTGA	CAGCCCTTGG	GSTTAAGAAA	1740
35	ACACTTGGCA	AAATCTCAGA	GTCCGAGGAC	ATAAATGAG	GATGAGAGAG	GAAAGTAGAG	1800
	CATCTCTGCA	GAGAGCCACG	AGGTACTCTT	CTGTTTGTGG	CGAGAGCAAA	AGA.CATCAAA	1860
	TAGATCATCA	CAGTACAGAG	CTTGAACATC	GTCTGCTCTC	CGAGTGGGTT	CAGACCTTAC	1920
	CTTTCAGGGA	CTGAGAGAGG	CAGAGCTGCA	GAGGCGGAGA	GGAGGAGG	TGATTCGGT	1980
	TCGATTGTGA	GGCGGAGAAA	CGGTTGGTGA	ACTTGTTCAA	GATATGATGC	AT	

Seq ID NO: 64 Protein sequence

Protein Accession #: NP_001194

	1	11	21	31	41	51	
45	MLLRGAGKIN	VGTHKEDGDS	TAPTTPRKVL	RCKDHHCPK	DSVNNICSTG	GYCFTHIED	60
	DGLPLPVYTG	CLLRBSPDGL	CHUPPIFQK	RITKCTEPM	EGKNDLPIYK	PLRRIKDFYD	120
	GPRIHALLLI	SVTVCSLLLV	LILFLCYFRI	KRQTRPRYS	IGLEQDRTII	PPGSSRLDLI	180
	BQSSSSGSS	GLPLLVQRTI	AKQIMVKVQI	QEGRYGEVNM	GMRGKQKAV	KVFPTTERAS	240
	WFRFETVYGT	VLAGHNELLG	FLAADIETG	SWTGLYITD	YHNGSLYDLY	LSSTTLQARS	300
50	MLRLAYSSVS	GLCHLETFE	STQGEIAFH	RLKRSNVLV	KRNQCTCLAD	LZLAVFEISD	360
	TNEVDIPFPT	RVGTIKYRPF	EVLDESILRN	HFQSYIMADM	YSFGLIWEV	ARRCVGGGIV	420
	REVQLPYVDL	VPSPDGYEDM	REIVCTIKLR	PSFPHRNSSD	ECLRGMQKLM	TECHARNPAS	480
	RLTALRVKKT	LARMSSEQDI	KL				

Seq ID NO: 65 DNA sequence

Nucleic Acid Accession #: NM_006475.1

Coding sequence: 28..2538

	1	11	21	31	41	51	
60	ACAGAGACTG	CAAGGAGAGG	ACTCAAGATG	ATTCCCTTTT	TACCCAGTGT	TCTCTACTTA	60
	TTCGTGTTTA	TTTAAAGGCG	ACACATCAAT	ATGAGAGAGT	CTTGTCTCAT		120
	AGTCGATATCA	GGGCTGGGGA	CGAAGGCCCA	AATGTCTGTG	CGCTTCAACA	GATTTTGGCG	180
	ACCAAAAGAA	AATACTCTAG	CAGTTGTAGG	AACGTGTATA	AAAGTCCAT	CTGTGAGCAG	240
	AAAGACGATG	TTTATATATG	ATGTTGGCCT	GTTTATATGA	GATATGAGAG	AATGAAAGCG	300
65	TGCGGACGCA	TTTATCTGAT	TATGAGACTC	TATGAGACTC	TGGGCAATGT	GGAGGCCACG	360
	ACAACTCAGC	GCTATTCTGA	CGCTTCAAAA	CTGAGGGAGG	AGATCGAAGG	AAAGGAGTTC	420
	TTCACCTACT	TGCAACCGAG	TAAATGAGCT	TGGGACAACT	TGATTTCTGA	TATCGGTAGA	480
	GTTTGTGAGA	GCACAGTGAA	TGTTGAATTA	CTGAATGCTT	TACATAGTGA	CATGATTAAAT	540
	AGAGGATGTT	CTGACAGAGA	CTTAAATAAAT	GGATATGATA	TCTCTTCAAT	GATATGATAT	600
70	TGGGGGCTTT	TCTATTAACA	TATCTCTAAT	GGGTTGTGCA	CTGTTAAATG	TGCTCGAATC	660
	ATCCATGGGA	ACGAGATTGC	ACAAATAGTG	GTGTTCCATG	CTATTGAAGC	TGTGCTTACA	720
	CAAAATTTGTA	CCCTCAATTC	AGACTTCATT	GAGCGAGAGG	ATGACCTTTC	ATCTTTTGAAG	780
	GCAGCTGCGA	TGCTATCTAG	CATATCTGGG	GCGCTTGGGA	GAGAGCTGCA	CTTCACTACG	840
	TTTCTGCCCA	CCAGTAGAGG	TTTGTAGAAA	CTTCCAGAGG	GTTGCTTAGA	AGAGTCTAGA	900
	GGAGACAGAG	TGGCTTCCGA	AGCTCTTAGT	AAGTACCAAC	TCTTAAATAC	TCTCCAGATG	960
75	GTGATGCTTA	TTTGGGAGAG	AGCAGGCTTT	GGAACCTGTC	AGGAGAAATC	AATTGUNGATA	1020
	GGATTTGAGG	TGACGACATTA	ACAGTAAAT	GGATCTGATA	TCTCTTCAAT	GATATGATAT	1080
	GTGACAATAA	ATGGTGTTAT	CGATTGATAT	GATCAGGTCC	TATTTCTGTA	TTCTGCCAAA	1140
	CAAGTATTTG	AGCTCGTGAG	AAAGACGCAA	ACCACTCTCA	CGATCTTTGT	GGGCCATATA	1200
80	GCGTCTGGAT	CTGCTCTGAG	GCAGAGATGA	GAACTAGCTT	TGCTGGCACC	TTGTGATAAT	1260
	GCATTTCTGG	ATGATATCTC	CACACATGTT	CAGGCTCTCT	TTAAATATAT	TCTTCAGATT	1320
	CACATATTGA	AGATAAAGAT	TGGCGTTAAT	GAGCTTTACA	ACGGGCAAAAT	ACTGGAATCC	1380
	ATGAGAGGCA	AAACACTCAG	AGTCTCTGTA	TATGTATACG	CTGTCTGCAAT	TGAAATATCA	1440
	TGCTGTGAGA	AGGAGGAA	ACAAGTGGAG	TTCACATATT	TGCAATATT	CCGGGATATC	1500
	ATCAGCGGAG	CAGAGAGATG	CGTCCATGAA	AAGTTAAAC	AGATATAGCG	TCTTAGACCC	1560
85	TTCTCGAGCC	TACTTGAAGC	TGCGACTGTG	AAAGGACTCC	TGACACAGCC	TGGAGACTGG	1620

	ACATATTATTG	TGCCAACCA	TGATGCTTTT	AAGGGAAATGA	CTAGTGAGAA	AAAAGAATTT	1680
	CTGATAGCGG	ACAAAATGCG	TCTCTCAAAAC	ATCATCTCTT	ATCACTGAC	ACCAGAGATT	1740
	TTCAATGGAA	AAGATGTTT	ACTACATTTT	TAAAGGCGC	ACAGAGAGC		1800
5	AAAATCTTTC	TGAAAGAGT	AAATGATACA	CTTCTGGTGA	ATGAAATGAA	ATCAAAAGAA	1860
	TCTCATCATCA	TGACAAACAA	TGGTTGTAAT	CATGTTGTAG	ATAAATCTCT	CTATCCAGCA	1920
	GACACACCTG	TGGGAAATGA	TCACATGCTG	GAATACTACTA	ATAAATTAAT	CAAAATCATC	1980
	CAAAATAGTT	TGATCTCTG	TACACAAATC	AAAGAATCTT	CGTGACTGCT	CTATCAACT	2040
	AAAATATATA	COAAAGTTGT	GGAACACAAA	ATTTAAAGTA	TTGAGGCGAG	TCTTCAGCCT	2100
	ATTTATCAAAA	CTGAAGGACC	CACATACTAA	AAATGCAAA	TTGAAGGTGA	ACCTGATTC	2160
10	AGACTGATT	GAAGAAGTGA	CACAAATACT	GAAGTGATC	GAAGAGGCC	AATTATATA	2220
	AAATGACCA	AAATCATTA	TGGAGTGGCT	GTGGAATTA	CTGAAGAAGA	GACACGAGA	2280
	GAACGATCA	TTACAGGTC	TGAAATATAA	TACACTAGGA	TTTCTACTGG	AGGTGGAGAA	2340
	ACAGAAGAAA	CTCTGAGAA	ATTGTATACA	GAAGAGGTCA	COAAGTCCAC	CAAAATCATT	2400
	GAAGTGGTG	ATGGTCATT	ATTAGAGAT	GAGGAATTA	AAAGACGCT	TCAGAGAGAC	2460
15	ACACCGGCA	GGAATCTG	AGACACAA	AAAGAAATCT	CGTGACTGAG	AGGATTAAG	2520
	GAAGTGCTT	CTCAAGTGA	ATCCAAAAC	CAGAAAATAA	TGTTTATACA	ACCTTAAGTC	2580
	AATAACCTGA	CCTTAGAATA	TTGTGAGGC	CAAGTTGACT	TCAGAGACTG	AAACATCAGC	2640
	ACGAAGAGC	ATATCATGAA	TAACTTCGA	CACAAATTA	ATATTTTTTT	TTCTGATATA	2700
	GAACATGAG	GGAATATGTT	GAGTTAGCT	CTCTGTGTA	AGGAATGGA	GAATAATATA	2760
20	CACCTTACAC	CCCTTTTCAAT	CTTGACATTA	AAAGTTCTGG	CTAATCTTGG	AATCCATTAG	2820
	AGAAAATATCC	TTGTACACAG	ATTTCATACA	ATTCAAATGC	AGAGTTGTG	AACGTGTATC	2880
	CCATTGAAAA	GACCGAGCCT	TGTATGATAT	TTATGGATAC	ATAAATGCA	CGCAAGCAT	2940
	TATCTTGCA	TGGAAGCTA	AGTTATATA	ATAGTCTCT	GGTGACAAA	ACTTTTATA	3000
	TCAAAAGGCT	TGCGACATTT	CTATATGAT	GGGTTTACTG	GTAATATATG	TTATTTTTTA	3060
25	CAACTATTTT	TGATCATCA	GAATGTTTGT	CATATGCTCT	TTGCAGTGA	TATTTTTTAA	3120
	TCTCAACCT	TTCAATATA	CCATTTTTTA	GATATAAGA	GAAATCTCT	AAATGTAGTA	3180
	ATTCAAGAA	ACTCAAGATT	TAACTTAAAC	AGTGCTTTTG	ACTTGGGAA		3240

Seq ID NO: 66 protein sequence
Protein Accession #: NP_064666.1

	1	11	21	31	41	51	
35	MIPLPLWFLG	LLLLIVNPIN	ANNHYDKILA	HSRIRGRDQ	RVNCAQQIL	GTOKKYPSTC	60
	KRWFFSGC	QNTGQVGL	POIMNSGRL	CGEVLPLDIL	VYGLGLVIA	TTQYSDA	120
	KLRERISQ	SPTYFAPSNS	AMNLSIDIR	RGLSNVNVE	LNALNLSHNI	NKRMLTKDLK	180
	NGMILPSMYN	NLGLFINHYE	NGVVTVNRCAR	ZIHGNQIATN	GVVHIVDRVL	TQIGTSTIQDF	240
	IRBBDLSSP	RAAATISDL	SALGDSHIFT	LAPTNHAEF	KLPKGVLESP	MDGNVASLAL	300
	MXILLATLQ	CEHILHGLV	PEFLATLIS	TCGDSBITV	NHLYNWKSD	LYVNGVIEL	360
40	IDQVLLPDSA	KQVLELAGRG	QTTFDLVLAQ	LGSLASALRP	GEYTLAPVNV	NAPSDDTSLM	420
	VRLLKLILQ	NHILKLVKGL	NELYNQILIE	TIGRQLGRVF	VYRTAVCIEN	SCMEGRSQQG	480
	RGNTHIPRE	IHKPARKSH	ELKLRDKRFS	TYLSLLSAD	LKELLTPQD	WLPVPFNDA	540
	FKQNTSEKS	ILIKRNLAL	NIIVHLPTG	VPIKGRPSP	WHLTKTQDQ	SKIPKRYND	600
	TLIANLKGK	SEDMINTGIV	HRVVKILYPL	ADTVPGNDQI	LEILNKLYK	IQIKFVRSGT	660
45	FKIEPVTVYT	TKILTRVPE	KIKVLESLQ	PI IXTDPTL	TKVKIGEPH	PLIKGEBET	720
	TEVIRGEBIT	KRYTKIDGV	PVEITKESTR	EBLITDPEI	KYTRISTGG	ETSPLEKLIL	780
	QSVTVKTVF	ISGDSHLPE	DEIEHLIQ	DTVPVRLQAN	KWYGSREEL	REGRSQ	840

Seq ID NO: 67 DNA sequence
Nucleic Acid Accession #: EOS sequence

	1	11	21	31	41	51	
	ATGCTCTGGG	CGTCTCCCG	GGCGCCCGCC	CGCGCGGAGC	CGGCTCTCGG	CGCTCGCGCA	60
	CTAGCGCTGG	TACTCTCGGG	CTGGGCTCTC	TGCTCTCTTC	CCACTCTCTC	GGATCTCTCC	120
55	TTCTCTCTCT	CGGCGCGCTT	CTGGGCTCTC	CGGCTCTCTC	CCAGCGCCCC	CGCTCGCGAG	180
	CAGTGCCTCG	CGCTGTGGGA	GTGCTCGGAG	GGAGCGCGCA	CAGTCAAGTG	CGTTAAACCG	240
	AATCTGACG	AGGTGCGAC	GGAGCGCGCC	GGCTAAGTGG	CGAACCTCTT	CGTACGCG	300
	AACGACCTGG	CCAGCAACCA	CTTCTTTTAC	CTGCGCGGGG	ATGTGCTAGC	CCAACTGCCC	360
60	AGCCTCAGCG	ACCTGGAATT	AGGATAATAT	TGCTGTGGTA	GCTTGACCTA	CGTGTCTCTC	420
	CGCAACTGCA	CACATCTAGA	AAGCTCTCAC	CTGAGAGACA	ATGCGCTCAA	GGTCTCTTCA	480
	AATGCGACC	TGCTGAGTT	CGAATCTCTA	CCGCAATCTA	GGTTTCTCTT	GGACATCTCT	540
	CCCTGGTCTT	CGCATCTGCA	CATGCGAGAC	ATGCTGAOCT	GGCTCAAGGA	GAACAGAGTA	600
	GTGCAAGGCA	AGAACCGGCT	CACCTGTGCA	TATCCGAGAA	AAATGAGAAA	TGGTGCTCTC	660
65	TGGAATCTCA	CAAGTCTGGA	CTGGAAGCTT	GACCGAGATC	CTTCCCGCAT	CGTCAACACT	720
	TCTATGCTCT	TGCTGAGACT	TGTTTTCAGC	CTGATAGAGC	CTATTTCTCT	CCGCTGTTTG	780
	TATTGGAAC	CGAAGGGGAT	AAATAAGTGG	ATGCAATACA	TCAGAGATCT	CTGACAGGAT	840
	CACATGGAG	GGTATCATTA	CAGATATGAA	ATCAATCGGG	ACCCAGAGAT	ACAAAGCTCT	900
	AGTTCTAACT	CGGATGTCTC	CGAGTGA				

Seq ID NO: 68 Protein sequence
Protein Accession #: EOS sequence

	1	11	21	31	41	51	
	MPFGCGSRGA	AGDGRILRLAR	LALVLLHGV	SSSPSTSSASS	PSSSAFFLAS	AVSAQPLPLD	60
75	QCPALCECS	AARTVACVNR	NLTIVPTDLP	AYVRNLPLTG	NQLASNHFLY	LEPRDLVQLP	120
	SLRLDLNLS	SNRLVPLTG	RNLNLSLSL	LEGNALVLR	NGLLALAGL	FTLPRVLRN	180
	PWYCGNAD	KWVLLKSTVE	VQGRDLTCA	YPERKGRVL	LEANSADLDC	DLPLPESLAT	240
	SVYFLGVL	LIGALFLVL	VLNRKGIKEN	MSNRIDACRD	HSGSYHYRVE	INADPRILNL	300
	SSNSDVL						

Seq ID NO: 69 DNA sequence
Nucleic Acid Accession #: NM_000095.1

	1	11	21	31	41	51	
85							

	CAGCACCOCAG	CTCCOCCOCCA	CGGCGATGGT	CCCGGACACC	GCTTGGGTTT	TTCTGTGCAC	60
	CTTGCTGTGC	CTGCGGCG	CGGACGAGCG	CGAGGCCCCG	TTGGGTCTCA	ACCTGGGCC	120
	CGAGATGCTT	CGGGAACCTG	AGGAAACCCA	CGCGCGCGTG	CAGGACGTGC	GGGACTGGCT	180
	GGGCGACGAG	CGGCGGAGA	TCACTTCTCT	GAJJAAACAGC	GTGATGGAGT	GTGACGTGGT	240
5	CGGATGAGTG	CAGTCACTAG	GCACCGGGCT	ACCGAGCGTG	CGGCGCCCTG	TCCACTGTGG	300
	CGCCGGGCTT	CGGCGGCGTG	GCGTGGCGCT	CATCAAGAGC	GAGAGCGGCG	CGGCTGGGCG	360
	CGCTGTCCCC	CGCGGGCTCA	CGGCGAAGCG	CTCGCACTGC	ACCGACGTCA	ACAGGTGACA	420
	CGCCACCCCC	TGCTTCCCC	GAGTCCGCTG	TATCAACACC	AGCCCCGGGT	TCCGCTGGGA	480
	GGCTTGGCGG	CGCGGGTGACA	CGCGGCCACC	CACACAGGCG	GTGGGGGGTG	CTTTGGCGCA	540
10	CGGCAACGAC	CGACCTTTCA	CGACAGATCA	CGAGTGTGAG	ACCGGGCAAC	ATACTAGTGT	600
	CGCCACCTCC	GTGTGGTCA	ACAACCGGGG	CTCTCTCCAG	TGGCGCCGT	CGGACGCCGG	660
	CTTGTGGGCG	GACACGGGCT	CGGCTGTGCA	CGGCGGGCGA	CAGCGCTTCT	GGCCCCGAGG	720
	CTGTCCGACG	GAGTGGCGAG	AGCATCGAGA	GTGGTCTCTA	AGGCGGGATG	GCTGTGGGCT	780
15	TTGTGTGTGT	CGGCTGTGCT	CGGCTGTGCT	CGGCTGTGCT	TTGTGTGTGT	ACATCTAGCT	840
	AGAGCGCTTC	CGGCGAGAGA	AGCTGTGCTG	CGGCGAGCGC	CAGTGGCGTA	AGGACAACTG	900
	CGTGACTGTG	CCCAACTCA	GGGAGGAGGA	TGTGGACCGG	GATGGCATG	GAGACGCGCT	960
	CGATCTGGAT	CGCGCGGGG	ACGCGGCTCC	CAATGAAJAG	GACAACTGCC	CCTGTGTGGC	1020
	GAACCGAGAC	CAGCGGAC	CGGAGCGGGA	CAGTGGGCG	GATGTGTGG	ACAACTGCC	1080
	CTCCGAGAG	AACACGAC	AAAGGACAC	AGACAGGAC	GGCGGGGGG	ATGGTGTGGA	1140
20	CGAGACATC	CAGCGGACC	GGATCCGCA	CCAGGCGGAC	AACCTGCCCT	GGGTACCCAA	1200
	CTCAGACGAG	AGGAGACGTA	ATGGGATGTG	TATAGGGAT	GCTGTGACA	ACTGTGCCCA	1260
	GAAGAGGAC	CGGATGTG	CGGATGTGGA	CCAGCTCTT	GTGGGAGAT	CTTTGTGAG	1320
	CGATCAAGAC	CAGGATGGAG	ACCGACATCA	GGACTCTCGG	GACAACTGTC	CCACGGGTGC	1380
	TAAACGTGCC	CAGGAGACT	CAGACACAGA	TGGCGAGGT	GATGCTCGG	ACGACGAGCA	1440
25	CGACATGAC	GGATCTGCG	ACGATCGGGA	CAGTGGGAT	CTGTGTGCTA	ACCCCGGCGA	1500
	CGGAGACG	GACACGAC	CGCTTGGGCA	CTGTGTGCGA	GACACCTCT	ATCGGACGA	1560
	GGTGTGAC	AAGATGTGCG	TGTGTGCGGA	GAAGCGTGAA	GTCAAGCTCA	CCGACTTCAG	1620
	GGGCTTCCAG	ACAGTCTGTC	TGGACCGGGA	GGGTGAAGCG	CAGATGTACC	CCAACTGGT	1680
	GGTGTCTAAC	CAGGGAAGG	AGATCTGTCA	GACATGAC	AGGACCGG	GCTGTGGCT	1740
30	GGTGTCTAAC	CGCTTCAATG	CGTGTGACCT	CGAGGACG	TCTCAATGCT	ACGACGCTCA	1800
	GGATGACGAC	TATGTGCGCT	TCACTTTTGG	CTACAGAGAC	AGCTCCAGCT	TCTAGTGT	1860
	CACTTGTGAG	CAGTGTGAC	AAAGTATTTG	CGAGGCGAAC	CGCTTCTGTG	ACTGTGGCGA	1920
	CGCTTGTGATC	CAGTCAAGG	CTGTGAGT	CTTCAAGCG	AGCTGTGGGA	ACTGTGGGA	1980
35	CGCTTGTGATC	CATACGAC	CACACATGTC	CCAGGTGTGCG	CCTGTGTGGA	AGGACCGGCG	2040
	AAAGCTGGGT	TGGAGAGACA	AGAAGTCTTA	TGTTGTGTTT	CTGACGACCC	GGCCCCAAGT	2100
	GGGCTCATCT	ACGGTGTGAT	TCTATGAGG	CGCTGTGAGT	GTGGCGGACA	CGAACTGGT	2160
	CTTGTGACACA	ACGCTGGGCT	CGGCTGGGCT	CGGCTGGGCT	CGGCTGGGCT	CGGCTGGGCT	2220
	CATGTGGGCT	AACTGTGCTT	CGGCTGGGCT	TGACACATCT	CCAGAGAGCT	ATGAGACCTG	2280
40	TCAGCTGGCG	CAGGCTTAGG	GACCAAGGTT	AGGACCGGCG	GGATGACGAC	CACCTCTACC	2340
	GGGCTGTGAT	GGGCGCTCTG	CACCCAGGCC	AGGCGGTGGC	CGTCTCGAGG	GGGAAAGTGG	2400
	AAAGGCTCAG	AGGAGACAA	ATAAGTGTG	TGTGAGGG			

Seq ID NO: 70 Protein sequence
Protein Accession #: NP_000086.1

	1	11	21	31	41	51	
45							
	MVPDTACVLL	LTLAALGASG	QGGSPGSGDL	GPQMLRELQE	THAALQDVHD	HLRQGVREIT	60
	PLHNTVMEDC	ACRGGQSVRT	GLFVVRPLLL	CAPGFCFPGV	ACITGEBGGR	CHCFRAGFTG	120
	HSHICTDYIE	CHMPCFPRV	ACITNSPFI	CSACGPGVSG	PTFGQVLAF	AKNRPCTID	180
50							
	IHCETQGIN	CVPNSVCINT	RFSFGQCFQ	PGFVMDQASG	CQRRGAFRCF	DGSPBSCSHH	240
	ADCVLERDGS	RSCVRCVGA	GNQILQDRDT	DLDPDPDEKL	RCPEPQCRH	MCVTPVPSFG	300
	EDVDHGGIDG	ACDPADGGD	VPRKGDGCP	VPRPQRDRT	EDKRGACBN	CEBQNGDQK	360
	DTGGGFGDA	CTDDLDGRI	RKNAWNCVR	PNISDQKDG	DIGDADCMC	POKSGTGGT	420
55							
	VDEHFPVGDAC	DSDDQDQDGG	HQDSRNCPT	VPNAGQESD	HDGQDADCD	DDNDGVFDS	480
	RNRCLVFPNP	QQRHDAKDGV	GVQVQDDPFA	DRVVDIDVC	PNAAEVLTID	FRAPFTVLID	540
	PSBAGIDBN	RYVLAQREI	VWRSPDGLP	AVQTTAFNV	DPBETIRVHT	VTDIDYAGFI	600
	FVYDRESEFY	VYVMQKSGT	VYQANPPFAY	AERQIQLEAV	KSTGTGQGLZ	KNALMHTGDT	660
	ESQVRLWIKD	PRNVGWEDKK	SYNFWLQHRP	GVQYIRVEFY	EGPRLVADSN	VVLDTMRGG	720
60							
	RLGVFCPSQE	NIHNAWLRIR	CHTIDIPEDYE	THQLRQA			

Seq ID NO: 71 DNA sequence
Nucleic Acid Accession #: NM_024626
Coding sequence: 71..319

	1	11	21	31	41	51	
65							
	GAGTACACCA	GGAGGCGAGC	GGCAGCTCCA	CTCAGCCAGT	ACCCAGATAC	GCTGGGAGACC	60
	TTGCCGAGCG	ATGGCTTCCG	TGGGCGAGAT	GCTCTCTGAG	AGCATATTTA	GCACTCATCAT	120
	TATCTGTGCT	GGGACATCTG	CAGTCACTAT	TGGCTCTGAT	ATTTCAGGGA	GACATCATCA	180
70							
	CACAGTCACT	ACTGTGCCCT	CAGCTGGGAA	CATTGGGGAG	GATGGAATCC	TGAGCTGCAC	240
	TTTGAAGCT	GACATCAAA	TTTCTGATAT	GGTGATACAA	TGGCTGAAGG	AAGGTGTTTT	300
	AGGCTTGCTT	CATGTGTCTA	AGAAGGACGA	AGATGAGCTG	TGGAGCAGG	ATGAAATGTT	360
	CGAGGCGCGG	AGGACAGCTG	TCTGTGTATCA	AGTGAATAGT	GGGATATGAT	CTTTGGGCT	420
75							
	GAJAAACGTT	CACATCTAC	ATGCTGTGAC	CTACAAATGT	TATATCATCA	CTCTTAAAGG	480
	CAGAGGGAT	GCTAACTAGT	AGTATAAAGC	TGGGCGCTTC	AGATGCGCGG	AAGTGAATAT	540
	GGACTATAT	CGACAGCTCG	AGCTGTGAGC	GTGAGAGGCT	CCGCTGTGTT	TCCCGGACAT	600
	CGAGTGTCT	TGGGACATCT	AGATGATGAC	CTGGAGGACAC	TTCTGGAGCT	TCTCCATGCT	660
	CAGCTTGTAG	CTAACTCTCT	AGAAATGTGAC	CATGAAGGTT	GTGTCTGTGC	TCTAAATGTT	720
80							
	TACGATACAC	AACATCACT	CTGTGTATAT	TGAATAATAC	ATTGCGAAG	CACAGCGGGA	780
	TATCAAGTGT	CGACTCTTAA	GGGCTGTGAG	GGGCTGTGAG	CTACAGCTAC	TAAATCTCAA	840
	GGCTCTCTGT	TGTATCTCT	CTCTTCTTGC	CATCAGCTGG	GCACCTTCTC	CTTCAGCGAC	900
85							
	TTACCTGAAT	CTAAATAAT	GTGGCTCGGC	CACAAAAGAG	CATGCAAGT	CATTGTGTCA	960
	ACAGGATCTT	ACAGAACTAT	TTTCAACACA	GATATGAGCT	AGTTTATAT	TTTGGGAGAG	1020
	AAATGATCTT	ATACTCTTGA	CTCTCTGAGC	ACGACACAG	ACGACACAC	AAAGAGAGC	1080
	CACAGACGGA	AGCTTCTCAT	ATGACACAGA	TAAATCTATC	TCTCAAGACA	TATTAAGAT	1140
	TGGGAJAJAT	ATTACTGTGA	ACTAGATCTA	ACTGTGTGAG	GCTTAAGAAA	CCCTGTTTTT	1200

	QAGTAGAAAA	GGGCGCTGGAA	AGAGGGGAGGC	CAACAATCT	GTCTGCTTC	TCACATTAGT	1260
	CATTGGCAAA	TAGCAATTCT	GTCTCTTTGG	CTCTGCTCT	AGCAGACAGA	GCGAAGACTC	1320
	TATCGGCAAC	CAGAGTAACA	TCTCTCGAGT	ACAGAGAGTG	ACAGAGGCTA	TGGGAATTC	1380
5	CTGATGGGAT	TATCTTCAG	TCTTTGAGCT	TCTAGTTTC	TTTCCCTCCA	TTCTACCCCT	1440
	CAGGCGAAGT	TCTGTAAAG	AAATGCTGTA	GTCTAGCTC	AGGTTTCTCT	ACTCTGAAAT	1500
	TAGATCTCCA	GAGCCGTGCT	GCGCAACAAT	CAATTTAAG	CACAAACAT	ATACCTTCCA	1560
	TGAAACACAC	ACAGACTTT	GAGAGCAAGG	CAATGACTG	CTGTAAATGA	GCGCTTGAG	1620
	AATGAAGCTT	TGAAGAGAAA	GAATCATTTG	TTTCCAGCCC	CTCTCCAGCA	CTCTTCAGT	1680
10	GTAAACCACT	GCGCTCTCGG	ACCTTGAGAG	CAGGCTGACT	GTATTACATG	TGTTTATAGA	1740
	AAACTGATTT	TAGAGTCTCG	ATGCTTCAAG	AGAATGATTA	AATATACATT	TCCATAAAAA	1800
	AAAAAAAAA	A					
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	Protein Accession #: NP_078902						
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	MAISLQILFW	SIISIIIIILA	GAIALIIGPG	ISGSHSITVT	TVASAGNIGE	DGLISCTFSP	60
	DIKLSDIVIQ	WLKEDVLVLG	HSFKEDKDEL	SEQDHFPRGR	TAVPADQTV	GRASLRALNV	120
20	QLTDAGTYRK	YLTITSKSKN	ANLEYKTGAF	SPVHVVDVFN	ASESLTCEIA	FWHPQPTVV	180
	WASQVDQGAN	FSEVENTSFE	LSNENVTMKV	VSVLNVNTIN	NTYSMIEND	LAKATGDKRV	240
	TESEIKRRSH	LQLMKSASL	CVSSFFPAIW	ALLPLSPYLM	K		
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30	CGGAGGGAG	CAGAGAGGCT	ACCAAGTTCT	TCCTCTCGGT	CTCTCTCGCC	TCGAGCTCCG	120
	CGCTGCGCGG	CAGCGCGGAG	CGATGCGAAC	CAGAGCCCCC	GCGCTCTCGC	GCGAGCGGCT	180
	CGGCGCGCT	CTCTCTCGAG	TGCTCTCGCA	CGTCCCGGCG	CGCTCTCGAG	CGCTCTCGAT	240
	CCCCAAGGGG	AGGCAAAAGG	CGCAGCTCGC	CGCAGCGGAG	GTGGTGAGCC	TGTATAATGG	300
	AATGTGCTTA	CAGGCGCGAG	CAGAGGTCGC	TGGTGGAGAC	GCGAGCGCGT	GGGCGCAATG	360
35	CATTTCGGGT	WLKEDVLVLG	TCCAGAGTGC	GATGAGATTC	AAAGGAGAAA	AGGGGAGTGA	420
	TCTTAGGAAA	AGTGTGAG	AGTCTGAGAC	ACCAACATTA	AGAGCTGTT	CATGAGTCT	480
	ATTGAATTAT	GCGATAGATC	TGGGAAAAAT	TGGGAGTGT	ACATTACAA	AGATCGGTTC	540
	AAATAGTGCT	CTAAGAGTTT	TGTTCACTGG	CTCACTTCGG	CTAAATACGA	GAATAGCATG	600
	CTGTCAAGGT	TGATATTCCA	CATTCAATGG	ACTGAAATGT	TCAGAGGCTC	TTCCCATATG	660
40	ACCTATATAT	TAGATAGTCA	AAGGAGCGCC	TGAATGAT	TCACACAATA	ATATTCACTG	720
	CACCTTCTCT	GTGGAGAGAC	TTTGTGAAG	AATTGTGTCT	GGATTAGTGG	ATGTTGTGAT	780
	CTGGGTGCG	ACTTGTTCAG	ATTACCCAAA	AGGAGTACCT	TGATCTGAT	GGATTTCAGT	840
	TCTTCGACT	ATATATGAAG	AGTACCAAGT	TAATATCTT	TATTTCTCT	TCTTACTCT	900
	TTTTTTTATT	ATGCTCTGGA	ATGCTGTACT	TAAATGACAT	TTTAATAAG	TTTATGATA	960
	CATCTGAATG	AAAGCAAAAG	CTAAATATGT	TACAGACCA	AAATGTGAT	TCACACTGTT	1020
45	TTTAAATCTA	CGATTATCTA	TTTACTCTCA	ATTTCAATAT	GTTTCAATAT	TTTTTTTAGT	1080
	TGTTTAAGAT	ACTTCTCTCA	TATCTCAAT	CTCTCAACT	ATATATATG	TTATTTGTGT	1140
	GGTCTTTTGT	TTTTTCTCT	AGTATAGCAT	TTTTAAAAAA	ATATAAAGC	TACAAATCTT	1200
	TGTACATTT	TAAATGTTA	AGAAATTTTT	TTATATCTGT	TAAATAAAAA	TTATTTCCAA	1260
	CAACCTTAAA	AAAAAAAAAA	AAAA				
	Seq ID NO: 74 Protein sequence						
	Protein Accession #: XP_057014						
55	1	11	21	31	41	51	
	MRPQPAASP	QRLGRLLLLL	LLGLPAPSSA	SEIPKSGKKA	QLAQREVVDL	YNGMCLGDLA	60
	GYPGRGDSGP	ANGITKPTGI	PDHDFPKKEK	GCLRLRSFSE	SWTNPYKQCS	MSLIMVIGIP	120
	SKIARCTFTK	MSHSLBALVL	PROSLARKK	RCQRVWFT	FWAGDSGFL	PIBALVLDQ	180
	GSPHSDNTIN	HSRTSVSEGL	CEGIGAGLNV	VAIMVOTCSN	YFKGDASTGN	NSVSRILIEE	240
	LPK						
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	Coding sequence: 248..1780						
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	CACAGCGTGG	GAGCAGCTCT	TGGGGGAGCT	CGAGCTGCCC	GATCAAGGCT	TCTTGGGGGT	60
	AGTCAAGGCT	GGGTGTGTAG	AACGGGCGCG	GGGCTGGGCG	TGGTTCCTCT	AGTGAGAGACC	120
	CAGGTGCGAG	AGGCAAGAAC	TCTGAGCTAT	CTCTGCTTCT	GGGTCAAGTC	CTTATTCAGG	180
70	TTCTGCGCGG	CGTCCGAGGG	AGTCTGCGGT	GGAAGCTGAG	AAAGCTGTGG	CAGTCTCTCT	240
	TTCAACCATG	CGGCTCTCCC	TGGGAGCGCA	GATGTGGGAG	CTGAGGCGCT	GCGCTGCTCT	300
	GCTGCTACTG	CTGGCATCAT	TTACAGCGCG	GTGCGCGCGG	GGTGAGCTGG	AGACTCTGAG	360
	GTGTGTAACT	GTGTGTGCTG	CGACGAGAGC	AAAGCTGCGT	TGCTCTTACG	GAGGGGAGCT	420
	CGGCGAGCA	GTGTGCGGAG	TGTCTAGGTC	TGGGTGAGAC	GCGGCGGAG	GCGCCAGGA	480
75	ACTAGCGGCT	CTGACATCCA	AAATAGGGCT	TCATGTGAGC	CGGCGTTACG	AGGGCGCGGT	540
	GAGGAGCGCG	CGGCGCCDAG	GCAACCCCGT	GAGCGGCTCA	GTGCTCTGCG	CGAAGCGAGT	600
	CGAGGCGGAT	GAGGCGGAGT	ACGAGTGGCG	GTTCTGAGAC	TGTCGCGCG	GAGACTCTCA	660
	GCGGCGCTGT	GCGCTCGGAG	TGCTGTGCGC	TGCTGTCGCG	TCAGTGAATC	CTGCTCGAGC	720
	ACTAGAGAGG	GCGCAGGGCG	TGACCTCTGCG	AGGCTCTGCG	ACAGCTGAGG	GAGGCGCAGC	780
	CCCCAGGTTG	ACTGTGAGCA	CGGAGGTCGA	AGGCAACAAG	TCGACGGGCT	CTCTTCAAGC	840
80	CTCCGCTCTT	GCTGCGCTCT	CGATCTGTGT	CGATCTGTGT	CGATCTGTGT	CGATCTGTGT	900
	CGACGAGCTA	ACTTGTGTGG	TGTCCATCTG	TGGGCTGCTC	CAGAGCAAAA	GGATCACCCA	960
	CATCTCCCAT	GTGTCTGCTT	TGCTGTGAGG	CTCTGTGAGG	GCGCTTGAAG	ACCAAAATCT	1020
	GTGGCAACAT	CGCAGAGGAG	GAGCATATCTG	CGTATGAGG	AGTGAAGGCG	AGGCGCCCTCC	1080
	CTCATCAAC	TGACGAAGCG	TGAGTGGGCT	TGCTCCAGCT	GGGATACAG	TGATGAGGA	1140
85	CAGTTTGGCG	TTTCCCGCCAC	TGACACATCA	CGACAGCGCG	ATTCAGCTCT	GCCATGTCAG	1200

	CAATGAGTTC	TGCTCAAGGG	ATTCTCAAGTT	CACGTGTGAT	GTCTCTGACC	CCCGAGGA	1260
	CTCTGGGAG	CACTGTGACC	TACTGTGAGC	CTCTGTGTGCT	CTGTGTGTGCT	TGATGTGCT	1270
	ACTCTTGTTT	TGCTCTCTGG	TGGTGTGTGGT	GGTGTCTAGT	TCCCGATACC	ATCGGGCCAA	1380
	GGCCCGAGCG	ATGACCCGAA	AATATGAGGA	GGAGCTGACC	CTGACGAGGG	AGAACTCCAT	1440
5	CCGAGGGCTG	ATATCTCCAT	ACACGGAGCC	CAGGAGCCAG	CCGAGGAGGA	GGTGTAGGCT	1500
	GGAGGCGGAG	ATATGTCCAA	GGACCAAGCT	GGACCAAGCT	CTGTGTGTGCT	TGTATGAGTA	1560
	AGAGGCGGAG	GGCCCGAGTT	ACTCCAGGCT	GACCAAGGCT	AGGAGATGAT	AAACACAGAC	1620
	TGAACTGCTG	TCTCAAGCTG	CTGGGGGGGG	CGAGGAGGAG	GAAGATCAGG	ATGAAGGCACT	1680
	CAAACAGGCG	ATGACAGCT	TGTTTTCAGGA	GATGTGGAGC	CTAGCGGAGCA	AGCCCAAGGCT	1740
10	CAATGTGCTC	TACATCAATG	GGCGGGAGCA	CTGTGTGTGA	CCGAGGAGCT	CCCTCTCTCT	1800
	CTAGGCGCTG	TGCTCTCTGT	TGCAATGGGA	GATTATTAGC	CATCTTGGGG	GGCTCCTCTAA	1860
	ACACCCCATC	TCTTGTGGGA	AGATGCTCCC	CATCCCACTG	ACTGTCTGAC	CTTTACCTCC	1920
	AAACCTTCTG	TTCATGTGGG	GGGCTCCGAC	CTGTGTGCTC	CTGCCACACT	GGTGTAGGCT	1980
	CACGTGTGTG	GTGTGTGTGA	CTGTGTGTGA	CTGTGTGTGA	CTGTGTGTGA	TGTGTGAGG	2040
15	TGACTGTCTG	TGGAGGGGCT	ACTGTGTCTG	TGTGTGTGAT	TATGCTGTGA	TATCAGAGCT	2100
	AAGTGAAGCT	TGGTGTATGT	GCCACGGAGT	TGAGTGGTT	GCGTGGGAGCA	CAGTGTGAGT	2160
	GTGTGTGCTG	TGTGTGTGAT	GCTGTGTGTG	GACCTCTGCT	TGAAAAGCA	GATATTCTCT	2220
	CAGACCCGAG	AGCATATTA	ATGAATGGGA	GTGTGTGTGA	GGAGGAGTGA	GACTGTGCTG	2280
	CAGACCCGAG	TGTGTGGGCA	TAGCTGGAGC	TGGAATCTG	CTCCGGTGTG	AGGGAAGCTG	2340
	TCTCTCTACA	CTGTGAGGCC	ATGGGGGGCA	GTGTGAAGCA	GCGACTCCCT	GGGTCAAGCA	2400
20	GAGGCTTGAA	CTGTGACAGA	AGCCCTCTGC	CTCTTGTGTG	CCCTTGGGCT	TGTGTGATCT	2460
	ACATATTCTG	TGAAATATA	CATGTGCCCG	GAGCTGTCTG	CAGGAATGCT	GCTGTGATCT	2520
	ACTTTTAAAT	TTTTTCTTTT	TTTTTCTCTG	CCCTTTCGAT	TAGTGTATT	TTTATTATT	2580
25	TTTTATTITT	ATTTTTTTTT	AGAGTTTGA	TCCAGCTG	AGGATATAGC	CAGAGCTGCT	2640
	CTGTAAAAAA	ACCAAAACCC	AAAAAAAAAA	AAAAAAAAAA			

Seq ID NO: 76 Protein sequence
Protein Accession #: AAH10423

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	MPLSLGAGDM	QPEAMLLLLL	LLASPTGRCP	AGELETSQV	TVVLGGDAKL	FCFTRGDSGE	60
	QGVQVAMAR	DAGGAGGELA	LLASISYGLIV	SPAYEGRVVE	PPFPRMPLDG	SVLLRNVAQA	120
	DSBIEYCRIV	TTPFGRGPR	KLARLVVPL	PSFLRNPLAE	EEQLPLAS	CTABSEPAIS	180
	VTMTVEVGT	TSSESEKISR	SAAVTSEPL	VPSRSMNQPV	LTCVSRHPLQ	LQDQIRITHL	240
35	HVSLPLASAV	RGLEDQNLNH	IGREGMLKLC	LSBQGPFPYS	NWTRLEDPLP	SGRVVDQDYL	300
	QPFPLTETHS	GLYVCHVISE	FSRSDSGVTV	DVLDDQEDSE	KQVLVBSAVS	VVVGVIAHL	360
	ICLLVWVVLV	HSHVLEHQA	QNTGTGTGAT	TLVREHSEH	SHSHEDPS	QFVSVEGLAA	420
	EHVPSLEMD	SSCSVSESEP	EGEYSYSLTV	VRIEFTQTL	LSPSGGRABE	EDQDQSIKQ	480
40	AMNHVQVQNG	TLRAKPTQNG	IYINGRHLV				

Seq ID NO: 77 DNA sequence
Nucleic Acid Accession #: NM_003474.2

Coding sequence: 37...3036

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45	CACCTAAGCT	CTTCTAGTCT	CCCGGGCCAA	CTCGGACAGT	TTCCTCATTT	ATTGCAAGCG	60
	TCAAGCGTGG	CTTGTGCGAG	AACGGGCGCC	CGCGACAGCA	CGGACACACA	CGGGGGGAAA	120
	CTTTTATAAA	AAATGAAGCG	TAGAGAGAGT	CAGGAGCGAG	GGGGGCGGCT	CCGAGAGGCT	180
	CCGAGAGCTG	CTCGGTCGAG	CAGGAATATC	CTCGGTCGAG	GAACCCCGCC	CCCGCTTGCG	240
50	GGCCGCGTGG	GATGTGTGAC	GGCTGCGCCG	CGCGCCCGAG	AGCTGTCTGA	CTGAGGCGCC	300
	GGAAGAGCTG	CAGCGCGGCC	GCTGCGCGTG	TCCCGCCGCC	GGGCCCTCTC	GCTGCGCGCTG	360
	GGCGGTGCTG	TGCTGTGCGC	CTGGAGGCGC	CGAGGGGTGT	GCTTAAGAAA	CGAAGAGAGA	420
	GCATGATGAG	TGTGTGAGTC	CTCTGTGTGG	AGTGGGAGCC	TCTGATATCC	AGTGAAGAGC	480
	TTGCACTCCA	AGAACTATCC	AGAAATGCTG	AATATTCCAG	TACAAAGGGA	AAGCAAGAGA	540
55	CTGATCATTA	ATCTGGAAGG	AAATGAAGGT	CTCATGTGCA	GCAATTTTCA	GGAAACCCAG	600
	TATCTGGGAG	AGCATCTACT	TGTCTCTCTC	GCTGTGAATT	ACAAGGTAT	TCTGTGTGAC	660
	TGTTACTACC	ATGACATGAT	ACGGGATAT	TCTGATTCAG	CAGTCAAGCT	CAGCAGCTGT	720
	TCTGTCTCTA	GGGGAGCTAT	TGTCTTTGAA	AATGAAGGCT	ATGTCTTAGA	ACCAATGAAA	780
60	ATGAGACACA	ACGATATACCA	ATCTCTTCCA	GGAAGAGAGT	TGAAAGAGCT	CGGGGATGCA	840
	TGTGTGAGCA	AGTGTGTGCA	AGTGTGTGCA	ATCTCTTCCA	ATCTCTTCCA	ACCAATGAAA	900
	CAGACATGCG	CAGAGAGGCA	TAAAGAGAGG	ACDCTCAGCG	CACATAGTGA	TGTGTGAGCT	960
	GTGATCTGTG	CAGACACGCG	AGATTTTCAG	AGGCAAGGAA	AGATATCTGA	AAAGATTAGG	1020
	CAGCATATTA	TAGAGATTGCG	TATATCATTT	GACATGATTT	ACAGACCACT	GAACATTCGG	1080
	ATCTGTGTTG	TAGCATCTGCA	AGTGTGTGCA	GACATGATTT	GACATGATTT	AAATCTGAGT	1140
65	CAATTCACCA	GCTCTCATGA	ATTTCTGGAG	TGGAGGAGAA	TGAGCTGCTT	ACCTGTCAAA	1200
	TCCCATGACA	ATGCGAGGCT	TGTCATGTGG	GTATTATTTCT	AAAGGAGCCG	CATGGGCACTG	1260
	GGCCCATATCA	TGAGCATGTG	CAGTGTGAGC	GACATGTGCT	GACATGTGCT	GGACATCTCA	1320
	GACCATATCT	TGTGTGTGCA	CGTCAAGCTG	GCAATGAGCG	GGGCAACACA	TTTCGGAGTG	1380
	AATCATGACA	CAGTGTGAGC	GGGCTGTAGC	TGTCAAATGT	CGTGTGAGAA	AGGAGGCTGC	1440
70	ATCATGAGCG	CTTCCACGCG	GTACCACTTG	CCCATGTGTT	TGACGAGTGT	CAGCAGAGAG	1500
	GACTTGTGAG	CAAGCTGTGA	CTCGAGAGTG	GGGGTGTGCT	ATTTTAACTG	CGCGGAGTGC	1560
	AGGAGCTGTT	TGGGGGAGCA	GAAGTGTGAG	AAAGATTTTG	TGGAGGAGAG	AGAGGATGTT	1620
	GACTGTGGGG	AGGCCAGAGGA	ATGTATGAAT	CGCTCTGCA	ATGCCACCA	CTGTGATGCT	1680
	AAAGCGGAGC	CTGTGTGGGC	ACATGSGCTG	TGCTGTGAAG	CTGTGCAAGT	GAAGCTGTGA	1740
75	GGAGAGCTGC	GGGCACTTCC	GGGCACTTCC	TGTGTGAGCT	CGAGGCTTCC	CAGAGGCTGC	1800
	AGGCTCTTCC	GGGCAAGACA	CGTGTGAGCT	CAAGTATGAG	ACTCATGTCA	GAATGTGTGCA	1860
	GGCTCATGCT	ACAAATGGAT	CTGCGAGACT	CAAGGAGCAG	AGTGTGTGAC	ACTCTGGGGA	1920
	CCAGGTGCTA	AACTCTGCCC	TGGAGATCTG	TTTGGAGAGG	TCAATCTGCT	AGGTGTATCT	1980
	TATGTGCACT	GGGCACTTCC	CTCGAGAGCT	TGCTGTGAGT	GGGCACTTCC	GAGAGATCT	2040
80	AAATGTGAGA	AAATCCAGTG	TCAAAGAGGT	GCCAGCGGCG	CAGTCAATGT	TACCAATGCC	2100
	GTTTCTCATG	AAACAACAGT	CCCCCTGCAG	CAGGAGGCGC	GGATTTCTGT	CCGCGGGAGGCT	2160
	CAAGTGTGCT	TGGGCGATGA	CATGCGGAGC	CCAGGCGCTG	TGCTGTGAGG	CAACAAGTGT	2220
	TCAGATGAGA	TGTCAAAATA	TGATGTGCTT	TGGGCTGCTA	TGTCAAAATA	TGATGTGCTT	2280
	GAGTGTGACA	TGTGTGTGCA	CGGCAAGAGG	GTGTGAGGCA	ACAGGAAGGA	CTGCCACTGC	2340
85	GAGGCGCACT	GGGCACTCTC	CTTCTGTGAC	AAGTGTGCTC	TTGAGAGAGG	CAGAGACAGC	2400

	GGCCCATCC	GGCAGGAGA	TAACCAAGGT	TTAACCATAG	GAATCTGGT	GACATCTCTG	2460
	TGTCCTCTT	CTGCTGAT	TGCTGTTTAT	CTCAAAAGGA	AGACTCTGAT	ACCACTGCTG	2520
	TTTCAAMTA	AGAAGACAC	CATTGAAAA	CTAAGTGTTG	TGCGCCCTTC	CGCGCACCCC	2580
	CTGTGCTCC	AACCTGTCA	GGCTCACTCT	GGCCACCTGT	GAAGAAGCCT	GATGAGGAA	2640
5	CGCGCAGATT	CTACCCACC	GAGGAGGAGT	CCGAGGAGAT	TGCTGGAGTG	TGCAAGATTT	2700
	GACATCGGA	GAGCTATCA	GGCTCTAAT	GTCTCTCAG	CCGATCAAC	TACCGAGTGT	2760
	CTTCTCTCCC	TTCCACGGGC	CCCACTGACC	CTAGAGTCCC	CTGCCAGACC	CTCTGCAGCC	2820
	AAAGCTGCAT	TTAGCGAGGC	CCAGGGAGAC	TGTAAAGCCA	ACCCCCCTCA	GAGGCTCTGT	2880
	CTCTGCAGTC	CTCTGGCCAG	AGCACTCTGG	CTCACTGAGC	CTTGGCCGAG	GACCCAGAG	2940
10	CAATGGGAG	CGACCTGCT	CTCTGACCC	CTCAGACCTG	CTCCACATA	TCCACAGACA	3000
	GTGCCAGAT	CCACCCACAC	GGCTCTATT	AAGTGAAGAG	CGACACACTT	TTTTCACAG	3060
	TGAAGACAGA	AGTTTGACAT	ATCTTTCAG	TCCAGTGA	GTTTTTTGTA	CCAACTTTAT	3120
	GGATTTTTTT	TAGTTTATA	AGCATCATTA	CTATTAAGAG	CTGTGGCTAC	TGCCCTGAT	3180
	GCTGTGCTGT	GTATGCTGAC	CTCTCTCAT	TGCACAGTA	CTGTAAAT	TTAAATTTAT	3240
15	GCAGATGTT	GATTACAGTG	CAGTGGCTGT	TAGTAGGCAT	TTTTACCATT	ACTGAGTTTT	3300
	CCATGGCAGG	AAGGCTTGT	ATCTCTTTAG	TATTTAGTGT	AACTTGAAT	ATCTTGCTGT	3360
	ATGGGATTC	GGACAGGATG	TGTTTGCTTT	CTGATCAAG	CAATTAATGA	AAAGCTCCC	3420
	CGACTACCC	CGAGCTGTG	TGATGTTT	AGATCGACT	CGAGATATCC	CAAGTAGAAT	3480
	CTCAGTTGAT	TTTCTGGAAT	CCCACTCTCA	GGCCAGAGCC	AAGGGGCTTC	AGGTCCAGCC	3540
20	TGTTGTTGGC	TTTACGGAG	GGCTCTGGCC	CTTTCAGTCC	TGGCAGCGAG	GCTTCCAGGG	3600
	ACACCTGGGA	GAATCTTGGC	TTCTGGCCAG	GAAGCTTTGG	TGAGAACCTG	GGTCCAGAG	3660
	AGGATATCTA	GAGCTGCTG	ATACCTGCT	AGAGACTGCA	ACCTAGACCA	AGTCCAGAC	3720
	TGACCTTGAG	CTGACCGACC	GTGACATGT	TTGGAAGGGG	TCTGTATGTG	CACTCAAGCC	3780
	GTGCTCTGAT	AGAAATGCCA	AGCACTCTT	TTTCTGGCTG	TGCTTTCTAG	AGACATGCCA	3840
	CCAGTAGGTT	ATTACTCTTG	GGAAAGTGTG	TGTTTCTGTA	AGAAACTAC	TGCCCAGCA	3900
	CTGCAACAG	CTCACTCTCT	ATACCTGCT	GGCTGAGCA	AATCAACACA	AACGTGATA	3960
	CAATGATCCT	GTATTCAGAC	AGATAGGAC	TTTCCATGGG	ACCACTACTA	TTTTCAGAT	4020
	TGAACATTA	ACCAAGTCTA	CTCAATCAAG	TCTGTTTACT	GCAAGGTCCA	ACTATTAAAC	4080
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30	TATAGTCTA	CTGCTCTATC	ATTATTCGTA	GATATTGGAC	AAAGAGACTT	CTCTATGCGG	4200
	CATCTCTTCT	TTCCACCTTG	GCTGCAGGAA	TCTTTAAJAG	ATGCTTTTAA	CAGAGTCTGA	4260
	ACCTTATTTT	TAAACATCT	CAACCTTACT	GTGAGCATC	ACCATGATGT	ATAGAGGAA	4320
	CAACTGCTTT	ATGACATCT	CTGCTGATG	GGAGATGGTG	TGGGAGCA	TGCCCTTGA	4380
	CTCTTCACTT	TTCAATGCC	TGACTAGGGA	GGCATGTTTC	ACAAGTCTTT	TAAAGTGACT	4440
35	AATGGCAGTA	GAATACAAA	AATACTCAGA	TAGGTAAJAA	TGCCATGATG	CTCTGTGCTT	4500
	CTGAGCATGT	TTTTCATCA	GAGACACATT	GACACACATT	ACATATCTCA	CTCTGAGTGT	4560
	TTTATAGAA	AGCTGCTG	ATGCTGATG	AGTTTCTCA	TCTTTGAAA	CAGAAJAA	4620
	TGTACCAAGA	ATCTTGCTTT	GCTCTTGCTA	AAACAAJAA	GCATTCTACT	TCTCCGGTGT	4680
	CTCCACTCTT	ATTGAGCAAC	CATAGTATCA	ATGACTATCT	ATAACATPAA	CAOTGTGAC	4740
40	AAACACACAC	AAAGGAGAC	CAGCTCTTAA	CTGATTCGCA	CTGTATATAC	ATGACATCTT	4800
	TTATCTATA	GTATTAAGT	CTCTTAAGT	CTGCAAAAT	ATATCTGAA	ATGCTGATG	4860
	AGATACATAC	AGATTAAGT	TAACTGATTA	CACCTGGTAA	TGTGATAAA	GCCAAACATA	4920
	TATATACIAT	TAAAGAGTT	TACAGAAITT	TATGTGCAAT	TACGTGGCA	TGTCTTTTTT	4980
45	AGATGCCCAA	ATCTCTAGAT	CTGCACTGTT	AGCCCTTCT	CCATATTATA	GAGGATATGA	5040
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Seq ID NO: 78 Protein sequence
Protein Accession #: NP_003465

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	YRGRVREYD	SAVSLFCSG	IKGLVFEKSI	STVLEPKISA	TRHYLFPAP	KLKSVRGSG	180
	SRNTPNLLA	KNVFPFSPST	WARRHKRSLT	KATKYVELVI	VADRREFQRQ	GKDLKVKQR	240
55	LIEIANRVOK	PVRPLNLRIV	LVGVEVWMD	DECSVQDPP	TSLEHFLDNR	RMKLLPKRSH	300
	DRAGLVSYV	PQGTETCMAP	IKMSCTADQS	GGVKNHSEH	PLGAAVTAH	ELGHPFDMH	360
	DTLDRCBCSQ	MAVEKGOCIM	NASTGYFFPM	VFSKSRKDL	ETSLKNGKV	CLFHPLEVRK	420
	SFGQKRCNR	FVSEGEEDCC	SPREOCBRC	CNATTTCTK	DAVCANGLCC	EDQLKLPAGT	480
60	AAACASNSDC	LPFETCGAP	ICSPNVYTHD	SHSQQDVLYK	CTNIIQCTHE	QCQVFLMGW	540
	ADAPALPCT	RVRSGGSGP	GGVHFRSSP	ACGCDRAK	GGTGGESA	RPIVITRHS	600
	IETNIPLOG	GRILRCRGTI	YLGDDMPDQ	LVLAGTKCAD	GKICLARKQD	NISVGVHRC	660
	AMQCRGQVNC	NRIKRICIEA	INAPFPCKY	GFGQSDSGP	IRQANDQSLT	LIQGLVTLCL	720
	LAQPIVYTLK	RLTLRLLEPT	NKRTTIFKRL	CVPSRPPRPG	FPQCDRIQLH	IGKLVKRPK	780
	DSYPRDMPR	RLGDCNDVI	SRPLGKLVN	CPQSTQVRLP	PLRSLPAPSE	VPRPLPAPK	840
65	ALLRAGQCTK	PHPPQKLPFA	DPLARTRLT	HALARTPQQ	ETGLRLAPLR	PAPQYPIQVP	900
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Seq ID NO: 79 DNA sequence
Nucleic Acid Accession #: NM_003714

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70	GAGGAGGAGG	GAJAAAGCGA	GCAJAAAGGA	AGAATGGGAG	GAGGAGGSGA	AGCGCGAAG	60
	GAGGAGGAGG	AGAGGAGAGA	AGAGGGGAGC	ACAAAGATAC	CAGGTCTCCC	GAGGAGGAGT	120
75	TATATCCAG	AACTCATGTT	AGCAAGGAGC	TGGCCAGACT	CATBAGCCCT	GCTTGCTGTT	180
	TGGCCACCTT	TGACCCGAGCG	CGGCGAGCCG	ACCCGACCAA	CCACCCGAGG	GCTCCCAAG	240
	ACAGGAGCTC	CCAGCAGAAA	GGCGCGGCTT	CCCTCGAGAA	TACAGCGAG	ATCCAGACAT	300
	OTTGTGTCAA	CGCTGGCGAT	GTGGGGGTGT	GTGTGTTTGA	ATGTTTTCGAG	AMACACTTTT	360
	GTGAGATGCG	GGGCTCATCT	GGGATTTGCA	TGCTTTCTCT	GCAACACTCT	GGAJAAATG	420
80	ATGCCAGGCG	CAGTCAATCT	ATCAAGAGCG	CTCTGAATAT	TAGAGCCCAT	GCTCTCGGCG	480
	ACAGGTTCCG	CTGCATAAGC	CGGAAGTGCC	CGGCGATCAG	GGAAATGTTG	TCCGAGTCTG	540
	AGCGGGAATG	AGCTCTCAG	CAGCAGCTGT	CGCGGCGTGC	CCAGAGAAC	ACCGGAGTGA	600
	TATGTGAGAT	GATCACTTCT	GGGATTTGCA	AGAGGCGCAT	ACCCACACAG	GTGCGAGTTC	660
85	ACTTGTCTGT	GACTCTCTGT	GAGAGGATGA	AGAGGCGCAT	ACCCACACAG	GTGCGAGTTC	720
	AGTGTGAGCA	GNACTGGGGA	AGCTGTGCT	CGACTCTGAG	CTTCTGCAC	TGCGGCACTC	780

	AGAAAGCTTC	CAGGAGGCC	CCGAGCGCC	AGCCCCAGGT	GGACAGAAC	AAAGCTCTCA	840
	GGGCCACCA	CAGGAGGCC	GGAGCCACG	CCCGAGGCG	CAGCAATAG	GGAGCTGCG	900
	GAGGTGCCA	GGGTGAGCG	GGTTCACGA	GGCAACCCAA	GGCCCATGCC	GGAGGCGAG	960
	TGGGGGCGCT	TGGGGGCTCAG	GGACCTTCGG	GGAGCAGCGA	GTGGGAGAGC	GAACGACTCT	1020
5	AGATTATCTGA	TATCGCGAGG	TGAATGATGA	GGAGCGGCCA	GGAATATCTT	CTCTCAAGCC	1080
	GTCCATTCTT	TATCTATGAG	ACGATCTTCA	TTGAGAGGAG	GGGATCTGAC		1140
	ACGAGAGATT	CTGTGGGACG	TGTGACATCT	ATGAGGTGTG	GTGTCTGGCG	ACGCGACAGG	1200
	TGAGATGGAG	ACCCCTGGGG	CCGTGGGGTC	TCAGGGGTGC	CTGGTGAATT	CTGCACTTAC	1260
	ACGACTTCAA	GGAGCGCGCC	CCGCTGTATC	CTGCTATGAT	TGCTCTCTTT	CGATCTGTGG	1320
10	AGTCAGGCTT	TGTGTGCGAA	CGAGGGGTGA	GGGAGGTGTA	CAGCGGAGAG	GGGCGAGAG	1380
	CGAGCGCCCT	CGAGCTGGGG	CCACACATGT	GGTCTGGGCG	CTCGCCCGCA	AGCTCTGGT	1440
	GACGACGCTT	CTGTGCTGTG	CTCCGCGGAA	GTGAGGGCGG	CTGGATTTCA	GGACAGGAGT	1500
	AGATGTAAAA	ATAAATATCG	CTTAGATATG	GGAGAGAGAG	TGGAGAGAGG	CGAGCGGCCG	1560
	AGGGGTGCTT	TGGTGGCGAA	CGAAATCTCA	GTCTTCTGTG	TGGGGCGCTT	GGTTCACAG	1620
	CTCTTGGCGA	GGGTGGAGGG	AGGAGTGTCA	TTTCTATGTG	TAAATTTCTG	GCCATTGTAC	1680
	TGTCTGGGCT	GGGGGGGACA	CTGTCCAAAG	GAGTGGCCCC	TATGAGTTTA	TATTTTAACT	1740
	ACGTCTTCAA	ATCTCGATTT	GACTTTTTTT	ATTATTCGAG	TATATCTAC	ATATCTGTCA	1800
	TCTAATAAA	TGGCTTCTCA	ACAAGCGAC	TGGCTCATTA	AAACGACCT	AAAGGSEITT	1860
	TAAAAAAAA	AAACCGAGCC	CATCTTTTGA	GGCTGAATTT	TCTTTTTTTT	AGTTCTTATT	1920
20	TAAAGAGCTA	TCAAACAGCG	ACATAGCCAT	ACATCTGACT	CGCTGACATT	GACTCTCGCC	1980
	CACCTTGGGG	AAACCTTATA	CCGAGAGGAA	AATACACACC	TGGGAGGTAC	ATTTCAGAAA	2040
	TTTCTCTTAG	GATTCTCTGA	CTTCACTCTG	ACCTCTGAGC	AGATATGGTA	AGCTTGTGTC	2100
	CTGCGCATTC	CAGGAGACCC	AGCTGGAAAC	CTGCTTCTCT	CATGTGAGGG	GATGGGAAAG	2160
	GAAGAGAGAG	AATGAGACT	ACTTAGTAAT	TOCCATCAGG	AAATGCTGAC	CTTTTACATA	2220
25	AAATCAGAGG	GACTCTGTGA	AATCTCTAG	GAGCAGAGAT	TTCCAGATCT	TAATTTGTCA	2280
	TTTACGCTA	AGGAGAGAG	TCCAGAGGGA	CAATTAAGAG	CACAGAGGGA	GGAGAGAGGA	2340
	GGGAGAGGAA	GAAGAGAGAG	AGAGAAAGAA	GCTCTGTGCC			
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	Protein Accession #: P03705						
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	MCARLQDM	FLNAILATFD	DAGTDATEP	FRPQPRSSQ	QKRLSLQMT	AEIQHCLVNA	60
	GGVQCCTG	PEINSECHND	LHICMTFLH	NAGKFDQAG	SFKIDALEK	AHALHHPGC	120
35	ISRKCPAIRE	MVSLQRECY	LKIDLCAAAG	ENFRVIVBM	HFKDILLBP	YVDLVNLLT	180
	CGSEVKEAIT	HSVQVCBSGN	WGLSLCILSP	CTSAIQKPTT	APFERQPOVD	RTKLGRASDH	240
	BAGHILPEPS	SRSTGQARG	EROSKSHPHA	HARGRWGLG	AQPSGSSEH	EDSQSEYSDI	300
	RR						
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	GAAGTATCTT	ATTATTTTGA	ATTATTTGTA	TGTCAGACGA	AGMCATATT	GGGAATATG	120
	CTATTACAGA	CCCATATATG	TTTCACTCAT	TATAACACAG	GTGGTGATGA	AAGCAACAGA	180
	AATACATCTT	CAATCGAGAC	TGCTCTCCAG	CATCTCTTCT	CTTTCACTCT	TGACCATATT	240
	GCATCTGTGA	CAGGAGAGAG	ACATCTCTCA	CCACACACCC	CTTCCCTCTC	AAATGTGAGT	300
	GGTGTGTG	TGATGACTTA	AGCATGTGAC	ACTCTCTTCA	TTTCTTTGTT	GTGCTCTTGA	360
50	AGGCATGTGA	GGGCGACGCC	TCAATATCCA	GAGACCTTGC	CTTCAGGATT	TGAGGTGGGC	420
	AAGAATGTGA	AAGAGAGACT	TGACCATCTC	AGTGTATATCA	AAAGCAATCA	CCAAAGAGAT	480
	TTTTCATCTT	GGCATGTGTG	TGGGACCTGC	ATACAGAGTA	CGTATGCTC	TCTTTACTGG	540
	ACAAGATTTT	ACATCTTTGT	AAGACAGATG	TACACCGAGT	GGAAATCTCC	TATTAATGAT	600
	CATGCGAGAA	TGTAAACATC	TTCTCTCTTC	ACCAAAATTT	TGATGTGAAT	AAACATGTAG	660
55	CCTTAAACTT	TATTTGCTTC	TCGGTCTCTG	CCATCTCGGG	GGCCAAAACG	TTTCAGAGAT	720
	AGGAATCTTG	TGACATCTGC	TGGATGTGAT	TGGABAGAG	AGTGAAGGTT	ACATATATCA	780
	TGGTCTCAT	ACGAGAGACT	TTACGAAATG	TTCCAGCTGC	GATTTACAGG	GAATCCCGCC	840
	TGACCCCTGG	ACGTGTGTTCT	CCTATTTCAG	TACCCCTGTG	CCG		
60	Seq ID NO: 82 DNA sequence						
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65	ATGCCAAATA	CTTCAGGAAC	AACCAGGATT	GAATTTTGCC	TTCTCGAAGA	GGCCGCCCGG	60
	CACCGAGCGC	TGTCGTCCGC	TTCTCTTCGG	GTAGTCGCCA	GGCCCGAGTT	GGCTCTGGCG	120
	CCCGAGTACC	GGGAGTGGCC	GGCTGCCGAT	GACCAATTTCA	CGCTCCGAGT	GATTTCAGAGT	180
	CAGATCATGT	GGAGAGAGCA	AGATCTGGTG	AGCTTTGCTA	TTCTCTGTTA	TGAAATTTTA	240
	GTGGGAGAGC	CTCTTTTGA	GGCAACAGAA	GTCCATGTAA	CGAAGAAAC	CATGCGGAGG	300
70	ATTTCAGCTG	CCAGCAAAAT	GATGTGGTCT	TGCGTGTGAC	TGGACATCAT	GTCTCTGTGA	360
	GATGGGTCTA	ACAGCTTCGG	GAAGGGAGCC	TTTGAAGGTT	CAAGACACTT	TCGCATCAGA	420
	GTCTGTGAGC	GTATGCGCAT	CAGCCCGCAG	TGAGGAGACT	TGGGACATCT	CCGTTTCAGT	480
	TCCACTCTCT	ATCTGGTATG	CCCTCTGGAT	TCAATTTTCA	CCCAACAGGA	AGTGAAGCCA	540
	AGAATCAGGA	GGATGGTTTT	CAAGAGAGGG	CGCACGGAGA	CGGAACCTCT	TCTGAAGTAC	600
	CTCTTGACA	GAGGATGGCC	TGAGAGGAGC	AACTCTCTTG	TGCCCCAGAT	CTCATATCTG	660
	GTCATCTGAG	GGAGAGAGCA	GGGAGATGTA	AGCTTGGTGT	CCACAGAGCT	GAGGAAGAGG	720
	GGTGTCACTG	TTTGTGCTGT	GGGGGTCAAG	TTTCCAGAGT	GGGAGAGACT	GCATGCACTG	780
	GGCAGCGAGC	CTAGAGAGCC	GACAGTGTG	TTGCTGAGC	AGGTGGAGGA	TGCCACCAAC	840
	GGCTCTTCTA	GGAGAGAGCA	CAGCGCGGAG	ATATCTCTCA	GGCCACGCC	AGCTGGAGCC	900
80	CCGAGAGCTG	CTTCTACGGA	GGGTTAATG	GGCATCTTCT	TGATAGGGCC	CTGTGACTGT	960
	CGCCCTCTGC	AGATGTGAGG	CACATGTGTT	CCAGAGGAGC	TGGACGGCTA	CCAGTCTGCT	1020
	TGCCCCCTGT	CTGTTGAGGG	GGAGGCTTAC	TGTGCTCTGA	AGCTGAGCTG	GGATGAGAGG	1080
	GTGCTGCTCT	TCTCTGAGAG	GGGAGGAGCT	GGGAGGAGCT	CTTCCTGAGG	CTTCCTGAGG	1140
	GGCAAGTCTG	TGTTGAGAGC	GTGTTGGGCG	GGCCTGTCTG	GGAGAGCTCT	TGGGGCCCGA	1200
85	GTGGTGTGTG	CCACATACAG	CAGGAGAGCTG	CTGTTGGGCG	TGCTGTGGGG	GGAGTACACG	1260

5	GATGTGCTGT	ACCTGTGCTG	GAGCTCGAAT	GGCAATCCCT	TCCGTGCTGT	CCCCACCTGT	1320
	ACGGGCAATG	CCCTGATGCG	GGCGGCAAG	CGTGCTCTCG	GGAGGCGAC	CAGGAGCGCT	1380
	CAGGACCGGC	CAGGTAGAGT	GGTGGTTTTG	CTCACTAGAT	CACACTCGCA	GGAATGAGTT	1440
	GGCGGGCCCA	CCGCTCAGC	AGGGGCGGJA	GAGCTCTCCC	TCCGTGGTGT	AGGCAGTGAAG	1500
	GGCGTGGCGG	CAGAGCTGGG	AGAGGATACA	GGCAGGCCAA	AGCATGTGAT	GGTCTACTCG	1560
	GATCTCCAG	GTGCTTGGCA	CGAATCCGCT	GAGCTCCAGG	GGAGGACTGT	CAGCCGCGAG	1620
	CGCCAGAGGT	CGCGGACACA	AGCCCTGGAC	CTGCTCTTCA	TGTTTGACAC	CTCTCCCTCA	1680
	GTAGGGGCCG	AGAAITTTTG	TCAGATGCG	AGCTTTGTGA	GAACTGTGTC	CTTCCAGTTT	1740
	GAGGTGACCC	CTAGGTGTAC	ACAGGTCCGC	CTGTGTGTGT	ATGCGACGCA	GGTCCAGAGT	1800
10	GGCTCTGGGC	TGGACACGAA	AGCCACCGCG	CTGCGATGCG	TGCGCGGCAT	GGGCGGCGAT	1860
	CCCTACTAGT	GGGTGTGGG	CTCAGCGCGC	ACCCGCTCTG	TGCACATCTA	TGCAAGAAGT	1920
	ATGACCGCTC	AGAGGGGTGC	CCGGCTGGGT	GTCCGCCAAG	CTGTGTGGGT	GCTCAGAGGC	1980
	GGGAGGAGGG	CAGAGGATGC	AGCGCTTCTC	GGCCAGGAGC	TGAGGAACAA	TGAGGATCTT	2040
	GTCTTGTGCT	GGTGGTGGG	AGTGGTCCCTA	AGTGGAGGCT	TGCGAGAGCT	GAGGATCTCC	2100
15	CGGAATCC	TGATCCAGT	GGCGACTTAC	GGCCAGCTCG	GGTACACACA	GAGCTGTCTC	2160
	ATTGATGGC	TGTGTGGAGA	AGCCAAAGCA	CCAGTCAACC	CTTGGAAACC	CAGCCGCTGC	2220
	ATGATGAGG	GGAGCTCGCT	CTCTGAGAT	GGAGGATACC	GCTCCAGATG	TGGGATGAGC	2280
	TGGAGGGCC	TGGACATCGA	AGCCCTGGAG	TGGAGCTGCT	GCTCTGTATG	TGTGAGCGAG	2340
20	GGATGATTC	TGGAGACGCG	CCTGAGGACG	ATGGCTCCCG	TGCAGGAGGG	CAGCAGCGGT	2400
	ACCCCTCCCA	GCAACTCAG	AGAGGCGCTG	GGCACTGAAG	TGTTGGCTAC	CTTCTGGAAT	2460
	GTCTGTGCCC	CAGGTCTCTA	G				

Seq ID NO: 83 Protein sequence

Protein Accession #: XP_061091.1

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	MPNTSOTTRI	SIMLLQEPFG	HRALVAALLP	VSPSPBELAA	PGYPPVPAAD	DRFTLRPHGG	60
	QMHEKVDLW	SLGLVCTREF	WKXPEPEANE	VIHVKETIKG	ISAAEEMWEC	SAANDIMPLL	120
30	DGNSVVGNS	PERSHFALIT	YCLGLDISPE	RVRVGAQFVS	STPHLEPFLD	EFSTGTQKVA	180
	R1KHVPFGR	RAKSHHFGY	HLARGLPGR	HAHPFILLII	VTGRSGVDIT	ALGKQLEKRA	240
	GTVPVAVVR	PFMELEHAL	ASEPQRQVIL	LAEQVEDATN	GLWSTLSSA	ICSATPAGS	300
	PELVFMRLLM	GIELIGPCDS	QFQONQGTVC	PGSLDQVCLC	CPFLAAGGAN	CAIKLSLEBR	360
	VDLLEFLDSS	AGTLLDPLFR	ANVVRKRVFV	AVLSEBSAR	WVATVAREL	LVAHVYVLE	420
35	DFVPLWBLD	G1PFGGCTI	TSLALPGGRI	RGPSASRTG	QGRPVVVL	LYESSEIRSE	480
	AGPARHARAR	ELLILGVGSE	AVRALEBEIT	GPSKIVHWYS	DRDQLFNPII	ELQKLGSRB	540
	RPQCTQLAD	LWFMLOTAS	VGFENFAQMG	SPVRSCLAQF	EVNPDVTQWG	LUVYGSQVGT	600
	LDVLTDFKPR	AMGLA19SA	TYLQVGGSG	TALLRETDV	KTYGKARGIS	VGAVVVLIG	660
	GRMLDAHVP	AGKLRNLSA	VLWVGCVPL	SLEBLERLAG	RDSL1HWAAY	ADLRVHQDVL	720
40	ISWLCSBAKQ	PVNLCKSPSC	WNDSQVLYGN	GSYRCKCRDG	WDSPIENRE	HSSCVCVVEG	780
	GNILETPLAH	MAPVQGGSSR	TPFNSYREGU	GTEHVTFVFN	VCALGP		

Seq ID NO: 84 DNA sequence

Nucleic Acid Accession #: E06 sequence

Coding sequence: 1..2424

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	TTCTCTCCCT	TCCAGAGAGT	CCATGTAGG	AAGAAGACCA	TGGGAGAGAT	TTGAGCTGCC	120
	AGCAAAAZA	TGTGTGCTC	GGCTCCAGTG	GACATCAVGT	TTCTTTTATA	TGGGTCTTAC	180
50	AGCTTCGGGA	AGGSGAGCTT	TGAAGGTGCC	AGGACATTTG	CCATCAGAGT	CTGTGACGCT	240
	CTGGACATCA	GCCCCAGAG	GGTCAGATGT	GGAGCATCTC	AGTTCACTTC	CATCTCCCAT	300
	CTGGAATCC	CTTGATGATC	ATTTTCAACC	CACACAGAG	TGAAGCAAG	AATCAAGAGG	360
	ATGTTTCTCA	AGAGAGGGG	CAGAGAGGCT	GACTTGTCTC	TGAATACTCT	TTCTGCACAGA	420
	GGGTTCCCTG	GAGGACGAAA	TGCTTCTGTG	CCCCAGATCC	TCACTATCGT	CAGTGAAGG	480
55	AGTTCGCAAG	GGATGTGGCG	ACTGTCCATC	AGAGCAGCTGA	AGGAAGAGGG	TGTCACTGTG	540
	TTTCCGTGTG	GGATCAAGTT	TCCCAAGTGT	GAGAGCTCTC	ATGCACTGCG	CAGCGAGCCT	600
	ACAGGCGGCG	AGGCTGTGTT	GGCTGAGCAG	GTGAGGAGTG	CACACACGCG	CTCTTCCAGC	660
	ACCTCCAGCA	GCTCCGCCAT	CTGCTCCAGC	GGCAGCGCCG	ACTCGAGGGT	CGAGGCTCAC	720
	CCCTGTGAGC	ACAGAGCGCT	GGAGATAGTG	CGGAGGTGCT	CTGGGACGTA	CCCATCTGAT	780
60	AGAGAGGCT	GTCTCTCTCT	TGATCTCTCT	CTGTGACATC	TGAGTCTTGA	CAGCTGAGAA	840
	AGAGTGTTC	TAACTCCACC	TGCCACCTGC	TACAGAGACA	CTGCGCCAGG	CCCTCTGTAG	900
	TGCGAGCCCT	GGCAAGATGG	AGGCACATGT	GTTCACAGAG	GACTGAGAGG	CTACCATGTC	960
	CTCTGCCCGC	TGCTCTTTGG	AGGGGAGGCT	AACTGTGCCC	TGAAGCTGAG	CTCGGAATAT	1020
65	AGGTCGAC	TGCTCTCTCT	CTGCGAGAGC	CTCTGGGGCA	CCACTCTGGA	CGGCTCTCTG	1080
	GGGCGCAAG	TCTTCTTGAA	CGCGTTTTTG	GGGCGGCTG	TGAGCGAGGA	CTTCTGGGCG	1140
	CGAGTGGTGT	TGGCACATA	CAGCAGGAG	CTCTGTGTGT	CGGTGCTGTG	GGGGATGATC	1200
	CAGATATGCG	CTGACTCTGT	CTGGAGCTGC	GATGGCATTC	CTTCTCGTGG	TGGGCCCTAC	1260
	CTAGAGGCA	GTGCTCTGTT	CAGAGCGGCA	GAGCTGTGCT	TGGGAGGCG	CAGCGAGACA	1320
	GGCCAGGACC	GGCCACGTAG	AGTGTGGTGT	TTGCTCACTG	AGTCACTACT	CGAGGATGAT	1380
70	GTTCGGGCGC	CAGCGCGCTA	CCGAGAGGGG	CGAGAGCTGC	TGCTGTCTGG	TGTAGGCGAT	1440
	GAGGCGTGTG	GGGCAAGGCT	GGAGAGATTC	AGAGGCGAGC	CAAGATATGT	GATGTGTCTC	1500
	TGAGATCTCT	AGATCTGTTT	CGACCAATTC	CTTGAGCTCT	AGGGGAGACT	GTGCGAGGAC	1560
	CAGCGCGGCG	GGTCCGGGAC	ACAAAGCCCTG	GACCTGTGCT	TCAATGTGGA	CAGCTCTGCC	1620
	TCAATGAGGC	CGGAAGATT	TGCTCAGATG	CAGAGCTCTG	TGAGAGAGCTG	TGGCTCTCAG	1680
75	TTTAGATGTA	ACCTCAAGCT	GACAAGGCT	GGGCTGTGTT	TGTATGGGAG	CGAGTGTGAT	1740
	ACTCTCTGTA	GGTCTAGG	CGAGGCGGCT	GGGCTGTGTA	TGCTGCGGCG	CATTAGGACG	1800
	GGCCCTCAAC	TAGGTGGGTT	GGAGCTCAGC	GGGACCGCCC	TGCTGCACAT	CTATGACAAA	1860
	GTATAGTACG	TCCAGAGAGG	TGGCGGCGCT	GGTCACTGCG	AGGCTGTGTT	GGTGTCTACA	1920
	GGCGCGAGAG	GCCGAGAGGA	TGACAGGCT	CTCTCCGCGA	AGCTGATGAG	CAATGCTATC	1980
80	TTCTCTCTCT	GGTCTCTGTT	GGGCGCTCTC	CTAAGTAGAG	GTCTCCGAGG	GGTTCGAGT	2040
	CCCCGGGATT	CCCTGATACA	GTGGCGAGCT	TACGCGGACC	TGCGGTATCA	CAGAGGAGGT	2100
	CTCATTAGGT	GGCTGTGTGG	AGAAAGCCAG	CAGCCAGCTCA	ACCTCTGTGCA	ACAGCGCGCG	2160
	TGCAATGATG	AGGCTCTGCT	CTCTCTCTCT	AAATGGAGCT	ACCGCTCGAA	GTGTGCGGAT	2220
	GGCTCGGAGG	GGCCGCACTG	CGAGAACGAT	GGATGGAGT	CTAGCTCTGT	ATGTGTGAGC	2280
85	CAGGATGGA	TCTTGAAGAC	GCCCTCTAGG	CAGATGAGTC	CGGTGCAAGA	GGGCAAGCAC	2340

CGTACCCCTC CCAGCAACTA CAGAGAGGCG CTGGGCACTG AAATGOTGCC TACCTTCTGG 2400
 AATGTCCTGT CCCAGGTCCT TTAG

Seq ID NO: 85 Protein sequence

Protein Accession #: Bos sequence

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5	MPPPLLEAV	CVFLPSRVPP	SLPLQEVHVS	KETIGKISAA	SPDMKCSAAV	DIMFLDGSN	60
	SVGKGSFERS	KHAIPTVCDG	LDISPERVRV	GAQPSPSTPH	LEPFLDSFST	QQRVKARIKR	120
10	WVFGKGRSTT	ELALSTYLLR	GLGGRNRSV	PQILLIVTGG	KSQQVVALPS	KQLKSRGVTV	180
	PAVGVRFPRM	REKLHASEPH	RQRIIVLLAQ	VEDATNGLPS	TLSASAI CSS	ATPCDVEBAH	240
	PCENHRLTEV	REFAGNAPCM	RGRSTRVLAV	AAHCFFYSWK	RVPLTHPATC	YRTTCGPGCD	300
	SPQCQNGQTC	VPEGLDGYQC	LCPLAFGGSA	NCAKLKSLBEC	RVOLFLPILDS	SAUTTLDDGFL	360
15	RAVRVPRFV	RAVLREYSRE	LIVAVFVGEY	QDVPVLVGLV	SGLPFRGGT		420
	LTQSALRQAA	ERSGPSATRT	QDQPRRVVVV	LITESHSEDE	VAGPARHARA	RELLLLGVGS	480
	BAVRASLEEI	TGSPGVVMVY	SDPQLDLNFI	PELQGLKCSR	GRGCRTQAL	LDVFNLDYSA	540
	SVGPEPQAK	QSPVSRSLAQ	PSVNPVDVTV	GLVVYGSVQV	TAFLDITRPT	BAAMLAIRISQ	600
	AFVLYFGDGA	STALILEITD	VNTYQGGASR	GVFNAFVVLV	GGHGLADRAV	PQKLFRRGTI	660
20	SVLVVGVQPV	LSQGLRRLAG	PRDSLILHVA	YADLRVHQDV	LIRMLQSAK	QPNVLKCPSP	720
	QENSGSCVLA	NGSYRCKEDR	GHEGPHCENR	EHSSCSVCVS	QGMILETELR	IDAPVQGEBS	780
	RTPPSNVREG	LGTEKVPVPM	NVCAPGP				

Seq ID NO: 86 DNA sequence

Nucleic Acid Accession #: Bos sequence

Coding sequence: 89..2356

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	AGAAACCATC	GGGAGATAGT	CAGCTGCCAC	CAAAATGATG	TGGTGTCCGG	CTGACGTGGA	240
	CATCATGTTT	CTGTTAGATT	GCTCTAACAG	CGTGGGAGAA	GGAGCGCTTG	AAAGTCCCAA	300
	CGACCTTTGC	ATCAACGCTT	GTGACGGTCT	GGAGACACAG	CCGAGAGAGG	TCAGAGATGG	360
35	ACATCTTGCT	TGACATCTCT	CTCTCACTAT	CGAATTTCCC	TGAGATTGAT	TTTCAACACCA	420
	ACAGGAAATG	AAGGCACAGAA	TCAGAGGAGT	GTTTTTCAAA	GGAGGGCGCA	CAGACACGGA	480
	ACTCTGCTGT	AAATACCTTC	TGCACAGAGG	GTTCGCTGGA	GGCAGAGAAAT	CTCTTGTCGC	540
	CGAGATCTCT	ATCATCTCCA	CTAATGGGAA	GTCTCCAGGG	GATGTGGCAC	TGCCATCTCA	600
	CGACCTCAGG	GAAAGGCTGG	TCACTGTTT	TGCTGTGGGG	GTACGGTCTT	CCAGGTGCTGC	660
	GGAGCTGCACT	GCATCTGCCA	GCAGCCTAGT	AGGGCAGCAC	GTGCTTGTGG	CTGAGCAGGT	720
40	GGAGATGTCC	ACCAACAGCG	TCTTCAGAC	CTCAGACAGC	TGGGCCATCT	GCTCTAGCGG	780
	CAGCGCCAC	TGCAGAGGCT	AGGCTCAACC	CTGTGACACC	AGAGCTGGAG	AGATGTCTCC	840
	TGCTATCTCT	GGCATATGCC	CATGCTGAGG	AGATACGGCG	GGACACCTTG	CGGTGCTGGC	900
	TGCACACTGT	CCCTTCTACA	CGTGGAAAGG	AGTGTTCCTA	ACCCACCTTG	CCACTGTGTA	960
	CAGGACACCC	TGCCCGAGCC	CCCTGTGACT	CGACGGCTGC	CAGATATGAG	GCACATGTGT	1020
45	TCGAGAGAGA	CTGAGAGGCT	ACCATGTGCT	CTGCCCGCTG	GCTCTTGAGG	GGAGAGCTAA	1080
	TGCTGCCCTG	AAAGTGTAGC	TGGAATTCAG	GGTGCACCTC	CTCTTCTCGC	TGGACAGCTC	1140
	TGCGGGCACC	ACTCTGAGCG	GCTTCTGCGG	GGCCAAAGTC	TTCTGTGAAC	GTTTGTGTGG	1200
	GGCCGCTGTG	AGCGAGAGCT	CTCGGGCCCG	AGTGGATGTG	GCACACATCA	CGAGAGAGCT	1260
	GCTGTGGGCG	TGCTCTGTGG	GGATATACCA	GGATFPGCTT	GACTGTCTCT	GGAGCTCTGA	1320
50	TGGCATTCCT	TTCTCTTGCT	GGCCCACTCT	GACGGSCAGT	GCCTTGTGGC	AGGCGGACGA	1380
	GGGTGGCTTC	GGAGAGGCCA	CCAGACACGG	CCAGCTAGAG	TGGTGTGTTT	TGGTGTGTTT	1440
	GCTCACTGAG	TGCACATCGG	AGGATAGAGT	TGCGGACCCA	GGGTGTGAGG	CAAGGGGCGG	1500
	AGGACTCTCT	CTGCTGTGTT	TAGCAGTGTG	GGCTGTGCGG	CGAGAGCTGG	AGGATATCAC	1560
	AGCGAGCCCA	AGCATATGGA	TGGTCTACTC	GGATCTCTAG	GATCTGTCCA	ACCAATATCC	1620
55	TGAGCTGCGA	AGGAGACTGT	GCAGCCGCGA	GGCGCCAGGG	TGCGCGACAC	AGAGCTGTGA	1680
	CTCTGCTCTT	GTGTTTGAGCA	CTCTGCTCTC	AGTAGGGCCG	GAGATATTTG	CTCAGATGCA	1740
	GAGCTTTTGT	AGACATCTCT	CCCTCCAGAT	TGAGGTGAAC	CTGACGTGTA	CACAGCTGTG	1800
	CTCTGTGCTG	TATGGAGAGC	AGGTGCACAG	TGCTTCTGGG	CTGACACCCA	ACACCCATCC	1860
	GCCTGTGATG	CTCGGGGCCA	TTAGCACAGG	CCCTTACCTA	GGTGGGAGTG	GCTGACCGGG	1920
60	CTACGCCGCT	GTGACATCTC	ATACAAAGAT	GATGACCGCT	CGAGGGGCTG	GGGAGGCTGC	1980
	TTCTCCCAAA	CGTGTGCTGG	TGCTCACAGG	CGGAGAGAGC	CGAGAGGATG	CAGCGCTTCC	2040
	TGCCCAAGAG	CTGAGGACAA	ATGSCATCTC	TGTCTTGGTC	TGGGGGCTGG	GGCCTCTTCT	2100
	AAAGTAGAGT	CTCGGGAGGC	TTGACAGTGT	CCGAGATTCG	CTGATTCAGG	TGGCAGCTTA	2160
65	CGCGACGCT	GGPACAGC	GGGAGCTGCT	CATGTGATGG	GGAGAGGAGC	AGGCCACGCA	2220
	GCCAGTCAAC	CTCTGCAAG	CCAGCCGCTG	CATGAATGAG	GGACGAGTGG	CTCTGCGAGA	2280
	TGGAGCTAC	GCCTGCAAGT	GTCGGAGTGG	CTGAGGAGGC	CCCCACTGGC	AGAACCCGAT	2340
	CTTGAGAGCG	CCCTGAGGCA	CATGCTCTCC	TGCAGAGGCT	GGACAGGCGC	TACCTCTCCC	2400
	AGCACTACA	GAGAGAGCT	GGGCTCTGAT	ATGGCTGCTA	CTCTCTGAAA	TCTCTCTGAA	2460
70	CCAGGTCTCT	AGAAATGTCT	CTTCCGCCCG	TGGCCAGGAG	CACATATTCT	ACTGAGGAGG	2520
	GAGGATGTCC	CAACTGCAGC	CATGCTGCTT	AGAGACAGAA	AGAGCATGTA	TGTCACCCAC	2580
	AAAGCATGTT	GTGAAAGAT	TTTGATGTGT	AGATTAATAC	CACTATTTCT	TACCTCTGTT	2640
	GCTTGTGTGA	GTGAAAGAT	TGTCGCTCT	CTCTCTGCTG	GATTAACAGC	GGGTCTGAGA	2700
	GACTTAARAT	TAGCGGCTGG	ACGTTCTCTT	GCACACAATC	AATGCTCGCC	AGAAATGTTG	2760
75	TGACACAGTA	ATGCCACGCA	GAGGCTCTTA	CTAGAGCATC	CTTTGAGAGG		

Seq ID NO: 87 Protein sequence

Protein Accession #: Bos sequence

	1	11	21	31	41	51	
80	MPPPLLEAV	CVFLPSRVPP	SLPLQEVHVS	KETIGKISAA	SPDMKCSAAV	DIMFLDGSN	60
	SVGKGSFERS	KHAIPTVCDG	LDISPERVRV	GAQPSPSTPH	LEPFLDSFST	QQRVKARIKR	120
	WVFGKGRSTT	ELALSTYLLR	GLGGRNRSV	PQILLIVTGG	KSQQVVALPS	KQLKSRGVTV	180
	PAVGVRFPRM	REKLHASEPH	RQRIIVLLAQ	VEDATNGLPS	TLSASAI CSS	ATPCDVEBAH	240
	PCENHRLTEV	REFAGNAPCM	RGRSTRVLAV	AAHCFFYSWK	RVPLTHPATC	YRTTCGPGCD	300
85	SPQCQNGQTC	VPEGLDGYQC	LCPLAFGGSA	NCAKLKSLBEC	RVOLFLPILDS	SAUTTLDDGFL	360

RAKVYVKRPF RAVLSSEDSRA RVGVATYSRE LLVAVPVGEY QVVDLVWSL DGIPFRGGPT 420
 LTVSALAKQA RRGFSQATRT GQDRPRRVVY LITSESSSE VAPGARARA REULLLVGS 480
 EAVLRLSEI TYSPEINVTY EDQDPLPDY PELQHLCSR QRPCTPRL DLYFRLDTS 480
 5 SVGPENFACM QSVFSCALQ FEYFNFDVTQ GLAVYGSQVQ TAPFLDTFT RAAMLRLSQ 600
 APYLLGVGSA GTALLHLYDK VMTVQGRAP GVPKAVVVL7 GGRGDAARV PAQLRLNNGI 660
 SVLVGVGVSP LSEGLRLKLG PRSLHIVVA YAGLAVTGQV LIEWLGSEAK QPVNLCKSPS 720
 CMHSESCVQL NESTKICKD QHGFHCENR FLURE

Seq ID NO: 88 DNA sequence
 Nucleic Acid Accession #: NM_019594
 Coding sequence: 1..1334

1	11	21	31	41	51	
ATGTTACAGG	ATCTTGACAG	TGATCAAGCT	CTGACAGGCT	TGATGTCAA	ACCCCTGGCC	60
AAAGCCCGTA	TCCCACATGA	GACCTTCAGA	AGAGTGGGGA	TOCCCATCAT	CATAGACATA	120
CTGAGGCTGG	CGAGTATCAT	CATTGTGGTT	GTCTCATCA	AGGTAAATCT	GGATAAAATC	180
TCTGTCCTCT	CGGGCAGGCG	TCCTCCATCT	ATCCCGAGGA	AGCAGCTGTG	TGACCGAGATG	240
CACCTGCTCT	CGAGGAGGAG	GACCTGTGAG	AGAGCTCTCA	CGAGGAGGCT	CGAGGAGGCT	300
CGATGGGACG	TCGATCTCTC	CAAGGACGCA	TOCACACTCG	AGGCTGTGGA	CTGGCGCACA	360
GGGAACTGGT	TCTCTGCTGT	TTTGGACAC	TTACAGAGAG	CTCTCGCTGA	GACAGGCTGT	420
AGGCAGATGG	GCTACAGACG	CAAAACCATC	CTCAGAGCTG	TGGAGATTGG	CCGACAGCAC	480
GATCTGAGTG	TGTTTGTAGT	CACAGAAATC	AGCCGAGGAG	TGCGCATGGG	GANTCTGAGT	540
GGGCTCTGTC	TCTCAGGCTC	CCTGGTCTCC	CTGACACTCT	TTGCTGTGGG	GAAGAGGCTG	600
AAGACCCCCC	GTGTGGTGGG	TGGGGAGGAG	GCTCTGTGG	ATTCTTGCCC	TGGCAGGCTG	660
AGCATCATGT	AGGACAAACA	GACGATCTGT	GGAGGAGGCA	TCTGTGACCC	CCACTGGGCT	720
CTCACCGGAG	CCCATCTGTT	CAGGAAACAT	ACCATATGTT	TCAACTGGAA	GTGTGGGCTA	780
GGCTCAGACA	AACTGGGACG	CTTCCCATCT	CTGGCTGTGG	CCAGAGTCAT	CATCATGTAA	840
TTCAACCCCA	TGTAACCCAA	AGACATATGAC	ATGCGCTCTA	TGAAGCTGCA	GTCCCACTCT	900
ACTTCTCTCG	CGACAGTCAG	GCCCATCTGT	CTGCGCTCTT	TGATGAGGAA	GCTCATCTCA	960
CGACACCCAC	CTGACATGAC	TGATGAGGAG	TTTACAGAGC	AGATGAGGAG	GAGAGATCTC	1020
GACATACTCG	TGACAGGCTC	AGTCCAGGTC	ATTACAGACA	CAAGGTGCAA	TGCAGACGAT	1080
GTCTACACAG	GGGAGATCAC	CGAGAGATGT	ATGTTGTGCA	GCATCCCGGA	AGGGGTGTGT	1140
GACACTCTCC	AGGATGACAG	TGTTGGGACC	CTGATATACC	AACTTACAGA	GTGGCATCTG	1200
GTGGGACAAT	TGATCTGCTG	CTATGGCTGT	GGGGCCGAGA	GCACCTGAG	AGTATACATC	1260
AGGCTCTCAG	CTCATCTCAA	CTGGATCTAC	AAATGTCGGA	AGGCTGAGCT	GTAAT	

Seq ID NO: 89 protein sequence:
 Protein Accession #: NP_061947.1

1	11	21	31	41	51	
MLQDPDSDP	LASLVKPTLR	KPRIMETPR	KVSPILIIAL	LSLASIIIVV	VLKVLIDLY	60
YFLCSQPLHF	IPRKLCDGE	LDCLPGEDEB	HCVKSPFPBP	AVAVLRKDR	STLVQLSDAT	120
GNVFSACFN	FTEALAEAC	RQMGYSKFT	FRVIEIGPD	DLVDVEITEN	SQELRMNRNS	180
OPCLSLSHLE	LICLACRSL	KTRPVVGGES	AVDSVHPQW	SIQYDQHVVC	GGSLIDNRWD	240
LTAHCFRKH	TQVNRVRA	GGDILGSPFS	LAVALIITB	PNMYFEIND	IALSKLFFPL	300
TSQTVREIC	LFPEDELP	ATPLAIKMG	FTEKNGKMS	DILLAQSVQV	IDSTRCHAD	360
AYQGEVTEK	MCAGIPEGV	DTQGGDSGGP	LVYSGDQNHV	VGIVSGYGC	GGPSTPGVYT	420
KVSAIYLIWY	NVWKAEL					

Seq ID NO: 90 DNA sequence
 Nucleic Acid Accession #: NM_002776.1
 Coding sequence: 82..912

1	11	21	31	41	51	
ACCAGGCGCA	GACCACAGCG	AGGGCAGAGG	CAAGTCTGGG	TCGCTCTCCT	CCTTCTATC	60
GGCGACTCCC	AGATCTGTGC	CATGAGAGCT	CGC-ACTCTC	AGCTCTCGCC	CGGCTCTTGC	120
CGCCGCGCTC	TGCGCAAGCT	GCTGCGGCTG	CTGATGGGCG	AACTCTGGCG	CGCAGAGGCG	180
GGCTCTGCTC	CCCAAAACGA	CAGCGCGCTG	GACCCCGAAG	CCATAGGCGC	CCGCTGGCGG	240
CGCGGCTCGC	AGGCTCGGCA	GCTCTGCTCT	TTCAAGCGCG	TCTCTCTCCA	CTGGCGGGGT	300
GTCTCTGGGG	ACCAAGATGT	GGTCTGACAG	CGCCGCGCTC	GGGGAACAGA	GCACTCTGAG	360
GTCTCTGTAG	GGGATACAGA	CCTCTGCTCT	CTTCAAGGCG	AGCAGCTCGC	CCGAGCAAGT	420
CGCTCTGTGT	TCCATCCCAA	GTACACACAG	GGCTCAGGCG	CCATCTCTGC	AAAGCGAACT	480
GATGAGGAGC	ATCTCATGTT	GCTAAAGCTG	CGCAGGCGCG	TAGTTCGGGG	GGCCCGGCTG	540
GGGCGCTTGC	AGTCTGAGCT	CGCTGTGCTT	CGACCGGAGT	ACAGCTGCGA	GCTTCTTGCG	600
TGGGGACAGA	CGGGCCCGCG	GAGAGTGAAG	TACAACAGCG	GGCTGAGCTC	CTTCAGCATC	660
ACTATCTCTA	GGCTTAAAGA	GTGTGAGGTC	TCTTACCTGT	GCGTGTCTAC	CAACACATGT	720
ATATGTGCTG	GACTGAGACG	GGGACGAGAG	CCTTGCGGAG	GTGACTCTGG	AGGCGCCGCT	780
GTCTGTGAGC	GATCTGAGCT	TGGTGGGCTG	TGGTGGGCTG	TTTACCTCTT	TGGCTGTGGC	840
CGCATCTCAG	CTGTCTACAC	CCAGATCTCG	AAATACATGT	CCGTGATCAA	TAAAGTATCA	900
CGCTCAACT	GATCCAGATG	CTACGCTCCA	CGTATCCAG	ATTTATGCT	CCTCTGATCA	960
CAGATGTCCA	GAGGCTCATC	GATCATCTCT	CTTCTCTCCC	AGTGGGCTGA	ACTTCTCCCT	1020
CTCTTGACAT	GATCTGAGCT	CTGCTGCGCT	CGACGACTCT	AAACCTCTAC	CCTCTGACT	1080
CATTCCCGCA	CTCTATACCA	TTCTCTGCTC	GTACTGAGCG	TGAATATGAG	GAGGTGGTGG	1140
CAAAGGTTTA	TTCCAGAGAA	GCGAGGAAGC	CGGTCTATAC	CCAGGCTCTC	AGAGCATGTA	1200
CTGGGCTGAC	CCACACTGAC	TTCTCTGCTC	ACTCCGCGCT	GTGTGACTTT	GGGCAAGCCA	1260
AGTCCGCTCT	GGGACACTCA	GTTCTCTGCT	CTGCAAAATG	GGACATGAGT	CGTCTCTACC	1320
TCTTAGACAT	GTGTGTGAGA	GACTATGATA	TAACTATGTT	ATGTAATCT	TCTATGATT	1380
GTGATGTAA	GCTTAAACCA	GTGGGTGGTG	AGTCTGACT	AAAGGTATAC	TGTTGTGGTG	1440
AAAAAAAA	AAAA					

Seq ID NO: 91 Protein sequence
 Protein Accession #: NP_002767.1

1	11	21	31	41	51	
MRAPHLHLSA	ASGARALAKI	LPLMAQLMA	AREALLPQND	TRLDPEAYGA	PCARGSQPQW	60

VSLFNGLSPH CAGVLVDQSH VILTAHNCNK FLMARVGDH LLLLGQEGLE RTTSRVVHPK 120
 YHGGSPILR RTHQRDLML LKLARVVPYK PFRYALGYPK RCLQPGQCTQ VAGRGTTAAR 180
 RVKYNKGLTC SSILITSPKE CEVFPYGVVT NNMICAGLER GQPCQSDSQ CLFVACBETLQ 240
 GILSNWVYPC GSAQHFAVYT QICKYNSWIN KVIKRN

Seq ID NO: 92 DNA sequence
 Nucleic Acid Accession #: NM_032044.1
 Coding sequence: 182-658

1	11	21	31	41	51		
10	AGAGATATAA	AGCTCCAGAA	ACGTTGACTG	GGACCACCTG	AGACACTGAA	GAAGGCAGGG	60
	GCCTCTTAGA	TCTGTGTTC	CAACACAGAT	TGCAGATCAA	GGAGTITCAA	120	
	AGAGGCGCTA	GTAGAGTCTC	TGAGATCTCT	GCACATGACT	CATCTCTAGA	GTAGATGACCA	180
	GATGGCTCTC	AGAGAGTCTC	GCCTGCTCT	ATTGTGTGAC	TGCTCTTCTG	AAACAGAGAT	240
15	CCTGTGOTGAT	ATCATCATGA	GACCCAGCTG	TGCTCTCTGA	TGTTTITTAC	CAAGTCTCAA	300
	TGCTATGTT	TACTTCAGGA	AGCTGAGGAA	CTGTCTTGAT	GCGAGCTCG	AGTGTGACTG	360
	TTACGGAAC	GGAGCCCAAC	TGCGATCTAT	CCTGAGTTTA	AGAGAGGCCA	GCACCATAGC	420
	AGAGTACATA	AGTGTCTAT	AGAGAGGCA	GCGCATATG	ATTGTCTCTG	ACACGCCACA	480
	GAAGAGCGAC	CAGTGCAGT	GGATTAGTGC	GGCCATGTAT	CTGTACAGAT	CCTGTCTGCG	540
20	CAAGTCCATG	GGTGGGAACA	AGCATCTGTC	TGAGATGAGC	TCCATATACA	ACTTTTAAAC	600
	TTGAGACAGC	AGAGATGCA	ACAGAGGCCA	ACACTTCTCT	TGCAGTACG	GACATTTAGG	660
	CAGAGATACA	GATTTCTAT	ACTCTGTGAC	AGGCCCTTCT	TCTTCTCTTG	TGCTAGCTCT	720
	GCTAAATCTG	CTCATATT	CAGAGGGGAA	ACCTAGCAAA	CTAAGAGTGA	TAGGGCCCTT	780
	ACTACACTGG	CTTTTTTAGG	CTTAGAGACA	GAATCTTTAG	CATTGGCCCA	GTAGTGGCTT	840
25	TAGTCTCTAA	ATGTTTGGCC	GGCATTCTCT	TTGCACATTA	TGCTTCTCTC	CTCTCCCT	900
	CTCTCTGCT	CTTAGAGCA	GTCTATCTGC	AGCTATGAA	ACAGCTGGAT	960	
	CTTTGGCAT	AGAGATGAA	GATTTGAGGA	CAGAGGGAAG	AAACTCAGGA	GTAAGCTTCT	1020
	AGACCCCTTC	AGCTCTTACA	CCCTCTCTGC	CTCTCTTCAT	TGCTGTGACC	CAACCCGACG	1080
	CACTCAATCT	CTGCTGTATT	TTCTCTTCTG	CATAGAGAGC	TTTACACATTA	GATCTCTCTG	1140
30	TAGTGTATG	TGGGCAATAC	ATTCTCTTAA	TAAACCATTG	TGTACATAGC	AAAAAATAAA	

Seq ID NO: 93 Protein sequence
 Protein Accession #: NP_114433.1

1	11	21	31	41	51		
35	NASRSMELL	LSECLARTGV	LGDIIRPSC	APGNFYHKSN	CTGYFKRLRN	WSDAELEQSS	60
	YGNRHLARI	LSHLEKATL	ETTSQVQRQ	PWHLGIDG	KRQWQWIDG	AMLYLRSWS	120
	KSMGNKHC	ENSRNFFLT	WSSNENRQ	HFLCKYRP			

Seq ID NO: 94 DNA sequence
 Nucleic Acid Accession #: XM_051860
 Coding sequence: 1..4086

1	11	21	31	41	51		
45	GAGCTAGGCT	TCAGACAGAG	CCGACGGGGG	TGCTATCGGA	CAGAGCGCTG	CGAGGCGAAG	60
	CGGCGCGGGG	AGCCACAGGG	GCTGACGGGG	GCGAGGGTCT	GAACCCAGAT	TTCCAGAGAT	120
	AGCTACCACT	CCGCTGTGCC	AGCCGCCGGG	AGCTCGGGCT	GCTCTGGGGT	CAGCGACCGA	180
	AGCTCCGGGG	CGGCTGGGCT	CCTGGGCGGC	GAGCGTTGAC	ACTGTCTGGT	CTACAGAGCC	240
50	AGAGGAGGCA	CAGCTCCAGG	ATGGGAGGCT	CTGGGAGGCA	GAGCTCTCTC	TTCAAGGCCA	300
	TCTGTGACAT	CAGCTGGCTC	ACTCTGACCT	GCTTCCCTGG	GGCCACATCC	ACAGTGGGTC	360
	CTGGTGGCC	TGACGAGAGC	CCTGAGTTTC	AACTCTGGA	CCTCGCATC	GACCAAGAAC	420
	ACCATGTGA	TATCTGCG	GGGAGAGCAC	TGCTGTCTAC	CTTCTCTGCC	ACGCTCTATT	480
	CCATCCACAT	CTCAGAGGGA	GGCAAGCTGT	TCAATTAAAG	CAAGAGAGAG	CGGATTTGTT	540
55	TGCGAACCCG	GCACATCTCT	ATTGACAACG	GAGGAGAGCT	GAGTCTGGGG	AGTGGCCTCT	600
	GGCTTTTCA	GGCGATTTCT	AGCATATT	TGTTATGAG	GGCTGATGA	GTTATTCAGC	660
	CGGATCTTCA	CTATGCTCT	AGATACATGT	GGGTTGGTAA	AGGAGGGGCT	CTTGAAGTTC	720
	ATGACAGACA	AAAGCTCTCC	TGGACATCTG	TGACACAGAC	CTTACACCCA	GGTGCGATGG	780
	CAGAGAGGAG	CTATTTTTT	GAAGAGAGCT	GGGCGACGCG	GCGGATTTAT	GTTCATGTCA	840
60	TGAGACCCCA	CTGACATCT	CTGACACCAT	TGAGACCTGT	TGGACCAT	AGATACAGAG	900
	AAAGAGTGA	AGCTCTGGTC	CAGTATTGTA	ACGGCGTGCC	GGATGCGAGG	ATCCTTTCTG	960
	TTGAGTGA	TGATGAAGGT	TCTGTGAATC	TGGATGACAT	GGCCAGGAAG	GCGATGACGA	1020
	AAATGGGAAG	CAACACCTTC	CTTGACCTGT	GATTTAGACA	CCCTTGAGAT	TTTCTTACTG	1080
	TGAGAGTGA	CTGATCTGAT	ATACAGGCTA	AGCATATGGA	ATATACAGTA	CATGAGGAT	1140
65	CTGCTCTGCG	CCGGGTATTC	AAATGTTTCC	AGACAGAGCA	TGGCGAATAT	TTCAATGTTT	1200
	CTTTTCTCAG	TGAGTGGGTT	CAAGAATGAG	AGTGGACGGA	GTGGTTGGAT	CAGATTAAG	1260
	TATCTCAGAC	TAAAGTGGG	GGAGAAATTT	CGAGCTCTGT	GAAAGCTCAC	CCAGAGAA	1320
	TATGACATG	TGCTTTGAT	ATACAGGCTA	TACAAATGGA	TGGAGTTTAC	CTCAGACAGC	1380
	AGGTTTCTTA	CAAAAAGAGC	CAGAGATTATA	GGTTTGGTGT	CTACGACCGG	GGCAGAGCTT	1440
	GCGGAGGACTA	CGTGTACGG	TTCTCTCTGT	GGAGGCTGTT	AGGCGCCAAA	CTACAGCTCA	1500
70	CCATTGACAC	CAGTGTGAC	AGACACCTCT	TGAGCTCTGA	GGATATGTA	CAGTACAGGA	1560
	AACTTGGAGA	TACCTTGGTC	ATTCCAGATA	CTGATTTACT	CATGTACAGC	GCAGAGAGAT	1620
	TCCAGGTGCT	TCTCTGAGA	TCTCTGGCCC	CCAACCAAGT	CAAGATGCGA	GGGAAACCAA	1680
	TGTACTTGCA	CATCGGGGAG	GAGATAGACG	CGTGTGACAT	GCGGCGGAGT	GTGTGGGCTC	1740
75	CGATCTCGAA	CATCTATGTC	CTGAGAGGAG	TGAGAGGACA	ATGTTACCCC	TACAGAGAC	1800
	ACATTTGCA	TTCTTTTAT	ATCGATACCT	TGTGGGCGCA	CATCAAGTTT	GCTCTGGGAT	1860
	TTCAGGAGC	ACACTTGGAG	GGCACGAGAG	TGAGCATAT	GGAACAGCAG	CTGTGGGCTG	1920
	ATGACCGACTA	TGACTTCCAC	CTCGGCGGTC	ATGAGAGCTG	AAAGGAGAGT	TATGATCCAC	1980
	CACTATACAT	CAGGAGAGC	TGACATCAT	ATGAGCTCTG	TGCTGGCTCT	ACATGCGAG	2040
80	GCTCCATGCG	CTGTGTATC	AAAGAGGTTG	TGGGCTATTA	CTCTTTGGGC	CAGTCTCTCT	2100
	TCCAGGAAGA	TGGCGCGAG	GAAAGCAACA	CTTTTGACCA	CTGTCTTGCC	CTCTCTTGTA	2160
	CTGTGTGAC	CTCTCTCCCC	TGCGAGCGTC	ACAGCAAGAT	TGCGAGAGT	ATACACAGAG	2220
	ACTCTTACCC	GGGATGAGT	GGAGAGGCCA	GGGAGAGCTG	CATGCTGGTC	TCCACATCT	2280
	GGATGCCAA	TCCCAACAC	AACTCTATCA	ACTGTGCGGC	TGCAAGATCT	GAGGAATAGT	2340
85	GATTTGGTGT	TATTTTTCAC	CAOGTACCAA	CGGCGGCCCT	CGTGGGAATG	TACTCCCGAG	2400

	GTATTTCAGA	GCACATTCCA	CTGGGAAAT	TCATTAACAA	CCGAGCACAT	TCCAACTCAC	2460
	GGCTGTGCAT	GATCATAGAC	AACGGAGTCA	AAACCACDCA	GGCTCTCGCC	AGGAGCAAGC	2520
	GGCTTTCTCT	CTCAATATAT	TCCTGCAGAT	ACGCTCTCTA	CCAGAGACCT	GCACCTCTGA	2580
5	AGCCCCGGGA	GCGGCCATC	ATCAGACATC	CTATTGCCTA	CAAGAACCCG	GACCACGGGG	2640
	CTCGCTGGTG	GGGGGGGGAT	GTGTGGCTGG	AGAGCTGGCG	GTTCCTGAC	AATGGCATTT	2700
	GCTCTGACCT	GTGATGGT	GGAACTCTTC	CCATATACCA	GGCTCTGAC	CAAGAGATTA	2760
	AGAACACGCT	GTTTTCTG	GAGGTGTGCA	ACCTGGGGAC	GGAAATGATG	GACATATAGA	2820
	TCCTGGGGCCC	TGGCGCTGT	GACCATAGCG	GAGGAGCCCT	CCCATATGCG	CAGAAATTTT	2880
	CAATTAGTAG	AATTCAGTTA	TATATATGCC	CCATACACAT	CCAAATATGC	ACTTTCCGAA	2940
10	CGTTTGTGCG	CTCTGAGGGC	GGCCGACACA	GGCTCCCTGG	CTTCGAGCTG	TAATATGCTT	3000
	GCACAGACCT	GCATCTATAC	ACCTGACGAC	GCATTGTGCT	TGAGAGATCT	CGGATTTCTT	3060
	CCAGAGTGTT	CTTCGGAGAG	CTCTGGGCGCT	GGTTCAACCA	GCTGGACATG	GATGGGGATA	3120
	AGACATCTGT	GTTCATATAG	GTGAGCGGCT	CTGAGTCCGA	GTACCTTGCG	TCTACTACCA	3180
	CGAGAAATGA	CAACTGGCTG	GTCCGACATC	CAGACTGCTT	CAATGTTCCC	GACTGGAGAG	3240
15	GGCGCATCT	GATGTGTGCA	GAGATGACGA	TGTATCATCA	AGCTCAACAG	ACCGATTAAC	3300
	TGGCAATGAA	GATCATCAAG	AATGACTCTG	CCAGCCACCC	TCTTTTACTG	GAGGGGGGGC	3360
	TCACACGAGG	CAOCCATTAC	CAGCAATACC	AACAGCTTGT	CACCTGTCAG	AAGGGCTTCA	3420
	CCATCCACTG	GGACCGCTG	CACTACCTGC	AGGCTGCTCT	CTGCTCTATC	GAGGCTTCA	3480
	AGGGGACTG	GATCCGATGT	GGGTCTGCT	ACCCGCGGCT	CACCAACATC	TGCATCTCTT	3540
20	GGGATGTTCA	CAATCGCTCT	CTGAAGCAAA	GGTCCAAGAC	GGGGCTCTTC	GTGAGGACTG	3600
	TGCGATATGA	CAAGATGAGG	CAGAGCTAAC	CTGGACGAGG	GCACACTACT	TGGGACGAGG	3660
	ACTCAGAGCT	GTGTTTCTCT	AGGCTGAAGG	CTCGACACGA	GAGGAGAGAG	TTTGTCTGCT	3720
	CTCTCAATGA	AGCTGTGCTG	GGATATAAGA	TTAAAGCTCT	GATTCACAAAG	AACCCAGGGG	3780
	TCAGTGACTG	CACAGGCCCA	GCTTACCCCA	AGTTTACCGA	GAGGGCTGTC	GTAGAGCTGAC	3840
25	CGATGCCCAA	GHAGCTCTTT	GGTTCTCAGC	TGAAACAAAA	GGACCATCTT	TGGGAGGATGA	3900
	AGATGGAGAG	TTCCAGACGC	AGCTCTCTTC	AGCTCTGGAA	CGACTCTGCT	TACATATGAG	3960
	TGGATGKGAA	GAAATGACCT	AGTTCCGAGG	ATGGCATCCA	GGTGGTGGTG	ATTATGCGGA	4020
	ACCAAGGGCG	CGTGGTGAGC	CACACGAGCT	TCAGGAATCT	CATTCTGCAA	GGCATACCAT	4080
	GGCAGGCTTT	CAACTATGTT	GGGACGCTCT	CTGACATCTC	CATATGCTCT	ATGGCATCAA	4140
30	AGCGAAGATA	CTCTCCGAGT	GGCCATATGA	CCAGAGTGCT	GGAAAGCTCT	GGGGGACGAA	4200
	GGGGTCTCAA	GTTTAAAGAG	CAATGGCAT	TGGTTGGCTT	CAAGGGGAGC	TTCCGCGCCA	4260
	TCCTGGGTGAC	ACTGGACACT	GAGGATCACA	AAGCCAAAT	CTTCCAAAGT	GTGCCCATCC	4320
	CTGTGGTGAA	GAGAGAGAGC	TTGTGAGGAC	AGCTGGCGCC	GGTGGCCACC	TGTTGTGATGA	4380
	CTATAGAGCT	GACTCTGCTG	AGCTCTGCTC	AGCCGACGAG	CTGGGCTGCT	GGGCTGGCTC	4440
35	CACAGCTGTC	CTGGGAAAGG	CGTCTTTCAG	CCCTGATGGG	CCAGAGGAAAG	GCTCATCAGG	4500
	ACCCCTGGTG	TGCCACTGTC	CCCTACTCAA	GTGCTTACCT	GGAGCCCGCT	GGGCGGCTCT	4560
	GGGAAATGCT	GGAAATGCTC	ACTTTCTGCT	GGGCTATGCT	GTGCTTCTCT	CTCATCTGTT	4620
	CCCTTTCAGT	GGGGTCTGCT	GGACATATAT	GGGACAGCTG	GGTTTCTGCT	ACACGACAGA	4680
40	TCGACTTTGG	CAGAGCGCCT	GACCCAGCTA	GGAGGTATGC	TGGAGGGCTG	GTCAATTCAC	4740
	GATCCCATATG	GTCTTCAGCA	GACAACTGAG	GGTGTAAAT	GTAGAGAGAA	GAGCCTTGGC	4800
	CTATAGAGAA	TCCTTTACCT	TGTAGAGAG	AGCCCAACTC	ACAGGATCTG	GAGCTGGGCT	4860
	AGACTTGCT	ATTCAGCTG	AAGAGGACGA	AGGAGGCTG	GGCTGATGCT	ACCTTTGAGG	4920
	AGACTTTGAG	TGGCAGGTT	GGACTTGGAC	TAGATGACTC	TCAAAGGCC	TTTATGTTCT	4980
45	GAGATTCCAG	AAATCTGCTG	CATTTCACAT	GGTACATGGA	ACCCAAAGAT	TCATGTGATAT	5040
	CCACTATAT	CCATGATGCT	GGGTGGCCCA	GGCACACG	GATGGAGGAG	TGAGACTATA	5100
	TGCTTACGTT	GAGGCTGCT	CGTCTCAGTA	GGGCGGCGAG	GGTGTCCAT	GCATCTCGCA	5160
	ATGCGAGGTG	GAGAAATCAC	AGAGAGGTAA	AGAGTGGGCC	AGTGCCATTT	CAGAGGGGAG	5220
	CTCGAGGAAG	GCTTCTTGCT	TACAGGAATG	AGAGCTGGCC	GATTTTCTGT	GGGGGGAGAT	5280
50	GAGGACGCT	CGGATATGCG	TCAGGATCTC	AGGCTCTCTC	GGCCGCTGCT	CAATGATGCT	5340
	GTGACTACGG	GGTCCGCCCT	TGCTCAAGTCT	TCTCTGGCCC	ACTCATGATG	GAGAGATGTT	5400
	CTCAGAGGGG	AGGATATGGC	TTTGTGCTCT	ATGAGCACAG	AGGAATTCAG	TCCCGAGGCA	5460
	GGCTGTGCTC	TGACTCCAGG	AGGGTGAAGT	CCACAGAGAT	GAGCTCTCTC	CTTAGGGGCT	5520
	CGTTTGCTCT	TCATCAAGGG	AGCTGAGGAC	AGGGGGCTCT	CAGAGAGCCT	TGATGTGCT	5580
	CGTACTCCCT	CGGCTCGGGA	TTTCAGAGCT	GGAAATATAG	AAATATATCA	GGCCAAAGCC	5640
55	TTCAITTTAA	CAGATGGGGA	AGTGTAGCCC	CCAGATGGG	AAGAACACAC	ACAGCTAAGG	5700
	GAGGGCTGGG	GGAGGCCAC	CTGAGCCCTT	CTGCGCACAC	CACATGCTCT	CAACACAGAG	5760
	CCGAGAGTGG	CCGAGGAGCT	CTGAGGTTAG	CTTCTCGAAA	TGGGAGCAAG	TCCCTCGAAA	5820
	GGAAAGGAAA	TGACTAGAGT	AGAAATGACG	CTAGCAGATC	TCTTCCCTCC	TGCTCCGAGC	5880
	GCACACAAAC	CGGCGCTCCC	CTGTGGTTTG	GGGCTCCCTG	TGGCCTTCAC	TTTGTGTAAT	5940
60	ACCTGTGAGC	CCAGCTGGGG	TGCGAGTAGT	CTGACATCTC	CCATGTGTTG	TACCTGGCTC	6000
	TCCTGTCTCT	CGACTCTCA	AGGTGAGGCT	CCAGCAGGCG	AGTACAGCTC	CCCATGTTCT	6060
	TGGTAGGCCA	ATTGGTGCTG	TCGTGGGTGT	CTGAAACAGT	ATTGGGTCCA	CCCGACTGCC	6120
	TTTCAGCTGG	TGCTTAATGC	CCCTGCTCTC	CCCTGGGCCA	CGTTATAGAG	AGGCCAAGA	6180
	GCTCTCTGTA	GAGGAGGAGA	GATATCTGTT	GTATTAAGAT	TTTCCACCA	CACAGATCTC	6240
65	TCCCTGGGCT	TTTGAAGGAA	TCATATTTCT	CCCTTTCTCT	CCGCTCAACC	CAAACTTTCT	6300
	CCTTCAAGGA	GGGCGTCCCT	GGCTCCCTCT	ACCCAACTGC	ACCCATAGAG	CTCGTGTCAA	6360
	GATGCTCTT	GGGCGCTGGG	AGGCACTGCT	CAGGAGAGTC	TTTCCACCA	AGCATATCTC	6420
	AGCTGCTGGG	AGCTGCTGGG	GATATCTGTT	TTTATAGAGT	ATGCTGCTCT	CAAGGCTGAC	6480
	AGTCACAGGA	AGGACTTCTT	CCAGGAGAGT	TAGTGGTGAT	GGAGGAGAGA	GTTTAAATGA	6540
70	CTGATGTCT	TTCTGTGCTCA	GGGTTTGTGT	GAGTTTTCAC	CTCTCTAATG	CAGGGTGTCT	6600
	ACAGCTGAAA	CCACTTATGA	TGTGATCACT	TCGAGGAGTC	CAGGATATGT	GAATGTCTTT	6660
	GGCTCAAGTC	ATTTATATAT	TGAAGGTTCT	CAGAGTTTCT	CAGAGTTTCT	CATATGTTCT	6720
	ACAGTACAGA	ATTCTGATCA	AAAGTTTCTT	TTCTTAAGCC	ATTCAACAG	AGGCAATATC	6780
	TAGGCAATTT	CTTGATAGCA	CAAAITTTCT	TATTTGCTAG	AAATTTGCTC	TGCTTGTAT	6840
75	TTCTGTGTT	AGACTTAAG	TGAGTAGGCT	CTTTAAGGAA	AGGACAGCTC	CTCTGAATCT	6900
	CTTGTCTGCT	TTCTCTTAC	GAAATAGTCT	GTCTTTTCTT	GGAGTATAGA	TGTATAGAT	6960
	GTTTGTATCT	AAACTTTCTT	TGTAGGATC	ACCATGAACA	AAGATATATT	TTCTATTATT	7020
	TTATTATATG	TGACTTCAA	GAAGTCACTG	TCAGAGAAAT	AAAGATTTGT	CTTAAATGTT	

Seq ID NO: 95 Protein sequence

Protein Accession #: XP_051860.2

1	11	21	31	41	51
MGAAAGQDFL	PRAMLTSMIL	TLFCFPGATL	TVAGCPDGS	DELQPNPHGH	DQDHHVHIQQ
85	GKLLTLTSSA	TVYSYHSISG	GKLVKIDHDE	PVILRTHRIIL	IDNGGELHAG
					SALCPFGNGP

Seq ID NO: 97 Protein sequence:

Protein Accession #: NP_065169.1

	1	11	21	31	41	51	
5	MSRRKQAKPQ	HIHSEEDQGE	QQPQQQTTFE	ADAAAPAAPA	GELGAPVWPF	GNEVASSEDE	60
	ATVKRLAREE	TRVCTFLEH	KDICTANPVP	LIMHDSQPV	PSEDPQGVNI		120
	SHQPTSPGKQ	DCIHRNGGSS	EDMKQKPDNE	SVVYLKTETA	LPFTPDQDYS	LAKGQVAMTN	180
	VTIQLALRTK	VAVNORSADA	LPAPVFGANS	ITWVLEQILC	LQQQQLQDII	LTEQIRIQVN	240
	MMASALHMS	GAGADITLTI	QSHMQQVYSA	AVALLSEKRG	SGQLSDIALK	QADLPHANTP	300
10	SATSLELRL	APFTLADQPT	PLALLQVHSL	PLALLQVHSL	SVLPQSPFT	VALETSRDKG	360
	GKPFNISAVD	VKTKDEALY	EHKCKCYEKV	FUTDSLLQIH	LESHITGERPF	VCSCVGRHPT	420
	TGKNLKVHFI	RHPQVKANPQ	LFARFDQKVA	ACNGIPVALS	VDPIDEPSEL	SILDSKPVLTU	480
	TSVGLPQNLS	SGTNPKDLTG	QSLPQDLQPD	PSFESBGQPT	LPQVGVPHYS	FRAGGQPSGS	540
	TFPQSGETLK	LQVAVHIDH	ATTDRHBLI	QHRVLEQSG	LMHYKRVTHS	SEFPCCKLQD	600
15	RAFTKTNLKL	THLGVHRYNT	SIKTQHSICP	QKQKFTNAVM	LQGHIRNEMG	QQTNPFTLPE	660
	NPCDTGSGEP	MTVGGNGSTG	AICHDVIESI	IOVEVSSQGE	APSSSSSIVPT	PLPISHSASP	720
	TLGFANWASL	DAPQKQVPAF	PHLQGRQSEB	NGSVESDGLT	HDSESLMDQD	EYKSGSPDIL	780
	ETTSQALQEP	ANQKLSSTGT	KSPDQSGRAE	SSHSIRTFWE	GSSLPFTPTI	BAFPTTVYVE	840
	VFGTFVGPST	LSFQNTPLLA	AQPRKARQKH	GCTRCGRNFS	SASALQIHER	TRTGEKPFVC	900
20	NICGRAPFTK	GNLKVHYMTH	GANNNSARRR	RKLAIENTWA	LIGTDGKRVS	EIPFKETILAP	960
	SWNDPVPVNM	QITSMNLGSL	AVKTEISIVT	QSGGVTPLPV	SLGATSVVMN	ATVSSMDQSG	1020
	SGISADVEKP	SATDGVKPRQ	FFPHISEMKI	AVS			

Seq ID NO: 98 DNA sequence:

Nucleic Acid Accession #: NM_006612.2

Coding sequence: 553..1095

	1	11	21	31	41	51	
30	TTCTCCGCGA	ACCTTCGCTT	CCTCTCCCTC	CGTCCGCCCC	ACCTCTAGC	CTCGACATCC	60
	CTCCCCCCCC	CAGCGCGGCG	CTCTCGCTTT	CGCGCGAACC	AACTGGAITTA	ATTTCACGCT	120
	TTCTGTTCTT	CTCGCTGTGT	TTCTTCTCCC	CTTGTGGCTCT	CGCCGCGCTCT	CGCTTCTCTC	180
	TTCTCCCCCT	CGCCTCTCTT	CGCGCCCCCG	CTTTCAGTCT	CACCTGTCTCT	CTCCACATAT	240
	CTCTGCCCCC	CTCTATCTAT	GATACACACG	CTGACCTATC	TTCCCGACAT	CTCTTCCCCC	300
35	CCGAAAAGTA	CACATCTGG	CGCCGCCCAAG	CCCGAAGACA	CGCCGCTCTC	CTCGACATAT	360
	CAGAGGAATY	CTCCCCCCCC	CCCCAAAAAA	AAAAGCAATC	CGCCGCTCTC	CGCCGCTCTC	420
	ACATTCTGGC	CCCGCGATCT	GGCGCAGAGC	CGCGTGGCAG	AGAGATGTCC	GGCGAGAGGG	480
	CCGACGCCCG	CGCTTGGSTT	CGGACACACG	ACGACGAGCG	TGGGCGCGAG	CGTCCGCCCG	540
	TTCCGACAC	CAATGGGAAT	CCCAATGGGG	AACTGTATGC	TGGTGTCTCT	CACCTTCTAT	600
	GCTTGTGCTT	CTGTCTGCAAT	TGCTGTCTAC	CGCCGCCAGT	AGACCCCTGT	CGCGCGGAGG	660
40	CTGTGTGCTT	CCCTTCGATG	CGTCTGTGGG	GAAGCGGAGT	TTCTACTTCAG	CAGCGCCGCA	720
	AGCGCTGTGA	CGCTCTGCGA	CGCTGCGATG	CTTGAGGAGT	CTTGTCTTCC	CAGCTGTGTA	780
	CTGCGCTCTC	TGGGACAGTA	CTGTGTCTAC	CGCGCCAAAT	CGAGAGGAGA	CGTGTGTGAC	840
	CCCTCGACCG	TGCTTCCGGA	CAACTTCCCC	AGATACCCCG	TGGGCAAGTT	CTTCCAAATAT	900
	GACACCTGGA	AGCACTCCAC	CCAGCGCTTG	CCGACGGGCT	TGCTGTCTCT	CTCTGTGTCC	960
45	CGCGCGGCTC	ACGTCTCTCC	CGAGGAGCTC	GAGCTGTCTA	TGGAGCGGAG	CGTCCACGCT	1020
	CCCGCTATTG	CTCTAGCAC	CCAGAGCCCC	GGCCAGGGGG	GGCGCCCCCG	AGAGATGTGAC	1080
	AGCAATCGGA	AGTGAGCAAA	ACTCGGCCAA	GTCTCGAGCC	CGCGCGCCAC	ATCTCTGAGC	1140
	CTCTCTCTGA	CCAGAGAGAT	TTCCATCAGG	TTCCATCCCG	AAAATCTCTC	GGTTCACGAT	1200
50	CGCTCTGAGG	CTTCTCTGTA	CCGACTTCCG	TGCTCCCCCT	TCCGCGAAG	AGCTCATCTT	1260
	CCTCGGCCCC	CTCATCGGG	CTGAGGAGC	ACAGCAGCAT	CTTCAACAT	GTACAAAATC	1320
	GATTGGCTTT	AAACACCTT	CACATACCT	CCCCCC			

Seq ID NO: 99 Protein sequence:

Protein Accession #: NP_006603.1

	1	11	21	31	41	51	
55	MGIPMGKSLM	VLLTFLAPAS	CCIAAYRPSE	TLCGGELVDT	LQPVCGDRGF	YPSRPASRV	60
	RRSRGIVREK	CFRSLDLALL	ETVCTAPAKS	ERDVSTPFTV	LPDNPFRYVP	GKFPDYDTWK	120
	QSTRLRLRGL	PALLARARRH	VLAKLEAPR	EAQRHRPLTA	LFTQPAHGG	APPFAPASNRK	

Seq ID NO: 100 DNA sequence:

Nucleic Acid Accession #: NM_004217.1

Coding sequence: 58..1092

	1	11	21	31	41	51	
65	GGCCGGGAGA	GTAGCAGTGC	CTTGGACCCC	AGCTCTCTCT	CGCCTTTCTC	TCTAAGGATG	60
	GCCCAAGAGG	AGCACTCTTA	CCCCCTGGCC	TACGGCCGAC	AGAGCTCTCC	ATCTCGGCTG	120
	AGCACTCTTC	CGCTCTGCTA	CGCTCTGCTA	GAGCTCTGTA	CGCCATCTCT	ACTGTGCTTC	180
	ATGAGCGCCT	CCAAATGTCA	CGCCACAGCT	CGCCCTGGCC	AGAAAGTGAT	GAGAAATAGC	240
70	AGTGGGACAC	CGACATCTCT	AAGGCGGACG	TTACATAATTG	ATGACTTTGA	GATGGGCGCT	300
	CTCTTGAGCA	TAAGCAAGTT	TGCAAGCTGT	TACTTGGCTG	GGAGAGAGTA	AAACCATTTG	360
	ATGTGGGCGC	TCAAGAGTCT	CTTCAATCTC	CAGAATAGGA	AGGAGAGGCT	CGAGCATCAG	420
	CTGCGCAGAG	AGATGGAAAT	CCAGGCGCCAC	CTGCACCATC	CCAAATCTCT	GGTCTCTTAC	480
	AACTATTTTT	ATGACCGGAG	GAGGACTTAC	TGATCTTAG	AGTATGCCCC	CGCGGGGAGG	540
75	CTCTGACGAG	AGCTGACAGA	GAGCGGCTAC	TTTGAGAGAG	AGCCACACAC	CAGGATCTGC	600
	GAGGAGTGGG	CAGATGTCTT	AATGTACTCT	ATTGGGGAAGA	AGGTATATCA	CAGAGACATA	660
	AGCCACAGAA	ATCTGTCTCT	AGGGCTCAAG	GAGGAGCTGA	AGATTGCTGA	CTTGGGCTGT	720
	TTCTGTGACAT	CGGCTCCCTT	AAGGCGGACG	ACAAATGTGTG	GCAACCTTGA	CTACCTGCCG	780
	CCAGATATGA	TGAGCGGCGC	CAGACAGATG	CTCTGTGTGT	CTCTGTGTGT	CATTGGAGTG	840
80	CTTGTCTATG	AGCTGTGTGT	GGGAGACCCA	CCCTTTGAGA	GTGCTACACA	CAACAGACCC	900
	TATGGCGCCA	TGTTCAAGGT	GACACTAAG	TTCCCCGCTT	CTGTGGCCAC	GGGAGGCCAG	960
	GACCTCATCT	CGAAAGTGCT	CAGGATTAAC	CCCTCGAGAC	GGCTGGCCCT	GGGCGAGGTC	1020
	TGACGCCGCC	CGGAGCTGGG	GGGACAGATG	TCGCTCCCTG	TGCTCCCTCT	TCGCTCTGTA	1080
	CTGTGCGGCT	GAGAGTCCCT	GCTACTTCACT	CGAGTGGGTG	TGTTTGTATG	CTTGTGTATG	1140
85	TATAGGGGAA	AGAAAGGATC	CCTAATCTGT	CCCTTATCTG	TTTCTTACTT	CTCTCTTGT	1200

TTAATAAAGG CTGAAGCTTT TTGT

Seq ID NO: 101 Protein sequence
Protein Accession #: NP_004208

5	1	11	21	31	41	51	
	MAQKNSYFM	PYGRGTAPSG	LSTLPQVRLR	KEPVTPSALV	LASRSNVQPT	AAPQKQVMEN	60
	SSGTPTDLTR	HFTIDDFEIG	RLPGKEKFGN	VYLAREKKSH	FIVALKVLFX	EQIKREGEVH	120
10	QLRREITIQH	HLHPIHILRI	VNYPFDRRI	YLILRYAPRG	ELVKRLQKSC	TFDQRTYAT	180
	HEELADALY	CHRWKHEIR	IKRILLGL	KGRKLADPS	HFPLAPSLER	KTMCITFLYI	240
	PFEMIEDRMH	HEKVDWLQIC	VLCEYLLVGN	PFESASHSE	TYIRIVKVDL	KFPASVPTGA	300
	QDLISKLRLH	NPSEIRPLAQ	VSAHMFVRAN	SRVLPPSAL	QSVH		

Seq ID NO: 102 DNA sequence
Nucleic Acid Accession #: AK025790
Coding sequence: 56..1642

1	11	21	31	41	51	
20	AGTATCCGAG	GAGAGCAAG	TGGCAAGTCT	TGGCAAGTCT	GCTGCCCCCT	CCGTATGTC
	GCAAGGGATC	CTTCTCCGC	CAGCGGGCTT	GCTGTCGGAT	GAGGATGCG	TAGTTTCTCC
	CAGTTTGGAG	TCCAGCACTC	CAGATTGGGG	GTCTGTGGTA	CGAAGAACC	TCGATATCTCA
	CTGCTCTGTC	GTCTCTATCT	CCGTAAGAGA	CAGACAGCAG	GTCTCATCTG	AGGACAGTAT
	GAGAGAGGTG	AAGTATATCT	TGAGGGTTTG	GCCCTTGTTA	CCTTCAGAGT	TGGAAGACAA
25	GGAAGATCAG	GCTGTTGTCC	GTATTAGAAA	TGTGGAGACC	CTGTGTTCTA	AGGACCCCAA
	GGAATCTTTT	GCCTCAAGAA	GCATAGAAC	GGGAATTGCG	CAGACGACAC	ACAGTTCTAC
	CTTTTCCGAG	ATCTCTGGG	CAGAGMTGG	AGAGCATCTC	TTCTTCAACC	TAATCTGTGA
	GAGATGGTGA	AGGATGTAC	TCAAAGGGCA	GAATCGGCTC	ATCTATACAT	ATGAGTCTAC
	TAATCTCAGG	AAAACCCACA	GAATCTCAAG	TACCATCAAG	GATGGAGGGA	TTCTCCCCCG
	GTGCTCTGGG	CTGATCTTCA	ATAGCTCCA	AGGCACACTT	CATCGAACAC	CTGATCTTGA
30	GCCTCTTCTC	TGCAATGATG	TAATCTGCTC	AGACACAG	CAGATCCGAA	AGGAGGAAAT
	GAGAAGCTGT	TCCTGTCTAA	ATGGAGGCTC	CCAAAGGAGG	GAGCTGTCCA	CTTCTCTTGA
	GAGAGTGTC	TACATCGAAA	GTGCGATAG	TACCAAGCAC	AGCTTGGACA	GTGGCATGTC
	TGGGCTCTCT	TCTATCAATG	AGTGTACCA	CAGTATGCCG	CTGGATGAAA	CAAGTATCTG
	ATGGGACGAG	CCGCTCTATC	CCCAATCTCA	ACACTCTGCT	CTTCTCTCTC	
35	GATCTCATTC	TTTGAGATCT	ACAAGCAACT	GCTTTATGAC	CTATTAGAAC	CGCTTAGCCA
	ACAGCGCAAG	AGGCAGACTT	TGCGGCTATG	CGAGATCAAA	AATGGCAATC	CCATATGTGA
	AGATCTCAAC	TGATTTCTAT	TGCAAGATGT	TGAGAGGCTC	TGAGAGCTCC	TAAGAAATGG
	TCTATAGAAC	CTATCTGATC	CTCAACACCA	CACTCAAGCC	TCGATCTCAG	
	CTATCTCTCA	ATCAGCATCC	TACACTCTCA	GGGGGAGGGA	GATATGATCC	CCAAATGATC
40	CAAGCTGTCA	CTCTGTATG	TGGCTGGCTC	AGAGGCTGCG	AAGATCAGA	AGAGTGGTGA
	ACGGTTGAGG	GAGACAGAGA	ACATTAACAC	CTCTCTACAC	ACCGTGAGCC	CTGTATATGC
	TGCTCTGTGT	CAAAAGCTGC	AGACAGCTGC	AAGACAGAC	CTGTGTCCTC	TCCTGTATGC
	CAGTTGACT	CGAGTGTC	AAAGTTCTCT	CACAGGCGGA	GGCGTTCTCT	GCATATGTG
	CAATGTGAAT	CCCTGTGATC	CTACTATAGA	TGAACATCTT	CATGTGCGCA	AGTTCTCTAGC
45	CATGCTGAC	CAGTGTACT	GTGACGCC	CACCTATGCA	ACTGSGATTC	CGATCTCTGC
	ACTGTTCAT	CAGGAGCAAT	AGTCTTCAG	TATCCCCAG	CTTAGAGAAA	GGGGCTTAGG
	CAGACACAGG	CTTGATGAT	GATATTGAAA	ATAGAGCTGA	CATCTCCATG	TATGGCAAG
	AGGAGTCTCT	ACAGTTTGTG	GAGCCATGTA	AGACACTCTT	TTTAGAGAAA	GCAGAGGAAA
	AGCTACAGCT	CGAGATGAT	CTCCAGATG	AAATTTGCA	TGAGATGTA	GAACAGATG
50	AACAGGCGGA	ACAGTGTGTC	AGTGAACATT	TGACACCCCA	AAGAGAACTA	TTGGAGGAAA
	TGTATGAGAA	AAATCTAAAT	ATCTCCAAAG	AGTCACGAC	AAATTTTATC	CAGAGAGAGA
	TTACAGAGCG	GGATGAGAA	ATTGAGAGC	TGAGAGCTCT	CTTGACAGAA	GGCAGACAC
	AGTCAATGCG	CCATACAGAA	TGAGAGTCTG	AATGTGCTCT	ACGGGCTGCA	CAAGGTTGTG
	CAGCTCTGCG	CTCCACCCAG	CAGCTTCAGG	AGGTTAAAGC	TAATATTACG	CAGTGCAGAG
55	CAGAGCTAAA	CTCTCAACT	GAGAGTGTG	ATAAGTATCA	GAATATGTTA	GAACACACAC
	CCTCAGCCAA	GCCTCTCACC	ATTATATGCG	ACAGAGANTT	AGAGAGGCTC	CGACAGATA
	TAGAGCTGTT	GGGACACAG	CTTCAGAA	TTGTGATCT	CTTCAACTCA	CCAGAGAGAT
	CTTGTGCA	CAGCATGCG	CGAGGAAAC	TTGTCTCAGC	CTTGACACT	TGTGATGCA
	TCTTATCTCA	ACAGACAGAC	ACTCTGGCTC	ACTGCGAGAA	CAACTGTGCG	CTAGTGAAAC
60	TGACCTCTG	GAGAGAGAGA	CGATATATG	CTAGACGATA	TACTACTG	TTGAACTCT
	AGGCGAGCTG	TTCTGCCAAA	AGGCGGCTTG	GTACCAACCA	GGAAATACAG	CAACCAACCC
	AAACACCAAC	AGGAGAGAAA	CAATCTCTC	GAAATTTACT	TCCCGGAACA	CCAACTCGCC
	AAAGCTCAAC	AGACTGCAGC	CCCTATGCGC	GATCTGATG	CTGACGCTGT	TCCCTTTTAC
	CTATATCTG	GCTCTCTGCA	AAAATGATG	AGGCTGTGCT	CGAAGAGAGA	GAAGGCTGCA
65	GGCCCTGAGG	TGGGTGATCT	ACTCTCTGCA	AGGAATAGGT	CTTCTTATCA	CTTCTTATCA
	TATCAGGAAT	TATATCCAGG	ATGCAATACT	CAGACACTAG	CTTTTTTCTC	ACTTTTGTAT
	TATACACCC	TATGTAACT	CATGTGTGTG	TTTTTTTATA	TTTACTATATA	TAATTTCTAT
	GCACAGAAA	ACATATATAT	TAAAGATAT	ATTGTGCTCA	TTTTTTATG	AATTCGAAT
70	GTAGCAAAAT	CATTAAACAA	AATTATAAAA	GGACAGAGAA	AA	

Seq ID NO: 103 Protein sequence
Protein Accession #: NP_005724.1

1	11	21	31	41	51	
75	MSQGLSPPA	GLSDDDVVV	SRMFSTAAH	LSGVRSRLL	SDCVVSTSL	EDQQVPSDE
	SRGVYVYLR	VRLPRLSLE	ROKRCQVRI	EVETIVLQA	PKDSFALKEN	SRHIOGATHR
	PTFSQIFQPE	VQGSFNFNT	VKEMVQVLYK	QGNWLIYTG	VTSNGKTHYI	QTTIDGGILL
	PRSLALIFNS	LQGLNHTED	LKPLLSNVI	WLDKSGRIQE	ENKLSILANG	GLQERLSTH
80	LKRSVIESR	IGTSSFDGG	IACLSSISQC	TSSSQLDRTS	RHWAGPTAP	LPFENLHRS
	INTSFEIYH	ELLYLLSFP	ROQRHRLA	LCQWNGVY	VEDIANHYH	DAEEMNLKQ
	VORHNGFAS	THLNQNSRS	HSIFRILRL	LQGRGIVPK	ISELSLDLIA	GSRECKDQS
	GERLKEAGNI	NTSLRLGRC	IAALRNQQRN	RSKQNLVPRP	DSKLTVRFGP	FTTGRGSRCH
	IVNVPCAST	YDSTLRVAPK	SALASQVICA	CPTATYDPI	PALHVGQT	

Seq ID NO: 104 DNA sequence

Nucleic Acid Accession #: NM_006952.1

Coding sequence: 11..793

	1	11	21	31	41	51	
5	AATCCGACA	ATGGCGAAG	ACAACCTCAAC	TGTTGTTGTC	TTCCAGGGCC	TGCTGATTTT	60
	TGGAAGATG	ATTATGTGTT	GTTCGGGATC	TGCGCTGACT	CGGAGATGCA	TCTCTTTTGT	120
	ATCTGACAA	CAGACATCT	ACCCACTCTCT	TGAAGACACC	GACACATGTG	ACATCTATGG	180
	GGCTCGCTGG	ATGCGACAT	TTTGGGCGAT	CTGCGCTCTC	TGCGTGTCTG	TTCTAGAGAT	240
10	TGTAGGCATC	ATGAAGTCCA	GAAGGAAATAT	CTCTCTGGGG	TATTTCATTC	TGATGTTTAT	300
	AGTATATGCC	TTTGAAGTGG	CATCTTGAT	CACAGACAGG	ACACAACGAG	ACTTTTTCAT	360
	ACCGAATCTC	TTTCAAGTGG	AGATGCTAGA	GAGGTACAGA	AACACAGCGC	CTCCAAACCA	420
	TGATGACACG	TGGAANAACA	ATGAGTCTAC	CAAAACCTGG	GACAGCTCCA	TGCTCCAGAG	480
	CAATTGCTGT	GGGTAAATG	GTCCATCAGA	CTGGGAAAAA	TACACATCTG	CTCTCCGAG	540
15	TAGAGATTAAT	GATGCTGACT	ATCCCTGGGC	TGCTCAATGC	TGTGTTATGA	ACAATCTTAA	600
	AGAAGCTCTC	ATGATGCTCT	AGGCTGGGCT	CTGTTTATCT	GAATCTATGG	660	
	CTGCTATGAA	CTGATCTCTG	GTCCAAATGA	CCACACAGCC	TGGGGGGTTG	ACTGGATTTG	720
	ATTTGCCATT	CTCTGCTGGA	CTTTTGGGT	CTCTCTGGGT	ACCATGTCTC	ACTGGAGCAG	780
	AATTGAATAT	TAAAGA					

Seq ID NO: 105 Protein sequence

Protein Accession #: NP_008893.1

	1	11	21	31	41	51	
25	MAKDNSTVRC	FQGLLIPNV	IIGCGIALT	ASCIFFVSDQ	HSLYPLLEAT	DNDIYGAAH	60
	IQIPVGLICLP	CLSLVIGVVI	MESSRKILLA	YFILMFIVA	FEVASCITAA	TQDFPTPNL	120
	FLAGMLSRHQ	NNSVFNNDQ	WNNGVNTG	DKLLADNCC	QWNPSPDWK	YTSAPRTBNH	180
	DADYTPHRC	CYNHLEKPE	KLENKGLVF	GFTHGQCYE	LIEGPNRRIA	MYVATGPAI	240
	LCMTFVLLG	TMFYMSRIY					

Seq ID NO: 106 DNA sequence

Nucleic Acid Accession #: NM_002740.1

Coding sequence: 178..1968

	1	11	21	31	41	51	
35	CCGCGTTCC	GGCTGCTCC	GGGAGCGAC	CCTTGCGTCG	GGCTCGCGG	CGAGTGGGC	60
	AGGTAGTGG	GGGAGCGGC	GGGTTCTCC	GGCAGCGCA	GGCGCGGAG	TCCCCACGG	120
	CCGCCAAGC	CCCCCCCGCA	CCCCCGGCT	CCAGCGTTGA	GGCGCGGAG	TGGMGAGATG	180
	CCGACACGA	GGGATGCTG	CCAGCTGTCC	CGAGCGCGG	CACGCGGAG	CTCCGAGCA	240
40	CATTCACCAC	AGGTCGGGT	GAAGCTCTAC	TACCGCGGG	ATATCATGAT	AACACATTTC	300
	GACCTTCCA	TCTCTTTGA	GGGCGTTTC	AATGAGGTT	GAGACATGTG	TTCTTTTATG	360
	ACGACACGAC	TCTTCACAT	GAATGGATA	GATGAGGAG	GAGACCGCTG	TACAGTATCA	420
	TCTCACTTG	AGCTTTATG	CTGTTATGAG	TAAACAGCA	TGCTCTCTCA	CTGCTCTCT	480
	TTGATCTTG	TGTTCCCTG	GTATCCAGAA	CTCTCTGGA	TGCTCTTCC	AGAGAAAGAT	540
45	AAATCCATCT	ACCGTAGAG	TGCAACCGCG	TGAGAGAAAG	TTATTGTGTC	CAATGCGCAC	600
	ACTTTCCAG	CCAGCGTTC	CAACAGGCT	GTCACATCTG	CCATCTGCAC	AGACGUAATA	660
	TGGGACCTG	GAGCGCAAG	ATATAGTGG	ATCACATGCA	ANCTCTTGT	CTATAGAAAG	720
	TGCCATAAAC	TGTCACAAT	TGAATGTGG	GGGCTATTCT	TGCCACAGGA	ACCATGATG	780
	CCCATGATCT	AGTCATCAT	GCATCTGAC	CATGACAGCA	CAGTATATCC	ATATAATCT	840
50	TCAATGCTAG	AGAGTTTGA	TCAAGTTGCT	GAAGAAAGAG	AGGCAKRTAA	CACAGAGGA	900
	AGTGCGAAG	CTTACTCAG	TCTAGTCTT	CGAGATTTTG	ATTTCCTCG	GTTAATAGGA	960
	AGAGGAAGTT	ATGCCAAGT	ACTGTGGTT	CGATTAAAA	AAACAGATCG	TATTATGCA	1020
	ATGAAAGTTG	TGAANAAGA	GCTGTTTAAT	GATGATGAGT	ATATTGATG	GTATACAGGA	1080
	GAGAGCATG	TGTTTGACA	GGCCCATAT	CATCTCTTCT	GGTCTCTCT	GCATCTCTCT	1140
	TTCGACAG	AAAGCAGTT	GTCTCTGTT	ATAGAGTATG	TAAATGAGG	AGACCTATG	1200
55	TTTCATATGC	AGCGACAAG	AAACTCTCT	GAAGAACATG	CCGATTTTGA	CTCTCGAGAA	1260
	ATCACTGCTAG	CATTAAATTA	TCTTCATGAG	CGAGGGATAA	TTTATAGAGA	TTTGAAGACT	1320
	GACATATGAT	TACTGGGCT	TGAAGGCCAC	ATTAAACTCA	CTGATACGCG	CATGTTAAG	1380
	GAAGATTAC	GGCCAGGAGA	TACAACGAC	ACTTCTCTGT	GTACTCTTAA	TTACATTTCT	1440
	CTGAAATTT	TAAAGAGGA	AGATTATGTT	TTCACTGTTT	ACTGCTGGC	CTTGGAGATG	1500
60	CTCATTTTGT	AGATGATGCG	AGGAAGGCT	CAATTTTATA	TGTTGGGAG	CTTCGATATG	1560
	CTTGACACGA	ACAGACAGA	TATCTCTCT	CAGTTTATT	TGGAANAAGA	AATTCGATTA	1620
	CCAGCTCTCT	TGCTGTGAAA	AGCTGCAAGT	GTCTGAGATA	GTTTCTTAA	TAGAGACCT	1680
	AAAGAACATG	TGTTGTGTCA	TCTCTCAACA	GATTTTCTGT	ATATTGAGG	ACACCCCTTC	1740
	TTCCGAAATG	TGATTTGGA	TATGATGAG	CAAAAACAGC	TGTAACCTCT	CTTTAAACCA	1800
65	AAATATTTCT	GGGAAATG	TTTGCTCTCT	CAGTTTATT	TGGAANAAGA	AATTCGATTA	1860
	CNGCTCACTC	CGATGATAGA	TGACATTTG	AGGAAGATTG	ATCACTCTGA	ATTGGAAGTT	1920
	TTTGAATATA	TCAATCTCT	TTTATGTTCT	GCAGGAAGAT	GTGTCTGATC	CTCATTTTTC	1980
	AAACATGAT	TCTACTATG	TTCGATTATA	ATGATGATCT	AAATCTGCTG	CAGGCTTGA	2040
70	TACATATCA	CTTTTATG	TTCGACCTCA	CAAAAACAG	CTCATTTCT	CTTCTCTCT	2100
	ACTATAGAA	TCAATTTATA	CATCTGTTT	ACTATGAAA	AAAAATTAAT	ACTACTAGCT	2160
	TCCAGCAAT	CATGTCAAAA	TTTAGTTGAA	CTGTTTTC	AGTTTAAAT	AGGCTACAG	2220
	ATGATTAATG	AGTTTACCTT	TTTGTTTAA	AAAAAAGAA	G		

Seq ID NO: 107 Protein sequence

Protein Accession #: NP_002731.1

	1	11	21	31	41	51	
75	MSHTVAGGS	GHSHQVRVK	AYRGDIMIT	HFSPSISFEG	LCNVEDMCS	PDNEQLFTMK	60
	WDKEDSDCT	VSSQLLEEA	PRLYELNDS	ELLIRVFPQ	PERPMPCPG	REKSTYRGA	120
80	IRNKLRYAN	GIPTDAACT	RLNGLDGRCY	CTGDCGLHLY	KCKRSLTLY		180
	CRNLSIPQEP	VHMQQSSHY	SDHAGTIPY	NFSSHSLDQ	VEBEKEMANT	RESGAKSSL	240
	GLQDFDLRLV	IGRGSYAKVL	LVRLEKTDRI	YAMKVVKEL	WNDEEDIMV	QTEKRVFSGA	300
	SRNPFVLGLH	SCPTSESLP	FLVEYVNGD	LMPENGROR	LFSEHARFYS	ARTSLANLY	360
	HERDITRDL	KLVNVLDS	GRKLTIVGLV	CKEKLSDPT	TESTCTGIV	IAPLLEKED	420
85	YQPSYDMKL	GVLPFEMAG	RSPEDIVGSS	ENFQNTEDY	LFQVILEKQI	RTPSLSEVKA	480

ASVLKSLFK DPKRLCQHP QTGPDILQGH PFTFVQVHM NMQKVVPFF KPHISGEFOL 540
DNFDSQFINS PVQLTFDDHD TVRKIDQSEF BQFYEINPLL NSEAECV

Seq ID NO: 108 DNA sequence

Nucleic Acid Accession #: NM_000349.1

Coding sequence: 127..984

1	11	21	31	41	51	
GGAGCTCAGA	GGCGAGCTT	GAGGGCTCA	GGAAGGACGA	AGAACACACC	TTAGAGAGAG	60
AGGCAACGAG	AGCGGGCGCA	GCGACGAGCG	CAGCGAGCCC	ACCACCTCCA	CATTTCGCCAG	120
GAACCAATGC	TGCTAGCGAC	ATTCAAGCTG	TGGCGTGGGA	GCTCCTACAG	ACACATGCGC	180
AACATGAGAG	GCGCTGAGCA	ACAGGCTGTG	ATGGCCATCA	GCCAGAGAGCT	GAACCGGAGG	240
CGCTCGAGGG	GGGCAACCCC	TAGACGCTGG	ATTACACAG	TTGGCGGCGG	GAGCTCTCTA	300
CTCGCTTCTC	GCGCTGAGGA	GAUCTCTCTC	ATGACACAGG	AGCTGGCTCA	TCTCCAGGAG	360
GGGGAGAGGG	CCATGCGAGG	GGCCTTGGGC	ATCCTTAGCA	ACCAAGAGGG	CTGGAAGAGG	420
GAGAGTCGAG	AGACCAATGG	GGACAAGATG	ATGAGTAAAG	TGTCCTCCAG	TGTGGGCAAG	480
GTGTTCCGAG	TGGAGAGCGT	GCTGACACCA	CCATGAGGGA	CGCTCTATGA	AGACATCTGT	540
GAGCTGTGCT	AGACCAATGG	GGAATGGAGC	CCCAATGTCA	AGGATATCAA	GOTCTCTGAG	600
ANGATCGGAA	AGATACATT	CATTACTCAC	GAGCTGGCTG	CCGAGGCGAG	AGGAAACCTG	660
GTGGGGCCCC	GTGACTTTGT	GAGCGTGGCG	TGTGGCAAGC	GCGAGGCGTC	CACCTGTGTG	720
CTGCTCTGCT	TGGAGAGCGT	CTTCCGAGAC	ATGCTCTGAG	AGAAGGTTGT	CATCGGGGCG	780
GAGCAACGGTC	CCACTTGCAT	GGTCTCTCAC	COSTTGGCTG	GAGTCCCTTC	TAGACACAA	840
CTTAAGTGGC	TACTACGAT	CGACTCAAG	GGGTGGCTGC	CCAGAGGAT	CATCAACGAG	900
GTCTCTTCCC	GAACCAAGGT	GATTTTGGCC	AAGCACTCTC	GCGAGCGCT	GGAGTCCGAC	960
CTCTGCTCTC	AGGCAACCGC	TGGAAGACCA	CGCTCTGGAT	CCGACATCTA	CTCCAGCTCA	1020
CTGTACACA	CGCTCATCAG	GAGAATCCCT	ATTGGAGGCC	TGCAAGTCTA	AGATCTCCAT	1080
CTGTGACAG	TGGGATGGGT	GGGTTCTGTT	TTTAGATGAT	GACACTAGGA	TTGAGATGG	1140
TGAAGTTTTT	ATGACACAGA	AAACAGGGAT	GAGGCTCTTG	GATTAAAGG	TACTTCATT	1200
CATGATGATG	CTGATAGGAT	AGGTTTGGCG	CCCTTAAT	AAATGTAA	CTTTTTTCT	1260
GGGCGCTTCA	ATGACACCT	AAACCATCTT	TTAAATGCT	ATGGCTGTAT	ATGGGTGTGT	1320
GGCAGTACAT	GTGACCAAG	CAGAATCTCA	GAGGCTCTCC	GCTCAAGAT	GCAATGCGCT	1380
CGAGCTGCA	GAGCAACCGC	ACACACAGAG	CAGTGGCTCA	CTTCCTCCCT	TGCTCTCCCT	1440
TATAGTCCAA	GCTTTCTCTG	TGGAAAAGAG	CAAACTCAT	TAGTAGACAT	GTTCCTCCAT	1500
TGCTTTTCA	GGCACAAGT	AGAATAAGA	ATCATATAT	ACACC		

Seq ID NO: 109 Protein sequence

Protein Accession #: NP_000340.1

1	11	21	31	41	51	
MLLATPKLCA	GSSTYRHRNM	KDLRQQAVNA	ISQELRRRAL	GGPTPSTWIN	QVRRSSLLG	60
SRLEETLYSD	QLAYLQQGE	EMQKALGIL	SNQEGMKES	QDNGDRKMS	KVVPQGVKFP	120
RLRFVVDQPM	RLRYELSELV	MEAMGEMNPN	VKEIKVLQKI	GKDTFTHEL	AAEAAGNLVH	180
PIEDVSVRCA	KRKSSTLYA	GGDTFDPNPI	EKGQVIRASE	OPTFQWHLPL	AGSPFKTLFI	240
WLLSIDLKN	LFKSIINQVL	SGTQVDPANI	LKRKLESHA	SEARC		

Seq ID NO: 110 DNA sequence

Nucleic Acid Accession #: E05 sequence

Coding sequence: 131..682

1	11	21	31	41	51	
GCTGGAGGCC	TGGGCGCGGA	GCGGGGTGAG	GCGCGGAGGA	GCGTGGGTGG	GGCGGGGGGG	60
CGAGATATGC	CACACTCTCG	CTGCTGTGTT	GCAACCTCTC	TGGACTAGGC	TGCTCTTGTT	120
AATCATGATG	ATGTTATATA	AGAGTTGCGA	GCGGCCAGCA	CACAGATGCA	GCAATGCTCT	180
CTCTCTPCAC	GCTCTAGCTA	TAGCTTGTTT	CGAGATGTTT	ATCTCTTCAG	AAAGCTGGGC	240
ATTTCGAG	AGCAACACAT	CTCTAAGTGT	GAGGCTCTCT	CTGCGCCTTA	CACATTTTCC	300
AAATAGCTTC	AAATGCTTTA	CTTGTGAAAG	CGCAGGGGAT	ATTATTAAC	GCAATGATGT	360
GGCAGAGAGC	AAATGTGTCT	CACAAATAC	ACAGTACTGT	TGACAGTTC	ATCACTCTCAC	420
CAGCGCATCA	AGACACCA	AAAGTGTGCT	TCCAGAGTCC	TCCAGAGTCC	AAATGCTTCT	480
TGTCTCTGCG	CACACACAGC	GAGATCTGGA	ACATACGAG	TGTAGGCTCT	CTGTGAGAG	540
AAATATCTGC	AAATGAGAAT	TACCCACCCA	TCACACTAAT	GCAGTGTGTT	CGTAAATGCA	600
OGCTCAGAGA	ACATCTGCGA	GAGTGGCCCC	CACACTCTAC	CTACACATGC	TTCGCTGGGT	660
CTTGTGCTCT	CGATCTGCTT	GATGCGACCG	TTCTCAGAG	AGGCGAGAC	CAGCTCTTAA	720
AGCACAAGCC	AAATACCTGT	TGACGGTGA	ACTTTGGAGT	GAGATCAAT	CTTGCACTTG	780
GTGAGAGTGT	CACATTGGAC	CTCAAGGGCA	AAGCCAGTGG	TTTGCTTGA	TAAATGTTTC	840
CGCATAGAGG	CCACAGAGCT	GAGATGAGGA	ATTGGCGAG	GCTCGAGAAG	ATGCTCTGAC	900
TTCCAGGCTT	CTGTGTGAA	GAGACTCTAC	TTTGGGACAT	TCTCCAGGA	GATCTCTGGC	960
AACTAGTCCC	ACCTGACTAG	GCCTTAGCT	GAAAGGATT	CTTGACCTCC	TTCAGTCTCT	1020
CAGAGGCTGC	CAGGTCAJAC	CTCTTGTTT	ATGTGATTAG	CTCAGAGCAT	CTCTATGAAA	1080
TCTAACCTTT	CCCTCTAGGA	GAAGGCAATT	TTCGCCACCA	ACAGCATAGT	CAATGAGAAA	1140
GGCACTGTGA	GGGCAAAAC	TTCACTGAG	ACTAATATGA	AACTCATTTG	CAATATATGG	1200
GGGAAATAA	AGCTTTTAAA	TTATCAATG	T			

Seq ID NO: 111 Protein sequence

Protein Accession #: AAW0908.1

1	11	21	31	41	51	
MLYTSRDRPA	HKVSLMLLC	ALAIAYVQIV	ITPESNAPAK	NINFTVREPP	LDPTTFPNSF	60
KCTFCBAGD	HNKCNWAGD	HKCFQTYQC	LTVRHPTSHG	RTSTITKCA	SRECHPVNG	120
HSRDSSEITS	CRSCCEMIC	NVELPTNTHI	AVFAVMAQR	TGSSSAFTLY	LPFLAWFVL	180
PLL						

Seq ID NO: 112 DNA sequence

Nucleic Acid Accession #: E05 sequence

Coding sequence: 228..884

	1	11	21	31	41	51	
	CGCCGCGCGG	CGCCAGCGGG	GTGCGCTGGG	AGCCTGGGCG	GGAGGCGGGG	TGAGGGGCGC	60
	GAGAGGCGCT	GTGGCGCGGG	CGCGCGGAGG	CTCTGCTGGG	CGAGGAGCTC	AGAATGTTTG	120
5	TTTTCAGGCT	GCTTTAAAG	TGATTTGAGG	AGAGCGGCTT	TGAGAGATAG	CCACACTGTG	180
	GGCTGCTGTT	GAGCTGAGG	CTCTCTCTGT	TAAACACAG	GATGTGTCTG		240
	ATTACTCTGA	GTGCAAACTT	TTTCACTGTT	CGAGGAGAGA	GGCTGAACAC	CAACTCTCTC	300
	TCTCAAGGT	GTGTGCTTAA	CTGCGGAGCG	TGACACAGATA	TAAGAGTTTG	GACCGGCCAG	360
	CHCACAGGT	CAGCATGCTG	CTCTCTCTGT	AGCCTCTGCG	TATAGTGTGT	GTCCAGATGG	420
10	TATCTCTCT	AGAAAGCTGT	CTCTCTCTGT	CACTCTCAAT	GTGAGGCTCT		480
	CTCTGCAACC	TACACCAATT	CCAAATAGAT	TGAAATGCTT	TACTTGTGAA	AACGCAAGGG	540
	ATAATTATAA	CTGCAATCGA	TGGGCAGAGG	ACAAATGGTG	TCCACAAAT	ACACAGTACT	600
	GTTTGACAGT	TGATCACTCT	ACCAAGCAAG	GAGAGGACAC	ATCCATCAC	AAAAGATGTG	660
	CTCTCAGAG	TGAATCTCAT	TTTTCGCTT	CTGACACAG	CGAGATATCT	GACATCAAGG	720
15	AGTGTAGGCT	TTGCTGTGAA	GGATGATGCT	GCAATGTAGA	ATTACCCACC	AATCACACTA	780
	ATGCAGTOTT	TGCGGTAAAT	CAGCTCTAGA	GACATCTGG	CAGCAGTGCC	CCCACTCTCT	840
	ACCTTACAGT	GCTTGGCTGG	GTCTTTGTTC	TTCATCTGCT	GTGATGCCAC	CATTCTCTAGG	900
	AGAGCGAGG	ACGACCTCTT	AAGGCAAGG	CCAAAGATG	TGTGAAGGCT		960
	GTGAGATCA	ATTCTGCAC	TGGTGAAGAG	TGCACATTGG	ACCTCAAGCG	GAAAGCCAGT	1020
20	GTTTTCCTTG	GATAAATGTT	TCCCGCATGA	GGCCACAGGA	CTGAGATGAT	GAATTGGCA	1080
	GGGCTGAGAG	AGATATGCTG	ACTTCCAGGC	TCTCTGTGTA	AGAGAGACTA	GTTTGGGCA	1140
	GTTCCTCAGA	GAGGATCTGT	GCACTAGTCT	CCACTGTACT	AGGCTTTTCT	CTGAGAGGAT	1200
	TTCTTGACCT	CTTGTAGCTC	CTCAGAGGCT	CGCAGGTCAA	ACCTCTTTGT	TTATGTGATT	1260
	AGCTCAGAG	ATCTCTATGA	AATCTAACCC	TTCCTCTCAT	GAGAAAGCAG	TTTTCCCAAC	1320
25	CAACAGGATA	GTAATGAGA	AAGGCAACTG	TACGAGAAA	ACTTCCAGTG	GAACTAATAT	1380
	GAAATCTATT	TGCAAAATTAT	GGGGGAAAT	TAAGCTTTTA	ATTATATA		

Seq ID NO: 113 Protein sequence

Protein Accession #: Eos sequence

	1	11	21	31	41	51	
	MDVADYSECK	PFHCSREEDP	NHILLKLVNC	LLERLTRYKES	SRPARKVSM	LLCHALAIYA	60
	VQVIFVES	WAPARICCTT	HYVLELWPT	PFHSPKCTC	BNDRNTNCH	WABDNCW	120
	NTQVCLTVRH	FTSRGSRSTI	TKKASHSES	HFVGGCHSR	SEHTCRSCC	BKIMQVELP	180
35	TNITNAVAV	MUAROTSGS	APTLVPLVIA	WVFLPLR			

Seq ID NO: 114 DNA sequence

Nucleic Acid Accession #: Eos sequence

Coding sequence: 402-1025

	1	11	21	31	41	51	
	ACTTCTCTGAG	CGCGGCTGGC	TGGTGGGAAA	CAGGCTCCTT	CGCGGCTGCC	CAGCGCTGGC	60
	CACATAACACA	CTGCGCGCCG	CTTGGGCTCT	CTTCAACCT	CGTGGTGGAG	CGCTGGGCTT	120
	TCCAGAGGGA	GGCGGGCGCG	GGGCTGCTCC	CTGCGCGGCG	AGGCTCACTT	GTCCCGGCC	180
45	GGCGGCTCTC	CGCGCGGAG	GTGGTTCAGG	CGAGGAGGGA	CGCGCGGCGG	CGCGCGGCGG	240
	GTAGACAGCA	ACGCGCGCCC	CAGCGCGGTT	CGCTGGAGAG	CTGCGCGCGG	AGCGCGCGGG	300
	GGGCGCGGAG	AGGCTCGGTT	GGCGCGGCGG	GGAGAGATAT	CCACACTCTT	GCTCTCTGTT	360
	GGCAACCTCT	CTGACGTAGG	CTGCTCTGTT	TAACTACATG	GATGTTGCTG	ATTACTCTGA	420
	GTGCAAGCTT	TTTCACTGAT	CGAGAGAGA	GGCTGACAGT	CGACTCTGCT	TTCTCAGATG	480
50	ATAAGAGTTC	GGACCGCCCA	GCACACAGAG	TGACATGCTT	GCTCTCTGTT	CAGCTCTGTT	540
	CTATAGCTGT	TGTCCAGATC	GTATCTCTCT	CAGAAAGCTG	GGCAATGTCC	AGAAGACATCA	600
	ACTTCEADPA	TGTAAGGCTT	CGTGGAGC	CTACACAT	TCCAAATGAC	TCTAGAGTCT	660
	TACTTTGTGA	AAACGCAAGG	GATAATTATA	ACTCGAATCG	ATGGGCAGAA	GACAAATGTT	720
	GTCCACAAAA	TACACGATAG	TGTTTGACAG	TTTCACTACT	CACCAAGCAC	GGAGAAGACA	780
55	CATCATCAC	CAAAAGTGT	GCTCCAGAGA	GTGAATGTCA	TTTGTGTGTT	TGCCACACA	840
	CGCGGATCT	TGACACATCG	GAGTGTAGTG	CTTCTGTGTA	AGAAATGATC	TGCATATGAG	900
	AATTAACCCAC	CAATCAACAT	AATGCTAGTG	TTGCGGTAA	GCACGCTCAG	AGAACTATCT	960
	CGACGAGTCT	CCCCACCTG	TACCTACAGG	TGCTTGCTCG	GTCCTTTGTG	CTTCATATGC	1020
	TGTGATGCA	CATCTCTCTAG	GAGAGGACAA	GACCAAGCTC	TAAAGAGACA	GCACAAATCT	1080
60	GTGTGAAGG	TGAATCTCTG	AGTAAATGAT	ACTCTGTGAC	TACTGTGAGG	GGGCACTGAG	1140
	GACCTCAAGG	CGAAGCCAG	TGTTTGTGCT	GGATAAATAT	TTCGCCATGT	AGGCCAGAGG	1200
	ACTGAGGATG	GGAAATTGGC	AGGGCCTGAG	AAGATGTGCT	GACTTCCAGG	CTCTCTGCTG	1260
	AAAGAGAGCT	ACGTTTGGGC	AGTTCTCTCG	AGAGAGATCT	GGCAATAGCT	CCACACTTAC	1320
65	TAGGCTTTGA	GGGACAGAGA	TTCTCTGAGC	TCTCTGACTG	CTGCGAGGCG	TCCAGATGTA	1380
	AACCCCTCTG	TTTATGTGAT	TAGCTCAGAG	CATCTCTATG	AAATCTAACT	CTTCCCTCTA	1440
	TGAGAAAGCA	GTTTTCOCCA	CCACAGAGAT	AGTCAATGAG	AAAGGCAACT	GTACAGAGAA	1500
	AATCTTCAAT	GGAACTAATA	TGAAATCTAT	ATGCAAAATTA	TGGGGGAGAA	TAAAGCTTTT	1560
	AAATTATACA	ATGT					

Seq ID NO: 115 Protein sequence

Protein Accession #: Eos sequence

	1	11	21	31	41	51	
	MLLITLSANL	FTVPERSLTT	TFSPRYKES	DRPARKVSM	LLCHALAIYA	VQVIFSES	60
75	AFARKINFTN	WFLDPTTF	PFHSPKCTC	BNDRNTNCH	WABDNCW	TGTCCLTVHF	120
	TSRGRSTYH	VKASRSBCH	FVGHSHRES	EHTECRSCC	BKIMQVELP	TNITNAVAV	180
	HAGRTSGSSA	PTLVPLVIAW	VFVLPL				

Seq ID NO: 116 DNA sequence

Nucleic Acid Accession #: Eos sequence

Coding sequence: 1-1059

	1	11	21	31	41	51	
	ATGGTATGGC	AGCAAGATTA	TGGAAACGAG	AGAGAGCACC	ATGGCTTCGG	TCTGGAATTC	60
85	TGCGGTGTAT	CTGCAAGGTT	CCCTTGCTTA	AGGCCCTTGA	CTCTCTTGAT	TATAGTTCC	120

	TCATCTGGCT	AGAGAGGATG	GGAGCTGCTG	GGAAGAGCAAT	TGTAAATCACT	CAGAGATGGG	280
	TCATGAGCA	TGGAAGAGATG	AGAGCTACAT	TACAATACAA	TGAGTCACAG	TGACGACGA	240
	GCTGCTGATG	AGAGAGCTGC	AGCAATGATG	CCAGATAGAT	TAGCTAAGAT	CATTGATGA	300
5	GATGTGAAG	GCATTTGACA	GAGAGAGATG	AGAGATCACG	TAACTCAAG	TAAGTAAGA	360
	ATGATGATG	ATGATGATG	ATGATGATG	ATGATGATG	ATGATGATG	ATGATGATG	320
	ATTATCCAG	CTGACATG	GGAATGATG	ATGCTCTGTC	ACCAAGTGTG	AGGCTCTGTC	480
	CTCACACAC	AGGATGATG	TGTGATATG	TGTGATATG	AGGCTTTCA	ACAGAGACA	540
	AAACACAAC	CCATGATG	AAATATATA	GAAATCTAG	CAGCTGTGTC	TTTCACTAT	600
10	GATATGAG	TGTGGACAG	GAGATGATG	GAGATTAAG	AGAAAGTGTG	CATTACTTCT	660
	ATGATGATG	ATGATGATG	ATGATGATG	ATGATGATG	ATGATGATG	ATGATGATG	720
	TATATCTAG	ATCTGACAG	GAGAGACATA	TGGTGTCCAC	AAATATACAA	GTACTGTCTG	780
	ACAGTTCAT	ACTTACACG	CAACGAGAAG	AGACATACAA	TCACAAAAA	TGTGTGCTGC	840
	AGAGTATG	GTCAATTTG	CGTGTGACAC	CACAGCTAG	ATTCTGAACA	TACAGAGTGT	900
15	AACTTCTCT	TGTGAAGAT	TGTGTCGAT	TGTGTCGAT	CCGCAATACA	CATCAATGAC	960
	TATGATGAT	ATGATGATG	ATGATGATG	ATGATGATG	ATGATGATG	ATGATGATG	1020
	CCATGCTGT	CTGCTGTGTC	TGCTCTCTCA	TGCTGTGTAT	GCCACCATCT	CTTAGAGAGAG	1080
	CAGAGACAG	CTCTTAAGG	ACAGACAAAA	AACTGTGTGA	AGCTGGAAT	TGTAGTGATA	1140
	GTATCAATT	GCATGTGTC	AGAGTGTGTC	ATGTGACCT	ATGAGCGAAG	AGCATGGTGT	1200
	GCTGATGAT	ATGTTTCCCG	TACATGGACA	CAGGATGAGT	GATGGGCTGT	GGGCTGTG	1260
	ATGATGATG	ATGATGATG	ATGATGATG	ATGATGATG	ATGATGATG	ATGATGATG	1320
	GCAGAGACA	TGCTGCACAC	TAGTCTCCAC	TGCTAGAGCG	TTTAGTGTCA	AGAGTTTGT	1380
	GACCTCTTG	ATCTGCTGAC	AGGCTGCCAG	GTCATAGACT	CTTGTTTATG	TGATTAGTAC	1440
	AGAGATCTG	TATGAAATCT	AACTCTTCCG	CTCATAGATG	ACGAGTTTGT	CCACCACTAT	1500
25	GCATGATG	TGATGAGGC	AGCTTTGACA	AGAGAAATCT	CAGTGAAGAT	ATATGAATAT	1560

Seq ID NO: 117 Protein sequence
Protein Accession #: Eos sequence

Protein Acetabularia 75 aa sequence							
	1	11	21	31	41	51	
30	MVWQDDYGR	REHNGCRLEF	CRVSAQCCPL	SPILTSLVIS	SSAERGEAAE	EEDEPFSRGG	60
	QRRMKERSHA	RIHKVQGEAG	GAEDEAAEAA	DDKVIQVKQM	RIYVRYTKEM		120
	CSRKFQNLIG	NVKGCHTDEM	LIRATQWML	PDQGVQVGP	PTQGVQVGI	LDNQAQENAT	180
	KIKPTDVKYK	SPSPVCLFTI	DIRVATCTE	RIKQKVSIS	MATPFGNSFK	CFTCEPAGTA	240
35	YICNKNAAEK	ECSTQVQPL	TVHHFISAGR	GTSLTKKAS	RSECHFGVLR	HSRSDSETEC	300
			TVHVFISAGR	GTSLTKKAS	RSLKLVVGLR	LL	

Seq ID NO: 118 DNA sequence
Nucleic Acid Accession #: XM_038659.6
Coding sequence: 528-1688

	1	21	31	41	51	
	ACTGATGGAG	TGGCGAGGAG	CAGATGATGA	DGGAAATGCA	ATCATCATTTG	ACCTCTGATC
	TGTTTATTCC	TGCTCCTCTT	AGGCTCTGAT	ATAAATGTTT	CAGGCGCATG	CCCAACATCTG
45	GATACGACCC	CACAGTGGCT	GATCTGGGAG	TAAACGCTTG	ATTCTGTCTG	ACACATGCGA
	CCTCTGCGCT	ACACCCCGGG	ATGATGACAT	GAGTGAAGCT	CGGGTCTGAG	CGCTGAGCTC
	GAATCTGAGT	GTGCGGAGAG	ACTCTGATCT	AGGCTGAGCT	CGGCTGAGCT	CGGCTGAGCT
	CTGCTCTGCT	CTGCTCTGCT	CTGCTCTGCT	CTGCTCTGCT	CTGCTCTGCT	CTGCTCTGCT
	AATCCGACGC	GGCAGCTGTA	CTGCTCTGCT	CTGCTCTGCT	CTGCTCTGCT	CTGCTCTGCT
50	CGGGAGCGCG	CTCTCTGCGG	CGCGAGCGCG	GTCCACAGCA	CAGGCGGCTA	CGACCTCTTG
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	CTGCTCTGCT	CTCTCTGCGG	CGCGAGCGCG	GTCCACAGCA	CAGGCGGCTA	CGACCTCTTG
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55	TTAAGCTGTA	AGACCTAACT	GTGCACACG	TCAACATTTT	AAAGAGGTGG	GTGCTCTGCT
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	ATTGTTGATG	GGAGAGCACT	GTGCACACG	TCAACATTTT	AAAGAGGTGG	GTGCTCTGCT
	TTGATGATGA	GGAGAGCACT	GTGCACACG	TCAACATTTT	AAAGAGGTGG	GTGCTCTGCT
	ATAATAAAT	TGCACTCTTT	CAGGCAACAG	TCAACATTTT	AAAGAGGTGG	GTGCTCTGCT
60	TGAGGCGTGA	TCTGCGCGTA	TCTGCAACAG	AGAGGCTCTT	TAGAGATGTT	CACACAGCTG
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	TACTCTTGAG	CCAGATGGGA	CTCTTCTTGG	CAGGAGAACG	TACCAAAAGT	CTGCTCTGCT
	GGGCACATCT	CAGTATGAT	AGAGCTGCTT	AGGCTGAGCT	TAGAGATGTT	CACACAGCTG
	GTGATCTTCT	CTGCACTCTT	AGAGCTGCTT	AGGCTGAGCT	TAGAGATGTT	CACACAGCTG
65	TTTCTGCGAG	AAATGAGTGA	GGAGAGAGAG	ACTCTGCACT	TCCTCACTA	GATGTCACAT
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85	ATGATCTGAT	TTCTGCGGAT	CTCTCTCTTA	CTCTCTCTTA	CTCTCTCTTA	CTCTCTCTTA
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	ATGATCTGAT	TTCTGCGGAT	CTCTCTCTTA	CTCTCTCTTA	CTCTCTCTTA	CTCTCTCTTA
	ATGATCTGAT	TTCTGCGGAT	CTCTCTCTTA	CTCTCTCTTA	CTCTCTCTTA	CTCTCTCTTA

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YSAVATRLP VDGLESELLEC IQQLVKLDGE WVPYSTEASL YIAPFTIGE PBLGVKPKPT 180
ALLFVLVAF GPTEPSSFTN PVELSHMPTV VYAHNGTGD CCKGHWYGS LPAQCDAVON 240
GQCVLMVLYO EDHITETVGT MQLVLYWINE DBSELATFP LDGI LIPVPT RRCILIDIAQ 300
50 WGEFVSEYRI LTMDLTLAL EGNRVREMPG SGTCACVCPV SDILYKGBTI HPTMENGPK 360
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Coding sequence: 121..1194
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5	TATGTATATA	TATATGTATG	TATATATATA	TATATATATA	TATGTGTGTA	CCCTCTTCTT	1920
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	TTAAGGCCCT	CTGGGCTCTC	TTCTCTAGT	GAGGGAACCT	TCTCTCTCA	CAGGAGACTT	2040
	TGCTCTATTC	TGCTCTGT	ATGCATAGG	TCTCATAGCA	CCCTTTCCCG	CAGGTATGAA	2100
	ATATTTCCTT	AGACACAGAG	GAATATGGTC	TAGCCCTGGG	GCTTGAGGAA	AGTTTCCGAG	2160
10	CCCTGTCTCA	TGAACTCAAT	CCCTCCGAG	GTCTTTCTCG	AGGCGCTCTT	GAGGCAATAT	2220
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	CTCGCCCTCT	ATCTCAATCC	TTCAGTATG	AATTGGAAGT	TCTACTAGAA	CCATGAAACAC	2340
	TGTGTCCTTT	CTGTCACTTC	CAGAGACTCT	GCCTGTCTCG	CAGCAACGCT	TGTGCGCTCG	2400
	CACCAAGCTG	CAGTGTGAGT	TTCAGTATG	ACAGATATCT	GGCGCTCTCT	AACTTTCTCT	2460
15	GAGAGCTGTT	GGATGATCAT	CAGTGTCTCA	CAGGTGTGAG	TGTGCTCTCT	TGTGTTTCTA	2520
	AAGGATCTCT	CAGAGCTCTT	GCTTATGCCA	TCAATCATAT	GGATTTTTTT	TTTTTTTTTT	2580
	GAGAGCGAGT	CTCAACTCTT	TGTGCGCAGG	TGACAGGTTA	ATGCAATGAT	CTGTGCTCAT	2640
	TGCAACTCTT	GCTTATGCCA	TTCAGTATG	GTCTCTCTCT	AGGCGCTCTG	ATGATCTGAG	2700
	ATGCGAGGCG	CTGTGACACA	CGCTAGTACT	ATTTCTGTAT	TTTTATAGTA	GATGGGGTTT	2760
20	CACCAACATG	GCGAGGCTCG	TCTTCAOCTC	CTGACCTTAG	TGATCCTACT	CTCCCATGAT	2820
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Seq ID NO: 121 Protein sequence
Protein Accession #: NP_059368

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25	MORDSYRIHYF	YDVGDDGFY	RSTTPSEDIN	KXPELVPPMV	TVHVSREPSP	QLWSPGTNVF	60
	GCADSETEBQ	DYKHAMRST	ASLIRKDCM	RFSTGTSELE	RVASDLVAG	AFSDFEPREP	120
30	ATPTDTPBLE	KQMLAPFFC	LLEPKIQAQ	SRSSPSRSC	AGSTITVKE	RSILSTREP	180
	ITAVRDLELD	PMHPIFIIS	IQQQINYAAP	PPFSCPEBQ	APKPMFKPEA	LIERAPGGD	240
	DKEDSEIVSL	PPVESEAQS	CQPEIHYDT	ERWTKCKVBS	YLERKRRNDQ	RSFLALADE	300
	VPALASCSRV	SKWMLVIAT	SYLHLELAES	ERHATEKRLQ	EQRRQLQKR	IRYLLSTY	

Seq ID NO: 122 DNA sequence
Nucleic Acid Accession #: AB006625.2

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40	GGCATAGAGG	TGGCTTAGAT	GGGTTCTCTG	GGCGACACTG	GGCGACACTG	GAGGTGAGCT	120
	TGCTCTCTCT	GATCTTCOCT	CTCTCTTGGA	GACGACTGGC	GGAGGAGAAG	GGGACTAGST	180
	CCAAAGACCTA	GGTGGCTGGG	TCCAGCCGGA	CAGCCGACCA	AAGGAGAGAG	TCACTGAGCT	240
	CTTGTCTCTT	GAGAGTACC	TGACCATCAT	CCCTGAAGAG	CTCAAGCTCT	GGGTGGAGAC	300
45	AAAAGAGCG	GAGACTGTCT	GAGACTGTCT	CACTCTCTCT	GAGAAATACA	AGGAGAGTGA	360
	CCAAACGAGA	GAGACACAA	ACAGTGAAGT	GACCAGGAC	GAGACATGGA	CCCGGAACAG	420
	AAGAGAGCTT	TCACCACTCT	ACTCAATCCA	TCTCTTCAGT	GGTGAACGGG	ACTGGGACCG	480
	GAGGCGCAG	AGCGAGACA	TGGAGCCAC	AGACCCCTGG	TCCGACACCA	GGACCCGAG	540
	AAGCAGAGTG	CTTCCGCGGG	ACTTTTCTCT	TCTTGTGGTG	GGAAALACAA	GCTTTGAAAT	600
50	GACAGAGAG	GACACAGGG	ACTCCAGGGC	TATGATGCC	CGATCTCAGG	ATGTGTAATC	660
	ATACCAAAAT	GTGTGTGACC	TGCTGTAGGA	CAGGAGAACT	CACACACACA	TCCAGGACAA	720
	CATGGAJAC	TACAGACAG	TGCTCTCTCT	GGAGTGTGAG	CTTCTGTGAG	ACGATGACCA	780
	CTCCCAAGAT	ACGACAGGGC	ACTCATCAAG	ATCCAGAGAG	AGTGGCTACC	CAGACACAGC	840
	CTGAGGTCTA	AAACTATGCG	CTGAAGCCAA	AAATCAACAC	CACCGCGGGG	GGATTGTGTA	900
55	AGATGTAACT	TCCACAGGAG	TGTATATGGA	AAATTCATCT	AGGATGTATG	CAGCAGTTGT	960
	CAAAATATG	AGACACAGG	ACTCAGACCA	CGGTCTCAG	AGATTCACCA	GAATGTGACA	1020
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	GTGTGTATAG	GAAACCTTCC	TCAATGATTC	TGCTGTGAT	GAGCAGCAAT	AAATCCACTT	1740
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70	AACTTTTAGG	CCGACGCCAG	CCCTTATATG	GTTCACAGAA	ATGTATGTGA	AAGAGGAAGT	1860
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85	AAGTGTTCTT	CGAGAGGGAT	CTGTGTGAGT	TAGAAGGAT	GGCGAATCTT	CTGTTCCGAG	2760
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5

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 AACCTCTACC TTGATAGATT AAGACAGCTA AAGACAGCTA GACCTCTAC 5040
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 TATATATAAA TAGCAATAA TGAACAAACA GTGATCAT ATATTGGAT TTATATGATA 5160
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 ACTGTTTGA AAGATAGATA CTTTAGCTTC TTTCTGAGC CATTCATCT GACACAGAC 5460
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 TTGTTTCTG GTTTTTTTTT TTTTTTAA CCACTCAATA TTGTTTGTAT GATAGTGAT 5640
 TGATAAACC CGAGCTTTT CCTGTAAAT CTTACATCT TGGCTTTAAA GAATGCGTAA 5700
 CACACTCAC TAGATGAGA TGTGTCTTAA TAGAGTTGA GACCTAGG AGAGGCTCT 5760
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 CTTAATCTC TGTGTTAT ATCTGACCT CTAACCTCAT GCTCAACTG CAT

55

Seq ID NO: 123 Protein sequence

Protein Accession #: BAA2956.2

60

VITKLGWVQV ETRTEKRIIE LLVLEQYLII IPEKLEPWVR AKCPENCEKL VILLENYKEN 60
 VQFDESDSD VTEKSPPLV HSFQGDWMD EKGRSDMEP KDRSHWYNI 66
 RSMUPRDLG LPVVAATFPE MDREDDRDS AYESSQDAE SYQNVDLAE DRKWNITQD 120
 NMENYKLLS LGVLALSDGD ESHQTQDRS RKRSAVPT SBLKTMPEA KESTDRGIC 180
 EDRESHGVIM EKFIDVSRH SESSRARESS DRSGRPFMS DNMKDISLN KRLVYIQGRV 240
 YDCAHPCGF RNSLTVSRH NVLSRKRHYV FDTGSGEIH GDRQKPEF FCGESRGEA 300
 MGVSLSSLS GPSPFESSPI DPQAMVYVD ECRSPFVSI EFVEHQIMET EBNLYEVS 360
 FTRSVAVSEV QKSQVGKRF ECKDGCTFF KSAALAEHR IHARGYLVEE ENQCECEAFM 420
 PPTPFSLELK IYGRMPCVE NVCKETPLHS SALIEBKIRH FGDDKIDRES HKREREREG 480
 ETRTPRALH ETRKTVSRI FLRSHQVQET FLRSHSLKE QKLTDRMF ENRGVCEET 540
 FTPOSLKRR KQTYNKEKLC DFTGDRDAP QSESLSEKQ IHSRKNLFEQ GRTEKSVLSH 600
 GPFTSEQKSH TITRELESD DEKAPTISM PYENQKIPK ENYEVKSRV RSVHLSIHS 660
 EQKSHSEVAG PPKPMVMAE TFGPFDLHM KVRAGGNTS EREYHSRVI HSLVASKPR 720
 SHGNHSLVS NEDESSHTI ELNDRERQI PARSHCEGG SKRYHSEV IQSVFAPQ 780
 KSVNPGSGE FKDGESFVP SBNVSRYKA RAKKXKIEE SNETSVHSL PFGBTFRPR 840
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 GQANRKCND PRQFPAETF LVTKQKIDY EKSHGESSG EYTDGRTHS EETHQSTIE 960
 DPTVCGSGS EYKQVGLG FVDTLHLS QVSHRCLY DSHETYSVI 1020
 ITHSISEYQ DYTGBQLYEC FKCBSEFHS SFLPESQRLH BDQLYSEMG CDQGTIALP 1080
 MKPRNRRAE RNFALAGSA RLCLCCQPTI HSSALAEHR IAREDDLLQ SQMAEALPI 1140
 GLALTEPQS QEEBAPCA VQGSFVFW KLADHVTYK NRPYEGSEY THSEFLPEI 1200
 KALFPYEC DQGFPHET WLREKELH RESEDEAA AAMAAQVE ANHYPOYVL 1260
 RIQALFVEA EFPEVAEPE VEAAEFVEA EPNGEABGP DGEALFGE AQGPHEABQ 1320
 FNGDAEPQG AGHDEPERA EEPBOKAEP EGDADEPDGV GIEDPEEGD QEQVREPTY 1380
 DCECTETFT SSTAFBHLK THASNIIEP AANAGBCSY IERASTGAG AQANDKEPK 1440
 CYVQGLFND RLELAGRNT ITO

85

Seq ID NO: 124 DNA sequence
Nucleic Acid Accession #: NM_007196
Coding sequence: 180..1942

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	GATTCGCCAT	TAAAGAGTAC	CAGATCTCTG	TACCGAGGAG	GAGGATGAGG	TACTCGGGCC	120
	TCCTCCACTG	GGTTCGGAATC	AGTAGGTCAG	CCCGCCCTGT	GATTCGTGAA	GACCTCACCA	180
	TGGAGCGGCC	CCGACCTCGT	CGCGCCAGAA	CTGTGATGTT	CCTGCTCTTG	CTGGGGGGAG	240
10	CTCGGGCAGG	ACACTCCAGG	GCACGAGGAG	ACGAAGTGCT	GGGGGTGTCAT	GAGTGCACAC	300
	CCCATTTGGA	GCTTCCCTGT	CTCGGGGCGA	GCACACTGATC	TTGTGGCTGT	TTGTGGCTGT	360
	TCCTTGTAGG	TGGCACTGCG	GTCTCTTACG	CTGCGCACTG	TAAAAAACCG	AAATACACAG	420
	TAGCGCTGGG	AGACCAAGC	CTACAGAATA	AAAGATGCCC	AGAGCAGAAA	ATACTGTGGG	480
	TTCACTGCAT	CCCAACACCC	TGCTAACACA	CGAGCGATGT	GGAGGACAC	ACCACTATCT	540
15	TGATGCTCT	TCAACTGCTG	CGCTGTGGTC	CAAGTGTGAG	CCCATCAGC	GGGATGCTG	600
	TGACGATCAT	TTGACAACCG	GAGTGCACAG	AGTGCACCGT	CTCAGCGTCG	GGAATGTCTA	660
	CCAGTCCCGG	AGAGATTTT	CCTGACACTC	TCAACTGTGC	AGAGATGAAA	ATCTTTCCCC	720
	AGAGAAAGTG	TAGAGATGCT	TACCGGGGCG	AGATACAGAA	TGGCATGCTC	TTGTGACCAA	780
	CGACCAAGG	GCGTCAACG	TGCGAGGCG	ATTGTGAGG	CCCTCTGTGT	TTGTATGCTG	840
20	CACCTCCAGG	CATCACTATC	TGGGGCTCAG	ACCCCTGTGG	GAGGTCCGAC	AAACTGGGCG	900
	TCTATACCAA	CATCTGCGCG	TACCTGGACT	GGATCAGAAA	GATCATAGCC	AGCAAGGCGT	960
	GATTTCTAGG	TAMGACATAG	ATCTCCCTTA	ATAAACTCAC	AACTCTTC		

Seq ID NO: 125 Protein sequence
Protein Accession #: NP_09127

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	MGRPRPRAAK	TWMLLLLLG	ANAGHSRAE	DKVLGHEEQ	PHSQPQNAL	FTQQQLLGG	60
	VIVGQNMVLT	AAHCKPKPT	VLRIHDSLQ	KGPQEIPV	VQSIPIHPCYN	SSDIVDRHND	120
30	LELLQLRDA	SLGSRPIEL	LADHETPOPG	KCTVSGNVT	TEPRSNFT	LAKCAVKPI	180
	QKQKZAVYQ	QITGHWYAC	SHSGADTQCG	DSGPFVWDD	ALQETSMGG	DFPCRSDEKP	240
	VTTNICYLD	MIKKIISRG					

Seq ID NO: 126 DNA sequence
Nucleic Acid Accession #: NM_014791.1
Coding sequence: 171..2126

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40	CGCGGTCTCT	TCAGGACAGC	AGGCCCTCTG	CCTTCTGTGG	GGCGCCGCTC	AGCGTGTCCC	120
	TCCGCGCCTC	AGGTTCTTTT	TCTAATTCGA	ATAAATCTGT	CAGAGGACT	ATGAAAGATT	180
	ATGATGACT	TCTCAAAAT	TATCAATTAC	AGCAACTAT	TGGACAGCT	GCTTTCTCAA	240
	AGGTCAAACT	TGCTTGCCAT	ATCTCTTACTG	GAGGATGGT	AGCTATAAAA	ATCATGAGTA	300
45	AAAAACATCT	AGGGATGTAT	TTGCCCGGGA	TCAAAAACGGA	GATTGAGGCC	TTGAGAGACC	360
	TGAGACATCA	GCATATATGT	CAACTCTACC	ATGTCTTAGA	GACAGCAAC	AAATATTCGA	420
	TGTTCTTGA	GTCCTGCCCT	GAGGAGAGC	TGTTTACTA	TATATATATC	CAGGATCCCT	480
	TGTCAGAAGA	GGAGACCCGG	GTGTCTTCC	GTCAGATAGT	ATCTGCTGTT	GCTTATGTGC	540
	ACAGCGAGGG	GTATCTCTAC	AGGGACCTCA	AGCCAGAAAA	TTTGCTGTTT	TGATGATATC	600
50	ATAAATTAHA	GCTGATTGAC	TTTGCTCTCT	GTGCAAAACC	CAAGGCPAC	AGGATATACC	660
	ATCTACAGC	ATGCTCTGG	AGTCTGGTGT	ATGCACAC	TGATTTAATA	CAGGCAAAAT	720
	CATATCTTGG	ATCAGAGGCA	GATGTGGA	GCATGGCGAT	ACTGTTATAT	GTCTTATGTT	780
	GTGATTTCT	ACATTGTGAT	GATGATAAT	TATGTGCTTT	ATACAGAGAG	ATTATGAGAG	840
	GAATATATGA	TTTCCCGAG	TGCTCTCTCT	CGATGACAT	CTCTGCTCTT	CAACAAATGC	900
55	TGCAAGTGA	CCCAAGAGAA	CGGATTTCTA	TGAATAATCT	ATTGAGCAAT	CCCTGGATCA	960
	TGCAAGTGA	CACTATCTCT	GTGTAGTGGC	AAAGCAGAAA	TCTTTTATAT	CACCTGATG	1020
	ATGATTTGCT	ACAGAACTCT	TCTGTACATC	ACAGAAACCA	CAGCACAACA	ATGAGAGATT	1080
	TAATTTCTAT	ATGATGATCT	GATCACTCTA	CGCTCACTCA	TCTTCTGCTT	CTAGCAGAGA	1140
	AGGCTCGGGG	AAACACGATT	CGTTTAAAGC	TTTCTCTCTT	CTCTGTGGA	CAGGCGAGTG	1200
60	TACCCCATCT	CACAGACATC	AACTCAAAAT	ATTGAGATCT	GGAGATGATG	ACCGCAAGTG	1260
	ATAAAATTA	TGTGGCGGGA	TTAATGACT	ATGATTTGTT	TGAAGATGAT	TTTCAACAGA	1320
	GTGCTCTTAC	TGCGGAGCA	TGCACTGCTG	GCACGATCA	AACTGGTGTG		1380
	AATCTAAATC	ATTACTCCA	CGCTTATGCA	GAACACTGCG	AAATAAATA	AAAGAACAAAG	1440
	AAATGTATATA	TACTCTTAAG	TTCTGTGTAA	AGATGAGAGA	GTACTTTATG	TTTCTGTAGC	1500
	CAAGACTCC	AGTTATTAAG	AAACGACATA	AGAGAGAAAT	ATCTCATGCG	CCAAATCTTT	1560
65	ACACTACAC	CTCAAAAGCT	AGAAACCGGT	GCTTAAAGA	AACTCTTAAT	AAATATCCAG	1620
	TAAATCTCAC	AGCAACACAC	AGATTAAATGA	CAGGTCTCAT	TAGCCGTTAG	AGCGCGTGCC	1680
	GCTCAATGGA	ATTGATGCTC	AACCAAGCAC	ATAAGAGAGA	GACTCCAAAA	AGAAAGGAG	1740
	CCAAAGTGT	TGGAGGCTT	GAAAGGGGCT	TGGATAGGCT	CTCAACAGAA		1800
	GCAAAAGAA	GGGTTCTGAT	AGAGAGCGG	CCGAGAGACT	AAAGCTTCA	TATAATATGA	1860
70	CTCAACATAG	ATTAGTGAAT	CCAGATCAAC	TTGTTAATGA	AAATATGCTT	ATTCTTCCGA	1920
	AGAAGCATGT	TGACTTTGTA	CAAAAAGGCT	ATACACTGAA	GTGTGAAACA	CAGTCAGATT	1980
	TTGGGAAAGT	GAAATATGAT	TTTGAATATG	AGATGTGCTA	GACTCAATGA	CCGATATGAT	2040
	TGGTATGATG	GCACGAGGG	CTTAAAGGGG	ATGCTTGGTT	TTCAAAAAGA	TTGTGGAGAG	2100
	ACATCTTATC	TAGCTCGAAG	GTTAATATGA	TGATTTCTTC	CATCTCGCG	GATGATGATG	2160
75	GGTGTAAATG	AGCTTACATA	AGAGCTTTTA	TGATGCTCTT	GATTTTAAAG	TTGATGTGAA	2220
	CTACCACTT	GTCTTCTTAT	AGACCTATAT	CTCTTCTGTT	TTTATGAAA		2280
	GATATATATT	TGTGTATGAA	TCTAAATCAA	GGCCACTGCT	CATATGTTTA	CTGTCTTTTT	2340
	TAATCATGTT	GTTTGTGATA	TTAATATATG	TTGACTTTCT	TAGATTCACT	TCCATATGTG	2400
80	AATGTAAAGT	CTTAATCATG	TCTCTTTGTA	ATGTGTAAAT	TCTTTCTGAA	ATAAAGCAAT	2460

Seq ID NO: 127 Protein sequence
Protein Accession #: NP_055606.1

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 AYVRSQGYAH RDLKPNLLP DEYHKJLKD I FGLCAKPKN KDYKLTCCG SLAYAAPELI 180
 QOKSLYLGSEA DVMSHILLY VLKOCFLPFD DNMYVALYK IMRGKYDVK KLSFSPSILL 240
 QOKLQVDPK RIMSHGLAH FHWQIDYTH VEWSSNFI HJDDDCUTEL EYVBNRRKPT 300
 NEDLISANDY DHEATLIL LAKANGKPY RLLSSPFGQ QASATPTLI KNNNSLEV 360
 TADSKNVYAG LIDYDWCED LSTGAATPRF SPTKYWTES NGVESKILPT ALCRTFANKL 420
 KIKENVYTFK SAVNIEEYPM FEPKCTPNK NQHKREILT PWRYTTSKA RNQCKLEPTI 480
 KIPWNTOTD KLTGVISPE RRCRVELDL NQAMSETPK RDAKRVFGL ERLDKRVYIT 540
 LTRSRKSGA RDSRBLHL TPVTTTFLV FQLJAREHS ILPKRVDYF QKTYTLKQT 600
 QSDFRKVTY FELEVQLQK PDVGVIRQR LKGDWVYTR LVEDILSSCK V

Seq ID NO: 128 DNA sequence

Nucleic Acid Accession #: E05 sequence

Coding sequence: 169-1323

1 11 21 31 41 51
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 GCAAGTTTGA GACTACCAAG ACCTCGGGAC TGGGCAATTCT CTTCACAACT GCGCCGCACT 180
 GCGTCTCCAG GACCTACCTG CACTCAGGAT GCGATCTCTG AGATATPCTI CTCTATCTAC 240
 TATGATACG TGGTAAGT GGCCTCTAT CTCTCCAGGA CTGATTTTTG TGTGGGCTCT CAGCGGGAAC 300
 CTCCTCTCTC TCATGGCTCT GCTCGGTTAG GCGGCTCGCA GCGGAGTGT TGGAGATTCT 360
 TGCCTGAATC TGCCATCTCT CAACCTCTAT CACTGCTCT CACTGCTCT CAGCGGCTCT 420
 TCCGCTGAGT GGCATTGGGT CTTCGGGAAT TCTTGTGCA AGATGTGTAG CACTCTTAT 480
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 ACACATGAAA ATCCCAAGAG TGTGTGGAAC TGCCACGCG ATTTCCGGCG CACTGGGAC 720
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5	ACATTTCCCT	GCTTCAAGTG	ATTTTTITAG	GGTGGGAC	ATGACCTAG	TAGAGCCAT	4320
	GAAGTGAAT	ATCATAGAA	GAGATGAGA	GAGAGCATG	AAACCGAAG	TGAGAGGTT	4380
	TGAGATCTG	AGCTACTCT	TCCTCCAGC	AACTCTCAG	AGGTGAGGA	GATGATCAT	4440
	GTGATGAGC	AGATCTGAG	GCACTGTGT	GAGCTTCAG	ATCAAGATC	TTCTGAGCT	4500
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10	Seq ID NO: 129 Protein Sequence						
	Protein Accession #: NP_001287.2						
	1	11	21	31	41	51	
15	MAATASPOL	ATEADSEHS	SPYTYDLE	VAFMLCRDA	VFSFGKPLV	VFSLIFVLG	60
	AGSILLALLV	LARTVPERRN	VEYLLNLAT	SNLLPLVTL	FWGIVAMSH	VPGSFLCQV	120
	STLYTINFS	GIFPISCHL	DKYLEIVHA	PYHRLRTRK	SILLATTVA	VSIAVSIDM	180
	VPVQTHENPK	GVNCHADPG	GHGTIWKLP	RFQONLLGL	LELLAMIPFY	SRIGCVLVL	240
	RFAGQRAALK	TAALIVVAF	STPIFNIL	FLRTLLDLQV	FWNCEVQRL	DIYALQTESI	300
	AFLLCCSPPI	LVAFSESRPS	YLKAFPLAV	LGNLALPQTA	QSLSCSSCS	FIITAQESMT	360
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	Coding sequence: 246..980						
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30	GTCTGGCTGC	TTCTCTCTG	GGACACAGAG	GTCCGGACG	AGCACACGA	GGGACCTAC	180
	GCACGCTGTT	CACTTCCCG	ACTCAAGAT	CCCGGAGCG	CCGAGGCTT	CGAGCGAGG	240
	CGGCCATGAA	GAGCTGATG	GTGTGCTGA	GTCTGATTC	TGACGCTCG	CGAGGAGAG	300
	AGAAATAGTT	GTGTCAATG	GACCCCTGG	ACAAGACATC	TACCCCTAC	CAAGCTGCC	360
	TCTACACTTC	GGGCGACTTC	CTCTGTGTG	GGGTCTTAT	CCATCCACTG	TGGTGCTTA	420
	CGAGCTGCA	CTGATLAAA	CGATTTCTC	GGGAGAGCT	AACTCTGGC		480
35	AAAGGGAGAG	TTCCGACAG	CAGAGTTCTG	TTGTCCGGCG	TGTGATCCA	CTCTGTGCT	540
	ATGCGCCGAC	CCATGACAG	GACATCATG	TTTGTGCGCT	GGCACGCCA	GCCAACTCT	600
	CTGATCTAT	CCAGGCTTT	CCCTCTGGA	GGATCTGCT	AGCCACAC	ACGACCTGC	660
	ACATCTCTGG	CTGGGAGAG	ACGCGATAT	GTGATTCTC	TGACACTATC	CATCTGTCT	720
	ACATCCACT	GGTGTCCCT	GAGGAGTGTG	AGCATGCTA	CCCTGGCCAG	ATCACCCAGA	780
40	ACATTTGTG	TGCTGGGAT	GAGAGTACG	GGAAGATTC	CTGCGAGGT	GATTTCTGG	840
	TTCCCGTGT	ATGTGGAGC	CAGCTCCGAG	GCCTTGCTC	ATGCGGTAC	ATCCCTCTG	900
	GTTCAAGGA	GAGCAGGA	CTTACACCA	ATGATCCAG	ATGATCCAA	TGGATCCAA	960
	AAACATTTCA	GCCCAAGTA	CCCTGACAT	TGACATCTC	CTCCGACTC	ACCACTCCAC	1020
	TGCTGTGTT	CAGAACTCT	CTCACTAGA	CTTGTGCTC	CTCTCTCTC	TGCCAGCTC	1080
45	TGACCCCTAT	GCTTAATAA	CCAGGCGAG	TGAGGCTCT	GATTTCTCT	GTTTATCCC	1140
	CGCTCATCT	CTTCTTCA	TGCGAGAGC	GTGATAGTG	AGGATCTGG	CTCTGCTCT	1200
	TACCCGCCAC	ACTAAGAGAA	TACAGGAAA	TCCTTCTAG	GCATCTCTC	TCCCCAACTC	1260
	TTCCACAGT	TTGATTTCT	CCCTGAGAT	CCAGGCGAG	TGTCGGAAT	CCGAGCTCT	1320
	CTGCTACTG	TGCGTCTCC	CTTGAGATG	ACCTTCTCT	ACTCGAGAT	TCTCACTCT	1380
50	AAGATGAGA	TAGATGAT	ACAGTCTCA	TACGGCAGT	GCTGTGAAA	AGATTTAAGA	1440
	TTTCAACCT	ATGACATCA	TGGATAGCA	CTCGGCGCG	CATGACTCA	ATAAAGATG	1500
	TAATTT						
	Seq ID NO: 131 Protein sequence						
	Protein Accession #: NP_002765						
55	1	11	21	31	41	51	
	MKKLMVLSL	IAAMHAEQN	KLIVHGPKDK	TSHPYQAALY	TSGLHGGV	LIRPLAVLA	60
60	AIKIKPRLV	FLGRNLRQ	ESSQSUSVY	RAVILPDYA	ASPDQIMLL	RLRHPKRLS	120
	LIQLPLERD	CSMTTSCI	LMGKTADD	FPDTTCAT	HLVRESCS	CTATCTGAG	180
	LCADDERVK	DSQCGSGG	LVGDHLAG	VSGHIFQGS	KELFQYTVN	CRYTHIQKT	240
	IQAK						
	Seq ID NO: 132 DNA sequence						
	Nucleic Acid Accession #: AY038071.1						
	Coding sequence: 1..1685						
70	1	11	21	31	41	51	
	ATGAGCAATC	AGTACAGGA	GGAGGGCTC	TCCGAGAGC	CCGATGCAA	AAGTAAATCT	60
	CCAACTTTGC	TCTCTCTCA	CTGATCGAC	AGCATCTGG	GCGGAGGAG	CCCTGCGAA	120
	ATGCGGTGTC	TGGGAGGCG	CAGAGAGTT	CTCTGCTCG	TGACAGGCG	CGCCGAGCTG	180
	GAAGAGCGC	TGACATCTC	CTCTAGAGC	CTGAGAGAG	CTCCAGCTCA	CGAGCTGCA	240
	TGCGCGCCA	AGCTGGGCG	CCCTGTACG	CGCGGCGGG	GCGGCTCTC	TGAGGCTGG	300
	CGAGCGGGG	CGGCGGGCG	GCGGCGGGG	GCGGCGAGC	CGCCACGCG	CAGCGGGGT	360
75	CCAGCGGGG	AGGCGCTTC	CGCGGACCG	CGACCGGCG	GGCCCGGGA	ACGGCGAGC	420
	GCGCGGGG	CGCGGCGCG	AGCGCGGCG	GCGCGGCG	CGCTCGGGA	CAGCTCGAG	480
	ATCAGCGAG	CGCGGAGGT	GAGCATCAG	CGCAGCAAT	GTATCCGGA	GACCGGGCG	540
	CCCTTGTGTC	CGCGCGGCG	CGCGCTGAG	GAGCTGGCG	GCGCGGGGG	GTCAACGAC	600
	CGGAGGAGC	GCTCTGCGT	GCGCGGCG	CGCGGAGCG	CGCGGCTGC	GGGTGTGAG	660
80	ACCGGAGC	AGCATAGAT	CTCTAGAGC	CTGAGAGAG	AGAGATAGA	GACCGAGGA	720
	GGGAGACTC	TGAGAGAGA	CGAGGAGAG	CTCTGTAGG	ACGACCGCG	CGCGCTGCT	780
	AAGGAGCCCC	CGGCTCTCT	TGTGGCGCG	ACTGCGGCG	TGGCGGAGC	AGCTCGGCT	840
	CGAGTGGCA	CAGAGGGGG	GAGGCTCTCA	CCGAGGAGG	AGCTGCTCT	GCACCGGGA	900
	GAGCTTAGG	CGAGAGGCG	CAGGAGAGC	GTGTGCTCT	CTGCGGAGC	CTAGCTAGG	960
85	GAGGCGCTC	TGAACGCAA	ACGAGAGGCG	TACCGACCA	CGTTACACG	CTACGAGCT	1020

Seq ID NO: 137 DNA sequence
Nucleic Acid Accession #: E05 sequence
Coding sequence: 1..939

1 11 21 31 41 51
ATGGGCGCGC GCGGGGCGCT GCTGCTGGCG CTGCTGCTGG CTCGGGCTGG ACTCAGGAAG
CGCATGCTCG AGAGAGCGCG GCCCATATCA GGACACATGCG GCGCAGGGGT CATCAGCTGCG
CGCATGCTCG ATGTGAGAGA CGCCCTTTGCG GGACGTGTGCG GAGCGCTGCG

	CTGTGGGATT	CCACGATGAT	CGGAGTAGGC	CTGCTCAGCC	ACCGCTGGGC	ACTCACGGGC	240
	CGCGACTGCT	TGAAACCTGA	CCTTAGTGAT	CCCTCGGGGT	GGATGTGTCA	GTTCGGCCAG	300
	CTGACTTCCA	TGCACTGCTG	CTGGGGCTGC	CAGCGCTACT	ACACCGTTTA	CTTGCTATCG	360
5	AAATATCTATC	TGAGCCCTCG	CTACCTGGGG	AATTCACCGT	ATGACATTGT	CTTGCTGGAG	420
	CTGCTGTGAC	CTGTCACTTA	CACTAAACAC	ATCCAGGCCA	TCGTGTTCCA	GGCTTCCACA	480
	TTTAAATTGG	AGAACGGGAC	AGACTGCTCG	GTGACTTGCT	GGGGTGACT	CAAAAGAGAT	540
	GAGGACTCTC	CACTCTCCCA	CACCTCTGCA	GAAGTTGAG	TGCGCTAT	AAACACTGCT	600
	ATGTGCAAC	ACCTCTCTCT	CAGTACAGT	TTCCGCAAGG	ACATCTTTGG	AGACATGGTT	660
	TGTCTGGCA	ATGCCCAAG	CGGGAGAGAT	GCTCTCTTGG	GTGACTCAGG	TGGACCCTTG	720
10	GCTGTAAACA	AGAGTGAGCT	GTGTGTACAG	ATTGAGATCG	TGAGCTTGGG	AGTGGGCTCT	780
	GTTCGACCA	ATCTCTCCCA	TTCTTACAC	ATATATCAAC	CCACCTTGA	GTGTATCGA	840
	AGGCTGATGG	CCGAGATGGG	CATGTCCAC	CCAGCAAGCT	CTCGGCACT	ACTCTTTTTC	900
	CCTCTTCTCT	GGGCTCTGCC	ACTCTCGGG	CGGCTCTGA			

Seq ID NO: 138 Protein sequence

Protein Accession #: Eos sequence

	1	11	21	31	41	51	
	MGARGALLLA	LLLRAGLRK	PEQEAAPLS	GPCRRRVITS	RIVGGEDAEI	GRMPWQGSRL	60
	LMDSHVGVS	LLSHRWALTA	ARCFETLSD	PSGHWVQFG	LTPSMFWSL	QAYTRYFVS	120
20	NIYLSRYLKG	NSPDIALLVK	LSAPFTYTR	IQPIQLQAST	PEFENRDTDC	VTWGYITKX	180
	ELSPSPHTLG	FVDAIAHNS	HNSLFLKYS	PRDIIPDHY	GGDAAGGGD	ACFGDGGDFL	240
	ACKNGLATGY	IGVSNWVGC	GRNRPQVIT	NIISHFENIQ	KMAQSGMSG	PDPSPHLLFT	300
	PLLWALPLLQ	FV					

Seq ID NO: 139 DNA sequence

Nucleic Acid Accession #: NM_014344

Coding sequence: 131..1444

	1	11	21	31	41	51	
30	CGCGCGCGGA	TGGGCGCGAA	GCUCCGCGAG	CCCCCGAGCC	CACAAACTGC	CGGGCCCCGC	60
	TGCGCGCGGG	GACCGCGGTG	CTGGGCGCTG	GCTTGAAGCG	CGCGCGCGGC	ACCGGCGACG	120
	CGCGCGGAGC	ATGGCGGAGA	GGATGCGGGG	CGCGCCCGCC	ACCGCGGGGC	TCGTGCTGCT	180
	GGCGCTCGCG	TGGCTGCTGG	CTGTGGGCTG	AGGGCTGTGC	CGCGCGCGGC	CGGAGCTGCG	240
35	CGCTCGCGCG	CGCGCGGAGG	ACCGACTGCC	ACCGCGCGCC	GCGCGGAGCG	CGCGCGCGCC	300
	CGCGCGCGCT	CGCTTCCCTC	TGCGCCCGCG	CGTGGCGTGG	GAGCGCGCGG	CGCGCTCCCT	360
	GAAGAACTTC	TGGGCGCTGC	TGACCTCTGG	CGCGCGCGCG	GACGCGCGCG	CGCGCTGCTG	420
	CGGAGCGGAG	CGCGCGCGCG	CAGCGCGCC	CGCGCGCGCG	CGCGCGCGCG	CGCGCGCGCG	480
	GTTGCAACGG	GGGCTCTTCT	GGAGCGCGCG	CGTGGAGGAG	CAGGTGCCCC	GGGCTTTTTC	540
40	GAGAGCCGAG	CGCGCGCGCT	GCTGTGAGCG	GGCTCGCGCG	GCGCGGATGG	TGGGCTCTGA	600
	CGCGCGGGAT	TGGGCGCGCA	GCTCGCAACG	ACTGGCGCTG	TTTGGCGAGC	GGAGCGCGCG	660
	CTGTGCTGCG	TGGGCGCGCG	CGTGTGAGCG	GATTCGAGCG	GAGGCGCGCG	CTTACTATCT	720
	GGCGCGCGCT	CTGGGCGCTC	AGCGCGAAGT	CGCGCGCGTG	GCACTGGCTC	GGGTGGAGCG	780
	TGGGCGCGCG	CAGTGGCGCG	AGGTCGAGGA	GAGCTGCGCG	CGTGGCGCAT	GGAGCGAGGG	840
45	CGAGCTGGTG	AGCTTCAGAC	CGTGGCTGCC	CAACTCTAGC	GACCTGTGGT	TGCGCGCGCG	900
	CTGAGCTTGG	GAGGAGCGCG	GTTCGCGCTG	CTCTCGGCTG	CGCGCGCGTG	AGCTGGCGCA	960
	CCTCAGCGAG	CGGAGAGCTGG	TGGACTTAAT	ACAATGGAGC	GACTTAATCT	TTTTGGACTG	1020
	CTGAGCGCGC	AACTTGCAAC	GGCTCTTAAG	CAACTCTTCT	AGCTCTCAGT	GGAGCGCGCG	1080
	CTCARTGAG	CGTGCACACA	GCAACTTGA	CGCGCGTGG	CGCGCGCGCG	TGGTCTTCTG	1140
50	GGCAATGAG	CGCGCGCTGG	TGCAACGCGTA	CGCGGTAGCA	GGCATTTGGG	ACAGTATATA	1200
	CAGCGCGCTG	TTGACTTCAG	TGTGCTGTGT	CGCGAGCGCG	ACCGCGCGCG	GGTCTCTGGA	1260
	GCTTGACCGC	GGACGAGGCG	CGCGCGCGCG	GCTGTGCGCG	CTCTTACCGG	CGCAACGAGC	1320
	TCCTCTGCC	GAGTGGCGCG	CGTGTGAGCA	CGCCCAAGCT	AGAGCTCTAC	AGCGCGCGCT	1380
	CGACTTCTCT	CGGACGACA	TTTTGCGTA	TAAGGCGAAG	TACGCGCGCG	GGTCTGGGAC	1440
55	TAGTGTGAC	CGGAGGAGAA	AGAGAGAGAT	CTGGGCGCTG	GGTATGGATG	ATGGGGGGAA	1500
	GGGCGGTGCG	CTCTGCACT	GTGAGGAGCC	AGCGCGCGCA	CGCCCAAGCG	CAAGAGTGTG	1560
	TAAAGCTCT	AGCTTTTCTG	CGACGCTGCC	CTTTTCTTCA	ATCCGAGCTG	GTTCCTTCTC	1620
	AAAGTTCTGG	GAGGAGGAAC	TCACCGAGGC	GAGAGATGTA	ACATCTCTCT	CACCCAGCTT	1680
	ATAAAGAGAT	TCCTTACTGT	CGCAGCAACG	GGATGTGATC	CGAGAGAACT	GGCTACTGGG	1740
60	CTTTGGCGCC	GAGTGGCGCG	TCCTGTGGGG	GAATGACGCC	CAFTCTTGGG	CGCCCTCTAT	1800
	TCCTTTTGG	AAAGAGGAA	ACTCTGCTTT	GAGCGCTTGA	GCTATATCTG	CAATTTTCTA	1860
	CGAAGAGAGG	CGTGGTGGCG	CGCGGAGGAG	GGCTGTGACA	TTGGCTGGTG	GGGCGGCTTC	1920
	CTGTGTCTCT	CCTTGTGCTG	AGCGCGCGCA	TGTTGAGATC	ACTGTTTCAA	GAGCGGGAGC	1980
	GGCTGCAATC	AGGCAAGGA	CGGCGCGCGC	TCGCAAGCTC	CGCGAGGACTC	CGAGGACTCT	2040
65	ACAAATATCT	TGACTCATCT	CTGACCTCTT	GCTCATTTGT	CTCGAAGGCT	AGAAATTCAG	2100
	GGTCAGCTGT	ATGCACTAAG	TCAAAATATG	AAATTTCTTC	TCCTCTCTCG	AAACGACCAA	2160
	AATTTTGGACA	ACGATGATGT	TCACCAAGAG	GAAGAAAAAA	TGAGTTTAT	GACCTTTATT	2220
	TGTTTGTGAT	TTTCACTTTT	TATTAAGAGAA	AAATTTTAT	TACAGAGAT	TACCTTCTCT	2280
	GTATATATGT	GCATTAAGTG	TGGTGTAAAT	ATACTAACA	AACTTATAT	TCAATAAAG	2340
70	GGAGTTTAAA	ATTTAAAAAA	AAAAAAA				

Seq ID NO: 140 Protein sequence

Protein Accession #: NP_055159

	1	11	21	31	41	51	
75	WRRNRGAAA	TGLWLLLAG	SLIALWGLLL	SPRTFLPASR	PPEDRLPRP	ARRGGAPAP	60
	RFLFPPPLAL	DARGSLKFT	RALLTLAAGA	DDPFFGRSR	FRMEVSRQP	RPRSAVVG	120
	GVFMRGLLE	QVPFPGSEAG	AAAMLEAARG	ARMVALERGG	GRSSNRLAR	FADTRACVR	180
80	YGIMFQIQG	EALEYTLARL	LGLQHRVPRG	ALARVEARGH	QRHQVQELR	AAHRTFVS	240
	SLTRWRLRL	ESGLRPLRGL	AEGLVQVHT	DLILFDLYLA			300
	NFBLRLNPL	SLQMDPRVQG	RATSLHRRG	QALVLYDNE	AGLVHYRYVA	GNMKYNEFL	360
	LQSVCFVRER	TARRVLSEHR	QGDAAARLLR	LYRRIRPRFF	ELALADPFA	QLQRRRLDFL	420
	AKHILHCKAK	YGRSGT					

Seq ID NO: 141 DNA sequence

Nucleic Acid Accession #: Eos sequence

Coding sequence: 11..574

5	1	11	21	31	41	51	
	GTCCGCCAAG	ATGCTCGGCC	CAGTCCCTCT	GCTGTCTGCA	GCCGACGCTT	CACCTCTTGT	
	CTGTGGGAAA	TGCTGTACAG	ACTCTTGCCG	ATGCTGTGTAT	GTACGCAAGG	ACGAGAGCTAT	120
	CAATGACCCG	GCTGGCAGGT	ATGATAGGAA	GCGCTCTCTG	TCACAGGATT	CATTCCGAGA	180
	CAATGACCCC	AAATGCGCTGT	CCTGCTGCCC	CCCAACCCCC	AACATCAAAA	TAGCCGAGAA	240
	AAATGCGCTT	CTCGAGACCA	AAATGTGTGT	GATGCTCTAC	AATCAGAAAAT	TCTTACAGTG	300
10	GCTCGAGCTT	TCGACACCTA	AACGCAAGG	TGTATGATCC	TATTCTCTGG	ATTATAGGCC	360
	TTCCAGAGGA	AGAGAGTGGG	CTCGACAGC	ACCAAGCACG	AGATATCAT	ATGGAGCTAT	420
	CACCAAGAG	AGAGACTACT	GCGCGAAGA	CACAGCATTC	GAGAGCTGGA	GAGAGAGAGG	480
	TTTCCGAGTG	GCTTTAAGC	TTGCTGTGCT	TGCTATTTC	ATCATTTGG	TGTTTGTCTA	540
15	CCTGAGCTGT	GAAATATAGT	CCTGTGTTGG	TTAAGTAATT	TAGG		

Seq ID NO: 142 Protein sequence

Protein Accession #: Eos sequence

20	1	11	21	31	41	51	
	MPAPVPLLSA	AQSPSPCMGK	ESTDFCPWLY	VRTDRASNDP	AGRYDRKPLL	QSDSPDPNDP	60
	KCLSLPPFP	NIKIAEKNAL	LGAKVVMVP	NKQFLQWPEA	STTKRRANVT	KCLDIKPSKG	120
	RHWABAPST	RITVGTITKSE	EDVCAEDQTI	ESMRSESPFV	GUKLALGLIF	IIVVYVLTLY	180
	EHKSLFG						

Seq ID NO: 143 DNA sequence

Nucleic Acid Accession #: XM_050163.6

Coding sequence: 39..365

30	1	11	21	31	41	51	
	GATTCTACCA	TCGAAAAGAA	GCGCAAACTT	CTATCATCAT	GGTGGATGTG	AAGTGTCTGA	60
	GTGATCTTAA	ATTGCAGAAC	CAACTGTAGA	AGCTTGGAAT	TTCACTGGCC	CCAATACTAC	120
	CTTCCACAGC	AAAGTGTAT	GAAAAAAGAT	TAGTACAGTT	GTGTGTCTCA	GCTCCCTGTG	180
	CAACCACTGT	GATGTGATG	CGAGAGAGC	TGATGATGAT	GCACGACAGT	GATGACAGCG	240
	AAAGTGGCTT	CGAAGAGCAC	CAAGCAACG	AATCATATAT	GGGATATCA	CCAAAGAGAG	300
35	AGACTACTGC	GCGGAAGAAC	AGACTATCGA	GAGCTGGAGA	GAGAAGGTTT	TCCCAAGTGG	360
	TTCAAGAGCTT	GCTGGCTGTG	GTATTTTCAT	CATTGTGGTG	TTTGTCTACC	TGACTGTGGA	420
	AAATATCTGT	CTTGTGTGTT	AGCTAATTTT	GAGCAAGAAC	AAATCTCAAC	CGACAGCTCT	480
	GCTCTTCACT	AAAGAACCAA	AACACTATCT	TGAAGGCCCA	GCGTACGCTG	CGACCTCTGG	540
	TTGCGAGGAG	ACCTTCCCTT	CACCTGTGCT	CTCTCACAGA	TCGGTGTCTG	GGCTCAGCCA	600
40	GCTGGAGAGA	CCTTCCCTTA	CGAGGCACTT	GTGTTAAGAG	CATGATGTTT	AGGAATATCC	660
	CCAAGTCATG	TCAGACTCTA	TTAAAGGTG	TTCCATATTT	GAGCGAGGCT	CAAC	

Seq ID NO: 144 Protein sequence

Protein Accession #: XP_050184.1

45	1	11	21	31	41	51	
	MYDVKLSDC	KLQNLKELKG	FSPGPILPST	ARKLYEKLQV	LLVSPPCAPP	VNNGPRELDG	60
	AQSDSDSEGG	KLQSHQAPESH	MLSPKRRKTT	ARKRLSRAG	EKKVSQMA		

Seq ID NO: 145 DNA sequence

Nucleic Acid Accession #: NM_002204.1

Coding sequence: 74..3229

55	1	11	21	31	41	51	
	AGGTGAACAG	GTCTCTACGC	CCAGCTCCGC	CCCTCTCAGC	GCTCTCGCCG	GGACCCCGCT	60
	TCCCTCTGGA	GCGATGTGGC	CCGGCCCCAG	CCCGCGCCGC	CCCGCCCCGC	GCTCTATGCT	120
	CTGTGCGCTC	GCTTGTATGG	TGGCGCGCGG	CGGCTGGGTC	GTCTCCGCGT	TCACACTGGA	180
	TACCCGATTC	CTGTGTATGA	AGGAGCGCGG	GAAACCCGCG	AGCGCTCTCG	GCTACTCGGT	240
60	CGGCTCTCAT	CGGCGAGAGC	AGGCGGACGA	GCGCTACTGT	CTCTTGGGCT	GTGCTCCCGG	300
	CGAGCTCTCT	GCATATGCTC	ACTGACGACG	CCGAGCTGGT	GCTGTCTACC	TGTGCCCCAT	360
	CACGTGCCAC	AAGGATGACT	GTGAGCGGAT	GAACATCACTA	GTGAAAAATT	ACCTGTGCCA	420
	TCACATATTT	GAGGACATAT	GCTCTTGAGT	GACTGTGGCC	AGCCAGGCGC	CTGACAGGAG	480
	AGTTCTTGCT	TGTGCCACCC	GCTACAGACCA	GCTGTGCTGA	TCGAGGCTAG	AAGGACAGAG	540
	GCGCATGTGT	GCATATGCTC	ACTGACGACG	CAATGACCTA	GAGCTGAGAT	CCAGTATAGA	600
65	CTGCGAGAAC	TACCAACAGC	AGATATGCAA	TAGCAACACA	GACTACTCGG	AGAAGGGGAT	660
	GTGCGAGCTG	GCGACAGCGG	GTGGCTTCA	CCGAGACACT	GTGTACTCTG	GCGCCGCCGG	720
	TGCTATACAC	TGAGAAAGAA	AGACATCACT	GATTCAGGCG	AAGAGATGGG	ACTTATCTGA	780
	GTATAGTTAC	AAGGACCCAG	AGGACCAAGG	AAACCTCTAT	ATTGGGTAGA	CGATCGAGGT	840
	AGGCAGCTTC	ATCTCGACCC	CCAAAACACT	CACCATTTGT	ACAGGTGCCC	CAGCGGCAAG	900
	ACATATGGCG	CGGTGTCTCT	TGCTGAGCCA	GAGGCGCAGC	GAGAGACTCG	GGAGGAGGCA	960
70	GCTGTGCTG	CTGTGCGACC	GGGGGCGCTA	CTTGTGCGAC	CGAATTGCCC	TGCGAGAGCT	1020
	GAACATGAT	GGGTGGCAGG	ACCTCTGTGT	GGGCGCCCCC	TACTACTTGG	AGAGGAAGAA	1080
	GGAAGTAGGG	GGTGCCATCT	ATGTCTTCA	GAACAGGCG	GGAACTGCT	TCCCTGTCTA	1140
	CCGCTCACTC	CTTCTTCAAG	CGCCGAGTGG	CTGTGCGTTT	GTTTTATCTG	TGGCGAGCAT	1200
75	TGTTGATCA	AAAGGCTCTA	TATGTGCTGA	TATGTGCTGA	GTGATCTGCT	TGAGAGCTCT	1260
	GCGCAATGAG	TACATATATC	ACGTGAGCTC	TAAAGGCGCT	CTTAGACAGC	CCGACGAGCT	1320
	AATCCATGGA	GAGAGAGCTG	GACTGCTGCG	GTTCGGCCAT	TTGCGCTATT	CCCTCAGTGT	1380
	CGAGATGGAT	TGGATAGAGA	GACTCTTACC	AGACTCTTCA	TTGGGAGAGC	TGTCAGACCA	1440
	CATTTGCTGT	CGTGGCGACC	GGGGGCGCTA	CACATGCTGT	CGAATGAGCT	TGCTGGCGAG	1500
80	GCGAGCTGTG	CTGAGCCCTG	CACCTTTCAC	GGGCACTCTT	TGTGTGCAAG	TGAGAGCTGT	1560
	CTTTGCTTAC	AAACGAGTGT	CCGGGAAACC	CAACTACAGG	CGAAACATCA	CCCTGGCGCTA	1620
	CACCTGTGAG	AGCTTCCAGG	ACCGCGCGCC	CGCCCGGCTG	CGCTTTGGCG	CGAGTATATC	1680
	GCGTGTCTTG	CGAGGCTCTA	TCTCATGCTG	CGAGGCGGCT	TGCCAGAGCG	TGAGAGCTGT	1740
	CCTGATGGAC	AACTTCCAGG	ACGAATCTCG	CCCAATCATC	ATCTCTGACA	ACTACTCTGT	1800
85	ACCTTTGCGG	ATGCGCGATC	GCGCCCGGCT	GGGGCGCTGG	TCCCTGGAGG	CTCAACCGAT	1860

	CCTCAACAG	GCACAGGCTC	TGGAGAAACA	CAGTGAAGTC	CAGTCTCCAGA	AGGAGTGAGG	1920
	CGCTGACAC	AAGTGAAGA	GTGAGGAGCA	GAATGCTTCCA	GCTCTCTCTG	CAGAGAGTCA	1980
	CGAGAAGCTG	AGCGAGCTCC	AGTACGACAG	AGA.CGTCCGG	AAATGTCTCC	TGAGCATCAA	2040
	CUTGAAGAAC	ACCGGAGCTC	GGGAGGAGTC	CGGGAGGAGC	GGCCACGAGG	GGCTGCTCAC	2100
5	CGTGTGTGTG	CCTTCGCGCC	TGCTGCTGTC	CTCAATGTGCG	CCCGCCGGGG	CGTGCACAGG	2160
	TAATGAGAGC	ACTTTGGGGA	CCTCTGGGAA	CCCTTCCAAA	CGAGAACGAA	GGATGGAGCT	2220
	GCTCATCGCC	TTTGAAGTCA	TCCGGGTGAC	CGTGCACACA	AGGAGCTTCC	AGGTGCAAGT	2280
	CGAGCTCTCC	AOSTGAGTCT	ACCAAGACAA	CCTGTGGCCC	ATGATCTCTCA	CTCTGCTGTG	2340
	GGACTATACA	CTCCAGAGCT	CGCTTAGCAT	GGTAATATCAC	CGGCTACAAA	GCTTCTTGGT	2400
10	GGGAGCAGTA	ATATGATGAA	AGCTGTGGAG	AGTGTATGGG	GGATATGGAA	GGCCCTTCAA	2460
	GTAATGATTC	CAGGTGTGGC	CAATGGGGGA	GGGCGTGTGT	GGCTTGAGGA	CGCTGGTCTC	2520
	AGGTCTGGAG	TGGCCCTACG	AAGTCAGACA	TGGCAAGTGG	CTGCTGTATCT	CCACGGAGAT	2580
	CACGCTGCAT	GGCAATGGGT	CTGGCGGCTG	CGGACGACCT	GGAGAGCTTA	TCACCCCTCT	2640
	CAAGCTCACT	CTTCTGAGAG	CTGAGACGAC	CGCATCATCC	CAGACAGGCA	GGGCGGCG	2700
15	GCTGGATCCA	GGGGGAGGCC	AGGGGCCCCC	ACCTGTCACT	CTGGCTGCTG	CCAAAAGAGC	2760
	CAAGCTGGAG	ACTGTGCTGA	CTGTGGCCAC	AGGGGCTGCC	CAGTGTGTGT	GGCTAGAGTG	2820
	CGCCATCCCT	GATGCCCCCG	TGTGCACCAA	CGTGAAGTGT	AGGGACAGAG	TGTGGAACAG	2880
	CGACTCATC	AGGAGAGGCC	GCACCTCCGA	CTAATPSTCT	GGGCTACCTC	GGGCTACCTC	2940
20	ATCTCTCCGA	ACCGAGATCC	CCACCATCAA	CATGAGAAC	AGAGCAAGT	GTTTCTCTGT	3000
	GGACATTGAC	TGGAGGCTGG	TGGAGGAGCT	CGCGCGGAAA	ATCGAGCTGT	GGCTGGTCTG	3060
	GTGGGGCTGT	GTTGACGGGC	TGCTGCTGTC	GGGCGTGAAT	ATCTCTCTCG	TGTGGAAGTG	3120
	CGGCTCTTC	AGGAGAGGCC	GCACCTCCGA	CTGTATGAAA	CGTAAAGAGC	AGAAAGGCGA	3180
	GATGAAGAGC	CAGCGCTCAG	AGACAGAGAG	GCTGACCGAG	GACTACTGAG	GGGCGAGGCC	3240
	CCCGCCCCCG	GGCCACTGGT	TGTGACTCTT	TTAAGGGGAC	CGCTATTAT	CAGATCATCG	3300
25	CCAGATPACA	CGCATGTGGG	ATCCGGGGAG	AGGAGCGGTA	CCCACTTCCA	CAGAGAGGCC	3360
	TGCGGACAA	GAACACCTGG	GTACCGAGCT	GGAGAGCTCT	GGATGACGAC	TACTGATCTC	3420
	CTCCCTGATC	CACACCGGCT	CTCCCGCAGT	GTCCCTCTTC	TTCTATTATTA	TCATAGTTTA	3480
	TGCTCTGAC	AGTCCACAGC	GGCCACACCC	TTTGTCTGGT	AGCAGCAGGC	TCAGACACAT	3540
	ACACCTGTTC	AGAGAGATTC	ACATGCTGTG	TGGCCCTGGG	GATCTTCTCA	CAGAGAGGCC	3600
30	AGGCTGTGG	ACCTTATGAG	CGCGAGACGA	CTGCATCTGT	GTGCCCTCTG	TGACATCTGG	3660
	GGCCACTGCT	AGTGTGAGCT	GCTGTGTGAT	CACGATGTGT	GCAATGGGCT	GGCGTGTCTC	3720
	AGGCTCTGCC	AGGCGGAGCG	CCRAAACCAAG	CCAAAGAGCC	TCCCAACAGA	GGCGGAGGGA	3780
	AAAGGCGCTT	GCAGATGTGT	GACACCTCTCC	CTTCTCACAC	TGATCTCCAT	CTGAGGCCA	3840
35	CGTCTCATC	ATGACTTTTG	CTATCAAGAA	TACTCAAGAG	GAGACGAGCC	GGGCGGCTGC	3900
	CGTGTGGGCG	CCCCAATTGA	CACCATATGC	AGAGAGGTGG	GGATCTCTCC	TAAAGTGTCT	3960
	TACGGGGGCA	CTTGGAGAGC	CTGGCGTGTG	CAGACCCCAAC	AGCAAAAGAA	CTAGAAAGAA	4020
	GGACCCGAA	GGCTGTCTTT	CTGTGAGGCT	CTGTGAGGCT	CTGTGAGGCT	CCAGAGATCT	4080
40	AACTCGAGAG	GATGTGCAGC	GGAAGGAACA	AGACAGGCGA	AACGCGCAAG	TAGCTGGGCG	4140
	TCACTGTCTG	GGGCGATGGC	GGGATCTCTC	ACAGAGAGGA	GGGAGCAAT	CTCGAGACGA	4200
	CAGATGTTTG	AGAGTATGAG	AGGAGATGCC	ACTTCTCACT	CACCATCAAC	AGGACAGCTC	4260
	CGAGAGGCC	CAGAGAGGCT	CTTGAAGGAG	ACGGAGAGGC	CTGACAGCTG	ATATGTATGA	4320
	TAGCAGAGGG	GGCGTCCAC	CCCATCCGAG	CAGACCCGAC	CTGAACTGAT	CGTCAAGGCG	4380
	CTAGAGGTGG	AGTTCTTAGC	TATCTTGGCG	TTTCTGTGCC	AGGCTGGCTC	TGCCCTCTCC	4440
45	CCATGGGCTG	TGTCTTAGGG	CCCATTTGAG	AGGCTGAGGC	TAGTTCCAAA	AACCTCTCTG	4500
	GACCGCTAC	TGTGGGAGC	CCACTGCCCA	CGGCGAGGCC	CTTCCAGATG	ACTCTGAGAG	4560
	GGGAATTCOC	TCCCCTCTCT	TGTGCTTTCT	TTTGTATATG	GCTTCTCAAC	CGACACATA	4620
	AACAGCTCCC	AGTTTGT					

Seq ID NO: 146 Protein sequence
Protein Accession #: NP_002195.1

	1	11	21	31	41	51	
50	MDPGPSRAPE	LPRLMLCALA	LXVAAGCGVV	SAPHLDTPL	VVKEAGNPGS	LPFGYSVALIR	60
	QTRQQRYL	LAPARELAV	PDGTYNRTGA	YVLCFLTAH	DDCERNMITY	KNDPHHIE	120
55	IMHVLQTVAS	QDGAQRVLVC	AHRYTQVLAS	GGSDGRVMVG	KCYVRNDILE	LDSDSDQWY	180
	RNMCMSTDT	YLETGQGLG	TSGGPTQWY	TPGAPADNM	KMSYPIATRK	ENDLSSTGK	240
	DPEDQNLVI	GTYNQWSEFI	LEPDNITITV	GAPRHRBMGA	VFLSLQEPAG	DLRRRLVLEG	300
	SQVQYAFGSA	IALADLNNDG	WQDLVLQGLY	YFERKEFVGQ	AIYVFMQAG	TSPFAPHSLL	360
	LVGVSIGSAP	LGVASIGDIN	QDQPDQIAG	APFEDIGLKV	YHSSSEGLIK	RQKQVTHSE	420
60	ELGLKATPE	QVLSQVSLVA	DSNFPLDLY	QSLSDHLY	RARVLDHVI	CTLPFRATV	480
	DPALCTATSC	VOVLECPAVN	QKAGNPHYTR	NITLALYTEA	DRDRRPPRLR	PAGSESAVPH	540
	GFPSHPKRC	OKLELLAMN	LKDKLAPLII	SMYSELPM	PDRPRLGLRS	LDAYFILNQA	600
	QALNTEFTVQ	FOKSCSPDKC	CENLHMRRA	PVSGDQRLK	RLQYSRDKVK	LLSHVITLQ	660
	FTSERGGDA	HEALLLQVPL	PALLLSVPLP	PGKQGNMSTI	PCSLGKQVST	HQMSHELLP	720
65	EVIGVTLIAR	DLQVQLQSLT	SSQGNLDMFM	ILLTLVDYTL	QTSLSMVNHR	LSFGFGVTVM	780
	GESMGKTVED	VGSELKYEYF	VOVMGEGVLG	LQTLVLGLEH	PIEVBNHGM	LYTFEITVHG	840
	NGSMPCRPD	DLINPLNLTL	SDQDRPESP	QRKRKLQDP	GGQGFPPFTV	AAAKSAKST	900
	VLCATGDM	QWLSGSLPD	APVTVTVYK	AKRREITVE	DTQDPRPV	NHMTLFLST	960
70	SIFTIMKMK	TWFSVDIDS	ELVSELPARI	ELMLVLVAVG	AGLLLLGLII	LLAKCGPFPK	1020
	RARTRALYA	KRQKAKMSQ	PSETERLTD	Y			

Seq ID NO: 147 DNA sequence
Nucleic Acid Accession #: NM_005501.1
Coding sequence: 74..3274

	1	11	21	31	41	51	
75	AGGTGAAGAG	GTCTCTACGC	CCAGCTCCGC	CCCTCTCACG	GCTCTCGCGG	GGACCCCGCT	60
	TCGCTCGACA	CGCATAGGCC	CGGCGGCCAG	CGCGGCGGCC	CGGCGGCCAC	CGCTGATGCT	120
	CTGTGCGCTC	CGCTTAATAG	TGGGCGCGGG	CGCGCTCGGC	GTCCTCTCTC	TCACACATCT	180
80	TACCCGATTC	CTGTGTAGTA	AGGAGCGCGC	GAGCCCGCGC	AGGCTCTTCG	GCTACTGTGT	240
	CGCCCTTCAT	CGGACAGACG	AGGCGGACGA	CGGCTACTGT	CTCTCGGCTG	CTGCTGCTGT	300
	GGAGCTCCGT	GTGCGCGATG	GCTACACACA	CGGAGCTGCT	GCTGTGTATC	TGTGCCACAT	360
	CAGTGCACAC	AGAGACATCT	CTGAGAGGAG	GACATCATCA	GTGAAATGAT	ACCTGCCGAC	420
	TCACATATTG	GAGGACATGT	GAGTGTGAGT	GACTGTGCGC	AGCCAGAGCG	CTGCGGACAG	480
85	AGTTCTGCTG	TGTGCCACAC	GCTACACCCA	GGTGCTGTGG	TCAGAGTGAG	AGAGACAGGG	540

	GCACATGGTG	GGCAAGTGTCT	AAGTGGCAGG	CAATGACCTA	GAGCTGGACT	CCAGTGATGA	600
	CTGGCAGACC	TACCAACAAG	AGATGTGCA	TAGCAACACA	GACTACCTGG	AGACGGGAT	650
	GTGTCAGCTG	GTGTCAGCTG	GTGTCAGCTG	GTGTCAGCTG	GTGTCAGCTG	GTGTCAGCTG	700
5	TGCTATCAAC	TGGAGAGGAA	ACAGCTACAT	GATTCAAGCG	AAGAGGTGGG	ACTTATCTGA	750
	GTATATTATC	AGGACCCAG	AGGACCCAG	AAACCTCTAT	ATTGGGTACA	DGATGACGGT	800
	AGGCAGCTTC	ATCTCGCATC	CCAAAATAC	CACCATTTGT	ACAGGTGCCC	CAGGACACGG	850
	ACATATAGGC	GTGTCAGCTG	TCTTAGAGCA	GGAGAGAGGC	GGAGAGAGGC	GGAGAGAGGC	900
	GGTCTGGAG	GGCTGCGAG	TGGGGGCTTA	TTTTGGCAGC	GCAATTGGCC	TGGCAGACT	950
	GAACAATGAT	GGTGGGCGAG	ACCTCTGGGT	GGGGGCCCCC	TACTACTTGG	AGAGAGAGAA	1000
10	GGAGGTAGGG	GGTTCGCATC	ATGTTCTTAT	GAGCAGAGCG	GGAACTCTCT	TCCTCTGCTCA	1140
	CCCTCTGACT	CTCTCTGAG	GGTTTATGTT	GGTTTATGTT	GGTTTATGTT	GGTTTATGTT	1200
	TGGTGACATC	AACCAAGATG	GATTTCAGGA	TATTGGCTGT	GGAGCTCCGT	TGGAAGCTGT	1250
	GGCGAAGTGT	TAGACTATTC	ACAGTAGCTC	TAAAGGCGCT	CTTAGACAGC	CCGACAGAGT	1300
	AATCATGGA	GAGAGTCTG	GAGTCTCTGG	GTGGGACAC	TTGGGCTATT	CCTGACGGT	1350
15	GCAGATGAT	GTGATAGAA	ACTCTTACG	AGACTTCTTA	GTGGGAGGCC	GTGTCAGACCA	1400
	CATTGTGCTG	CTGGGGGCC	GGCCAGTATC	CAACATGCTC	CACAGACCT	TGGTGGCAG	1450
	GGCAGCTGTG	CTGACAGCTG	CACCTTGGAC	GGCCACCTCT	TGTTGGCAG	TGGAGCTGTG	1500
	CTTCTTCTAC	ACACAGATG	CCGGAGACG	CACTACACAG	CCCTGGCTCA	CCCTGGCTCA	1600
	CCCTGGAG	CTGTCAGGG	ACCGCGGCC	CCCGCGGCC	CCCTGGGCC	CCCTGGGCC	1650
20	CCCTGCTCTC	CAAGGCTCTC	TCTCATGCTC	CGAGATGGCC	TGGCAGAGC	TGGAGCTGTG	1700
	CTGATGAGAC	AGCTTGTGCT	ACAAATCTCG	CCCATGATC	ATCTCCATGA	ACTACTCTTT	1840
	ACCTTGTGCG	ATGCGCATC	CCCTCGGCTC	GGAGTGGGG	TGCTTGGAG	CCTACCGAT	1860
	CCTACACAG	GCACAGCTG	TGGGAGACCA	CAGTAAAGTC	CAGTAAAGTC	AGAGTGGAG	1920
	GCCTGACAC	AGTGTGAGA	GCACATGCA	GATGGGGCA	GCTTGTGT	CAGAGGACGA	1980
25	GCAGAGCTG	AGCAGCTCC	AGTACAGAC	AGAGTCCGG	AAATGCTCC	TGAGATCAAC	2040
	TTGAGACAC	ACCGGACCT	CCGAGAGAC	CCGAGAGAC	CCGAGAGAC	CCGAGAGAC	2100
	CTGATGGT	CCCTGCTG	TGCTGCTG	CTGATGGT	CCCGCGGG	CCCTGCTG	2160
	TAATGAGAC	AGCTTTTGG	AGCTGGGGA	CCCTCTCAA	CGAGACGAA	GGATGGAGT	2220
	GGCTCATGCC	TTTGGAGCA	TCGGGGTAC	CCGAGAGAC	AGGAGACTTC	AGGTGAGCT	2280
30	GCACATCTG	AGTGGAGCT	AGTGGAGCT	ATGATCTG	CTCTGCTG	CTCTGCTG	2340
	GCATATACA	CTGACAGCT	CCCTTAGCAT	GTTAAATCAC	CGCTACAAA	GCTTCTTGG	2400
	GGGAGCAGT	ATGGGTGAT	CTGGACGAA	AACTGTGGAG	GATGTAGGAA	GGCCCTCTAA	2460
	GATGATATTC	CAGTGGGAC	CAATGGGGGA	GGGGTGGT	GGCTGGGGA	CCCTGCTGCT	2520
35	AGGTCTGAG	TGGAGTCTG	AGTGGAGCT	CTGCTGATG	CTGCTGATG	CTGCTGATG	2580
	CACCTTCCAT	GGCATATGG	CTCTGGCTC	CCACCATCT	GGAGACCTTA	TCACACTCT	2640
	CAACCTCAT	CTTCTGACC	CTGGGGAGAC	GGCATCATC	CCGACGCGA	GGCGCGACCA	2700
	CCGAGTCA	GGGGGAGCC	AGGGGGCCCC	CCCATGACT	CTGGTCTGT	CCAAAAGAGC	2760
40	AGCTCTGAG	AGCTCTGAG	TGAGAGAGCT	AGGGGTGCTC	CACTTGTGAC	CTGAGTGGT	2820
	CCCATCTCT	GATGGCCCC	TTGTCAACCA	CGTACCTGT	AGGACGAG	TGTGGAGAC	2880
	CACCTTCATC	GAGGATTACA	GAGACTTTGA	CCGAGTCCG	GTAATGGCT	GGGCTACCT	2940
	ATTCTCTGCA	ACGACATCC	CCACCATCA	CATGGAGAC	AGACATGCT	GGTTCTCTGT	3000
	GGAGCTTAC	GAGCTCTGG	ACCATATCA	CTGCTGCTA	ATGAGCTCT	GGCTGCTG	3060
45	GGTGGCTGG	GGTGGAGGC	TGCTGCTG	GGGGCTGATC	ATCTCTCTG	TGTGGAGAGT	3120
	TGACTTCTTT	AAAGGAGCC	GCTATATACA	GATCATGCC	AAATACACG	CAGTGGAGT	3180
	CCGGAGAGAG	GAGCTGTAC	CACCTCCAG	GAGCAGCTG	CCGACAGCA	AGCATGGT	3240
	GGCAGCTGG	CAGCTCTGG	ACCATATCA	CTGCTGCT	CCGATGCC	ACCCCTCTCT	3300
	CCCGAGTGT	CCCTCTTCT	CTTATTATC	ATAGTTATG	CCTGACAG	TCCACAGGG	3360
	CCACATCT	TGGTGGT	CAGAGAGCT	AGGACATAC	ACCTGCTCA	GAGCATGAC	3420
50	ATCTCTGCT	CCCTGGGCA	TCTTCCACA	GGAGGCGAG	CGTGTGGC	CTTACAGAG	3480
	CGATGGCAT	GCATCTCTG	GCCTAGATG	CAGTGGGCG	CCATGCTG	TGAGCTGTG	3540
	TGGTGCATCA	CGATGGTGC	ATGGGCTGC	CGTGTCTAG	CCTCTCCAG	CGCCAGCGC	3600
	AAACAGAGC	AAAGAGCTC	CCACAGAG	CGGAGAGAA	AGGCGCTCT	AAATGTGTG	3660
	CACCTCCCT	CTTACAGCT	GATCATCTT	GAGAGCGCA	CTCATGGAT	TGATCTTCT	3720
	CTTAAACAT	CTGACAGGA	CGAGCCCCG	GGCGCTGCG	TGGTGGGCC	CCATATGCA	3780
55	CCATGCCAG	AGAGTGGGG	ATCTGCTGA	AGTTTCTTA	CGGGGGCACT	TGGAGGAGCT	3840
	GGGTGCTCA	GACCCAGAC	CAGAGGACT	AGAAAGAGG	ACCCAGAGG	CTTCTTCTC	3900
	TGATCTCTG	TGAAGCTCT	CTCTCTGGC	ACAGACTGAA	CTCGAGGGA	GTGACAGG	3960
	AGGAGACAA	GACAGGCAA	CGGCAAGTA	GCTCTGGCT	ACTGTGCTG	GGCATGGCG	4020
	GATCTCCAC	AGAGAGGAG	GGACCAATC	TGACAGACA	GATTTTGGG	GGATACAGG	4080
60	AGAGTGCAC	TTCTCATCA	CCATCATGAG	CGAGCTCCA	GAGGCCCCA	GAGAGAGCT	4140
	CGAGAGACA	GGAGGAGCC	GACATCTGA	TGTTATATA	CGGAGGCGG	CTCTGACCT	4200
	CACTCCAGCA	GAGCCAGCT	GAACTATGG	TCAGGGGCT	AGAGGTGGG	TTCTTATGA	4260
	TCTTGGCTCT	TCTTGGCAG	CCCTGGCTG	CCCTCCCCC	ATGGGCTGT	TCTTATGACC	4320
	CATTGAGAA	GAGTGGCTA	TCTTCAAAA	CCTCTCTGA	CCCTGCTCA	TTGGGAGCC	4380
65	ACTGCGGAG	CCGAGCTCT	TGCAAGTAT	TGACAGAG	GATCTCTCT	CCCTCTCTG	4440
	TGCTCTCTT	GTATATAGC	TCTTCAAGC	GACCAATAA	CAGTCCGAC	TTTGT	

Seq ID NO: 148 Protein sequence
Protein Accession #: NP_005492.1

70	1	11	21	31	41	51	
	NPDPGRAPR	APRLMLCALA	LAVAAGGCVV	SAFNLDTPL	VYKZANPQS	LPQSVALAR	60
	QTERQRYLL	LAPAGRELAV	PGYVNRCTA	YLPLCLTAH	DCBERNITV	KNDPGHIE	120
	ENMLGVTVAS	QPGAPRLVAC	MRITYQLVMS	GSDQRRWVC	KCYVRNDLE	LDSDSDQTY	180
75	ENHMSMTD	YLETKQCQLG	TSQGTPTNV	YFAPGAGNN	KNSYMIQRE	BWLSSETSY	240
	DFPDQNTV	CTMNGHST	LAPNITVIT	GAPSRHSHV	YFLSDSAGD	DLBRGRLG	300
	QWQVAGYPSA	IALADLNNDG	WQDLVGLAFY	YFERKEEVOG	AIYVFNQNG	TSFPAPHSLL	360
	LHPSGSAFQ	LSVASIGDIN	QDGPQDIAV	APFEGILQRY	IYHSSKGLL	RQPOQVTHG	420
	KLGLPLATF	GTSLSGNGG	DENFYPLLIV	GLSDHIVLL	KARPVNIVH	KLTVPRFVAV	480
80	DPALCTATSC	WYELCEAFN	GGAGNRYVR	HTLATATLA	DEBRAPFLE	PAGRSNIVH	540
	GPFNSWPRC	QKLELLLPD	LEKLRPIII	SPNYSPLRN	PORFRLGLRS	LDTPILMGA	600
	QALNHSIEGQ	FQKQEDPNK	CESNLQHRAA	FVSGDQKRLS	RLQYSRVRK	LLLSINVTM	660
	RTSERGSDA	HEALLTVLP	PALLSSEVR	PQACQANET	PCRLGPRFR	NGRMLLIAP	720
	EYVGLATK	DLQVLCAT	SESNVWGLA	ITLLVNTIV	GTSLSVNRR	LQSPSTVM	780
85	GESQNTYED	WSPLYCEYFQ	VPQMBGLVG	LGLTLVGLXN	PYEVSNIGWL	LYPTETVHG	840

NGSWPCRPFG DLINPLALTL SDGCDRPSST QRRRRQLDPO GGQPPPPVTL AAKKAKSET 900
 VLTCATGRAH CVMLECPIDP APVTVTVTVK ARVNVSTFIE DYRDBDRBVRV NGWATFLRT 950
 SIPTINMENK TWTFSDVIDS ELVELPARI ELWLVLAVG AGLLGLLGLI LLLWKCDFFK 1020
 RTRYQIMPK YHVRVIRESE RYPPGGSTLP TKRHVTSHQ TRQYY

Seq ID NO: 149 DNA sequence
 Nucleic Acid Accession #: NM_006424.1
 Coding sequence:

1	11	21	31	41	51	
1	1	1	1	1	1	
10	GGGGCCAGGT	TTCAGGCTC	GGCGCGCGCC	TCCATCCGAG	CACCTGCGGA	GGGAGCGCTG
	ACCATGCTCT	CCTGCGCCTA	ATTGGGAGAT	GGCCAGACCA	ACCCGAGATA	GTACCTCGAA
	GGGCGCGGAG	GTCCAGGCTC	GATTAAGACT	GAAGACACAA	CAAAACAGAT	180
	240	AACATGAGCC	CACCTGTAAAC	CAGAGATTGA	CTCTCGCCTC	CGCTACACTG
15	ATAGATGAGC	CCACTGAGGT	GGATGAGGAC	TGGACCTATC	CCACTCTCCA	GGAGCTGGGG
	ATCAAGTGTG	CAGAGAGAGA	CHCCAAAGGG	AGAGTTCTCT	GTTCCTTCCA	AGGGATATGG
	AGATGATTAT	TACTGAGAT	ATTCCTCAG	TTTCTTGAGT	GTCCACGAGA	TATTCCTGAT
	AGCSGCTTCC	AGCTGGTTGG	AGGAAAAATG	GGAGGACAGT	TCTTACGCAA	CAGCTCTATT
20	ATGTCCAAAC	CTTTGTGGG	GGTGTGATC	GGGGTGTCTG	TGACGCTCTT	GGTGACAGAG
	TCGACGACTC	CAAGCTTCAT	GTGTGTGAGC	ATGGTGTCTC	CTTCATGTCT	CAGCTTTCGG
	GCTGCCATCC	CCATTATCAT	GGGGGCGCAG	ATTGGAGGCT	CAATGACCAA	CAGTATTGGT
	GGCTCATCTC	AGGTGGGAGA	TCGAGTGAGT	TTCAGAGAGG	CTTTTGAGG	AGCCACTGTG
	CATGACTTCT	TCAACTGGCT	GTCCGTGTGT	GTGCTCTTCC	CCGTGGAGGT	GGCCACCCAT
25	TACTTCGAGA	TCATAACCA	GCTTATAGTG	GAGAGCTTCC	AGTTCAAGAA	TGGAGAGAGT
	GGCCGAGATC	CATCTACTAG	CATCCCTAAG	CCCTTCAGAA	AGCTCATTTT	CGAGCTGAGT
	AAAAAGTTTA	TCAGCAAAAT	TCGAATGAAC	GATGAAAAAG	CGAAAACAAA	GAGTCTTGTC
	AGAGTTTGGT	GCAAAACTTT	TACCAACAA	ACCCAGATTA	AGCTCACTGT	TCCCTCGACT
	GCTACTGACA	CTCCGCTCTC	CCTCTGTGTG	AGGATATGGA	TCCAAAACGT	GACATCATAG
30	ATATGACTCT	ACAAAGAGAA	CATCCGCAAA	TCCAGAGATA	TTCTTGAAA	TTTCACATCT
	CCGAGTCTTG	TCTGGGACAC	CATCTGTCTC	ATACTCTCCC	TGCTGTGCTC	TCTGGGTGTC
	CTGATCATGA	TTGTCAAGAT	CCTGGGCTCT	GTGCTCAAGG	GGGAGCTGCG	CAGTGTCACT
	AGAGAGACGA	TCAACACTGA	TCTTCCCTCT	CTCTTGTGAT	GTTTAGCTGT	CTACCTGGCC
	ATCTCTGTGG	CGTCTGAGAT	GACTCTGATV	GTACAGAGCA	CCTCTCTGTT	CAGCTCGGCC
	TTGACCCCCC	TGATTGGAAT	GGCGGTATTA	ACCAATTGGA	GGGCTTATCC	ACTCAAGCTG
35	GGCTCCACAA	TGGTGCACCA	CACCAACCGCC	CCCTAGCCAG	CCCTGGCAAT	1540
	GCATTGAGGA	GTTCACGATC	GATGCCGCTG	TCCTTCACAT	CTCCGCGATC	1560
	TGCTVGTGCT	ACCGATATCC	GTCTACTGCG	GTGCCCATCC	GGATGGCCAA	GGGGCTGGGC
	AAACATCTCT	CCAAGTATCG	CTGGTTCGCG	GTCTCTTACC	TGATCATCTT	CTCTCTCTCT
	ATCCGCGCTGA	CGGTGTTTGG	CCTCTGCTCG	GGCGGCTGCG	GGGTGCTGCT	TGTTGTCTGG
40	TTCTCCGCTG	CGTCTGAGAT	CGTCTGAGAT	CTCTGCTGCT	GTCTGCTGCT	GTCTGCTGCT
	CCAGCGCTCT	TGGCGAGAAA	ACTCCAGAAC	TGGCAACTCT	TGCCCGCTG	GATGCTGCTG
	CTGAGGCGCT	GGGATGCCGT	GTCTCTCAAG	TTCAACGGCT	GCTTCAGAGT	GGCGTCTGCT
	TACGTGCTCC	GGGTGCTGCT	CCGCGCGCTG	TGCTGTGCTGT	GTGGCTGCTCC	CAGTGTGCTG
	CGCTGCAGCA	AGTCTGCTG	GACGCTGGAG	AGGGCGAGGA	TGTCTCTCT	2040
45	AGGCTCTCTG	AGACTTTTGA	TACATATACC	ATTAGCAGAG	AGGCTCAGGG	TGAGTCTCTT
	GCTCTGGACT	CAAGAGCCGA	ATGCAAGGCC	TTGTAGGGGA	GGCCGAGAT	TGTCAAGGAT
	GGGGGGATGG	GTTCTGAGTT	TGCACTGCTC	TCTCTCCTCC	CAGTCTTCCA	CCCTTTCACC
	ACCTCGAGGA	GATTGTCTCC	CCATTAGCCA	ATGAATATGA	TGCACTCTTA	AAAAAATAAA

Seq ID NO: 150 Protein sequence:
 Protein Accession #: NP_006415.1

1	11	21	31	41	51	
1	1	1	1	1	1	
55	MAPPELQDA	QPNPKYLEG	AAQQQTAPD	KSKEIKNTDN	TEAPVTXIEL	LPSTSTATIL
	DEPTFVDYDP	NLPFLQDGI	KMSERDTRK	LLCPFGQGR	LILLLFLFVP	PVCSLDLLES
	APFLWQDMA	GQFFNNSIM	SNPLLLGLVIO	VVLVTVQSS	STSTSVSM	VSSSLVFA
	APIIINGANI	GTSTNTIVA	LQWVDRESE	RRAFAGATVE	DFPHMLVLV	LLPVEVATRY
	LEITQLIVE	SRPHNGEDA	VDLLKVTPTG	FTKLVLQKLD	KVLSQIANDH	EPARKESRLK
60	THCKTPTNK	QIETGAGAT	NCSTGSLCKA	DSIGTNTTVP	VTYKMLAK	QILPHNPLP
	DLAVOTILLI	LSBLVLQCL	IMVXLKLSV	LQKWQATVIE	KINTDFPFP	PANLTGTLAI
	LVGAGTFIV	QSSSFVPSAL	TPLIQIGVIT	ISRAYPLTLO	SNIGTTTTAI	LAALASPRHA
	LESLQIALC	HPFNNISGL	LWPTIPNTH	PIMAKGLQHL	ISAKYWEAV	PLIIPFPLI
	NLPVPLQLLA	QWVLTGCVN	PVFPFILLVL	CLLLGLQVHC	RVLQELQGN	NFLPMREIL
65	KPKDAVSKF	TGCPMKKCY	QCVVCRACL	LLOGCPKCKC	CSKCEDLISE	AGQDQVFFVK
	APETFDNITI	SREAGRVPA	SDSKTECTAL			

Seq ID NO: 151 DNA sequence
 Nucleic Acid Accession #: U11119
 Coding sequence:

1	11	21	31	41	51	
1	1	1	1	1	1	
70	ATGACCGGCA	GGCCACCGCA	CAGGCGGGGC	AGCGGCTGCC	TGGGCATAT	GGAGGTGAAG
	ACAGAGTGTG	GAGCTGUAAT	TGTTGTGTTT	TGCTGTGAAA	GATCAAAACC	TGGAAAATT
75	GAGAGTGTTT	ATGAGTATCT	ACACAGTGTG	CATTAAGATC	CCAGATGTGA	CGTTTGAGA
	GGCTATGCGC	AGACCCATGC	AGACTTACTA	CCATAAATA	ATGATGATTA	TTATCACTGA
	CGTGTTCGCA	GGGCCAATCC	ACTGCTTAGG	ATATTATATC	AAAGAGAGGA	AGAGAGAGAC
	TACAGTGCTT	TGTGTACAGA	CAGCTAATA	AAAGAGAGGA	ATGTTTAAAC	CAAGATATTG
	CCTCTTACAA	ACCATAGAAA	ATGTTTATTA	ATATCATTA	GATGCCCA	AGACTTGA
80	CTGTGTCTTT	CTATTATGA	CGGAGTATT	CTCCAGAGA	CGATCTGAT	GTAAGTCTT
	TACAAATAGC	AGCGAGAGAA	ACCCCTAGGA	TTCTACATTA	GGGATGGCTC	CAGTGTGAGA
	GTACACCAAC	ATGCTGTAGA	AAAGTTTCCA	GGGATCTTAA	TATCCAGGCT	TGTCCAGAGA
	GTCTGTGCTC	AAAGTACAGC	AGCTTATGAT	GTTAATATAG	AAATTTTGA	AAATATGAG
	ATAGAGTTT	CAGGAGAGG	CCCTGATCAA	GTACAGAGCA	NATGATTCC	AAATAGCGT
	AACCTCATCA	GTACAGTAGG	ACCGCAAAAC	CAGAGGAATA	ATGTTGTGAG	GAACAGTGT
85	ACTCTTGCCA	GTTCGGTCCA	GTCTACTGAT	AACAGCGCTC	TGCGTATACC	ACAGAGATT

GAACCAAGCT TTGAGCCGGA GATGAAGAC AGCAAGAGG ATGACATTAT CATTGAAGAC 900
 AATGGAGTGC CACAGCAGAT TCCAAAGCT GTTCCATAA CTGAGAGCTC GGAGTCATTA 960
 ACACAGATAG AGCTAAGCTT TGAATCTGGA CAGAATGGCT TTATTCCTCT TAATGAAGTG 1020
 AGCTTAGCAG CCGATGACAG CAGCTCAACG ACGAATATGA AAACACATGC TCCAGATCAA 1080
 5 AACTCTTAG AAGAAGATGG AACATCATA AACTATTA

Seq ID NO: 152 Protein sequence
 Protein Accession #: XP_030559

1 11 21 31 41 51
 10 MNKSHRHGAG SGLGTEHVK SKFOAEFRFP SLERSKPGKFP EEPYGLLQNV HKIPNVDVLV 60
 GYADIHGDLI PINNDNYHVK AVSTANPLLR IFIQKEEAD YSAPGTDTLL KKKVLTNVL 120
 RPNRHKRKH IVISNPKQFA PYSILIDVDL LPETRRVHL YKGTSEKLLD FVIDHSRVR 180
 VTRHLEKLV GTFISLQVGL GIAGSTGLLA VNDVLEVNG IEVSGSKLQD VTDMLANSR 240
 15 NLIITVRFAP QRNNVNRNS TSGSGQSTD NSLLGYPQOI EPSFEPEDED SEEDDILIED 300
 MVVQQIIFKA VPTNESLESL TQIELSPESG NGNPFISNRV SLAALASSNS TEFTHAPQD 360
 KLEEDGTII TL

Seq ID NO: 153 DNA sequence
 Nucleic Acid Accession #: NM_003064.2
 Coding sequence: 23..421

1 11 21 31 41 51
 25 CAGAGTCACT CTTCTCTTCA CCGTGAAGTC GAGCGGCTTC TTCCCTCTTC TGGTGTGCTC 60
 TACCTTGGGA ACTCTGGACA CTGCGCTCTC GGAAGCTCTT CCAAGCTCTG 120
 AATCTCTCTT CCGTAAGAAAT CCGCCCACTG CTTTATGATAC AGAAGAACCT AGTGCCAGAG 180
 TGACTGGCAG TGTCCAGGGA AGAAGAGATG TTCTCTGACG ACTTGTGGCA TCAATGCTCT 240
 GGATCTCTGT GACACCCCAA ACCCAACAG GAGGAAGCTC GGGAAATGCC CAGTGAATCTA 300
 TGGCCAAATG TGAATGCTTA ACCCCCAAA TTCTCTGAG ATGAGAGGCC AGTCCAGAGC 360
 30 TGACTTGAAG TGTGTGATGG GCAATGTGTGG GAAATCTGCG GTTCTCCCTG TGAAGCTGTG 420
 ATTCTCTCCA TATGAGGAGG GCTCTGAGAT CCGTCTCTGT GTGGTCCAGC TCTCTTCCAC 480
 CTCGAGACTT GGTCTCACCA CTGATATCTC CTTTGGGGA AAGGCTTGGC ACACACAGAG 540
 CTTTCAAGAA GTGCCAGTTG ATCATATGAT AATAAAGCA GCTTATTTCT CTTTGAC

Seq ID NO: 154 Protein sequence
 Protein Accession #: NP_003055.1

1 11 21 31 41 51
 40 MKSSGLFPFL VLLALGTLP WAVEBSGKSP KAGVCPPKES AQCLAYKKFP QQSDWQCPGK 60
 KRCCFDTGSI KCLDPVDTPN PTRRKPGRCP VTGQCLMLN PFNPFCEMDQG CKRDLACMG 120
 MCSKSPGVSV KA

Seq ID NO: 155 DNA sequence
 Nucleic Acid Accession #: NM_001306.1
 Coding sequence: 199..861

1 11 21 31 41 51
 50 AGTCCGACAC GAGGCGAGGT GCAGGCGCAC GCGGCGAGAG CGTATGAGAC CGAGCGTTTA 60
 GCGGCGGCGC TGGTGTGAGTC AGTCCGTGCG TCGCTCGCTC CGTCCGGGCG CGCAGCAGTCC 120
 CGCAGGCGCC AGCAGGCGCG GCCTCTGTCT TCCCGCACCC CGAGGCCACC CGGTGTGAGCG 180
 GGCCTTCCCG CCGCAGGCGAT GTCCATGGCG CTGAGATACA CGGACACCGC CTGCGCTCTG 240
 CTGGCGCGGC TGGGACACAT CAGTCTCTGC GCGTGTCCCA TGTGGCGGCT CTGGCGCTG 300
 55 ATCGGACGCA ACATATCAC GTGCGAGAAC ATCTCGAGAG GCTCTGTGAT GAACTGCGTG 360
 GTGACGAGCA CGCGCGAGAT GCAATGCAGG GTGATGACT CCGTCTGTGC ACTGCCACAG 420
 GAGCTCTCAG GCGCGCGCGC CAGTATGCTG GTGGCATCTC TGTGTGCTGC CTGGCGCTGT 480
 CTAGTGTGCG TGGTGGCGGC CAGTGTGACC AACTGTGTGC AGGACGACAC GCGCAGAGCC 540
 60 AAGATCACCA TGTGTGAGAG CAGTCTGTCT CTCTCTCCCG CCGTCTCTAC CCGTGTGCGG 600
 GTGTCTGTGT CCGGCGACAC CATTATCCGG GACTCTTACA ACCCGTGTGT GCGCGAGGCG 660
 CAGAGAGAGG AGATGGCGGC GGGCTCTTAC GAGGCTCTTAC CGCGCGCGGC GCTCTGAGCT 720
 CTGGGCGGCG CAGCTCTCTG CTGTCTCTGT CCGGCGACAC AGGAGAGATA CAGCGCCACC 780
 AAGGTGTCTCT ACTCTCGGCC GCGCTCCACC GCGCCCGGAG CCGAGCTGGG CACAGCGTAC 840
 GAGCCGAGAG ACTACGTCTA AGGACAGAGC GAGGAGAGAC CCGACACACA CACACACCAC 900
 CACACACACC ACCACACACA GCGACGTGAG CCGGACACAG GCGCTCTGAG GTGACAGCTT 960
 65 GCTCTGAGG CCGAGCCACC CCGACAGAGC AGGAGCCCC GCGCTCTGAG TGGGCGAGCT 1020
 TCGCCAGCAG CCAAGCGTTT GCGGCGCGGG CAGTGCATTT GCGGCGCAGC GAGCAACACT 1080
 GAGTGTGACT TGAAGACTCA CCGTCTCTGA GAGCGCGGCC TGGGTUAGCC CCAATATCTG 1140
 ACCACCGGCT CGACCGGCTAT GCGGCGCGCT CCGGCGACAC GCGCTCTGAG GCGGCGGCA 1200
 GCGTCTGAG GCGCACTTGA TATTTTCA TAAAGCCTTC TCGTTTATG

Seq ID NO: 156 Protein sequence
 Protein Accession #: NP_001297.1

1 11 21 31 41 51
 70 NSMGLSTDT ALAVLWGLT IVCCALPWR VSAPFGSNII TSONIMELM MKCVVSGTGG 60
 75 MCKRVDSLL ALPGLDQAR ALTVLITILA AGVLVNLG AGCTICVQD TAAKATITVA 120
 GVLLLAALL TLVPVNSAR TIIRDYFNV VPQAKRENG AGLVGNWAA ALGLLGGALL 180
 CCSFPREKK TTATKVYSA PRSTGPGSL GTYDRKDYV

Seq ID NO: 157 DNA sequence
 Nucleic Acid Accession #: NM_005564
 Coding sequence: 1..597

1 11 21 31 41 51
 80 ATGCCCCGAT GTCTCTGTG GCTGGGCTTA GCGCTTGTGG GGCCTCTGCA TGCACAGCC 60
 85 CAGAGTCCA CTTCAAGACT GATCCAGACC CCACTCTGA GCAAGATCCC TGCCAGCAG 120

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AACTTCCAGG ACAACCAATT CCAGGGGAAG TGGTATGTGG TAGGCGTGGC AGGGAATGCA 180
ATTCTCGAGG AAGCAAGAAG CCGGCAAGG AATGATGCCA CCACTCATGA GCTGAAGGAA 240
GACAAGAGCT ACAATGTGAC CTCCTCTCTG TTTAGGAAAA AGAAGTGTGA CTACTGGATC 300
AGGACTTTTG TTCCAGGTTG CCAGCCCGGG GAGTTCACGG TGGGCAACAT TAAGAGTTAC 360
CTGTGATTAA CGAGTTACCT GTTCCGAGTG GTGAGCACCA ACTACAACCA GCATGCTATG 420
GTTTCTCTTA AGAAGATGTT TCAAAACAGG GAGTACTTGA AGATACACCT CTACCGGAGA 480
ACCAAGGAGC TGACTTCCGA ACTAAAGGAG AACTTCATCC GCTTCTCCA ATATCTGGCC 540
CTCCCTGAAA ACCACATCGT CTTCCCTGCT CCAATGGACC AGTGATAGA CGGCTGA

```

Seq ID NO: 158 Protein sequence
Protein Accession #: NP_005555

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1 11 21 31 41 51
| | | | |
NPIQLLHLLEL LLGALHQAQ QDSTSLPIA PPLSKVPLQG NFGDNQPGK VYVVLGAGNA 60
ILREKDKPGK MYATITELKE DKSINVTSLV FRKKCKDYNI RTFVPGCPQG EPTLGHIKSY 120
PGLTSLYLVK VSTNYNQAH VPFKKVQSNR EYFKITLYUR TKELTSELKE NPIRPSKYLGS 180
LPENHIVFPV PFDQCIDG

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Seq ID NO: 159 DNA sequence
Nucleic Acid Accession #: NM_006853.1
Coding sequence: 26..874

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1 11 21 31 41 51
| | | | |
AGGAATCTGC GCTCGGGTTC CGCAGATGCA GAGGTTGAGG TGGCTGGGGG ACTGGAAGTC 60
ATCGGGCAGA GGTCTCAGAG CAGCCAAAGA ACTTGGGGCC GCGTCTCTCC CCGTCCAGGC 120
CATGAGGATT CTGCAATTAA TCTCGTTTCC TGTGGGAGCA GGCCTCTTMS GGGGAGAGAC 180
CAGGATCATC AAGGGGTTGG AGTGCAAGCC TCACCTCCAG CCGTGGCAGG CAGCCTCTGT 240
CGAGAAGACG CCGCTACTCT GTGGGGGAGC GCTCATCCCC CCGAGATGGC TCTTGACAGC 300
AGCCCACTGC CTCGAAGCCC GCTACATAGT TCACCTGGGG CAGCAACACC TCCAGAGAGA 360
GGGAGGCTGT GAGCAGACCC GAGACCCAC TGGTCTCTC CCGACCCCS GCTTCAAGCA 420
CAGCCTCCCC AACAGAAGCC ACCGCAATGA CATCATGCTG GTGAGAGTGG CATGCCAGT 480
CTCATCACCC TGGGCTGTGC GACCCCTCAC CCGTCTCTCA CGCTGTGTCA CTGCTGGCAC 540
CAGTCGCTTC ATTTCCGGCT GGGGCGAGAC GTCCAGCCCC CAGTTACGCC TCGCTCAGAC 600
CTTGCATCAG CCGACATCA CAGTCAATGA GCGACAGAG TGTGAGAGCS CTTACCCCG 660
CAGCATCACA GACACCATGG TGTGTGCGAG CGTCAGAGAA GGGGGCAAGG ACTCTGTCCA 720
GGGTGACTCC GGGGGCCCTC TGGTCTGTAA CCGTCTCTTT CAGGCAATTA TCTCTGGGG 780
CCGAGATCCG TGTGCTGTCA CCGGAGAGCC TGTGTCTAC ACGAAGCTGT GCAATATGT 840
GGACTGGATC CAGGAGAGGA TGAAGAACAA TTGAGCTGGA CCGACCCACC ACAGGCCATC 900
ACCTCCATT TCCACTGGT GTTTGGTTCC TGTTCACCTC GTTAATAGA AACCTAAGC 960
CAGACCCCTC TAGGAACRIT CTTTGGGCTC CTTGAGCTAC AGGAGATGCT GTCACTTAAT 1020
AATGAACTGS GGGTTGAAA TCACTGAGAC CTGATGTGCA ATTCGCGCT GAAATATGT 1080
GACTCTGGGA ATGACAGAC CTCGTGTTGT CTCTGTGTGA TCCCCAGGCC CAAGACAGC 1140
TCTGTGCCAT ATATCAAGT TTCAATAAAT ATTGCTAAA TGAGTG

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Seq ID NO: 160 Protein sequence
Protein Accession #: NP_006844.1

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1 11 21 31 41 51
| | | | |
MRILQLILLA LATGLVGGET RIHKQPECKP HQPHQAALP ENTRLLCGAT LIAPRMLLTA 60
ARCLKPRYIV HLGQINLQKE EGCEQTRTAT ESFPHPGFPM SLPHKDERND IMLVEMASPV 120
SITMAVRPLT LSSRCVTATG SCLISGWGST SSPQLRLPHT LRCANITIE HQCENAYPG 180
NITDAWYVCS VQGGGDDSCG GDSGGFLVNC QSLQGIISWG QUPCAITRKP GYVTKVCTV 240
DNITQETQGN

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It is understood that the examples described above in no way serve to limit the true scope of this invention, but rather are presented for illustrative purposes. All publications, sequences of accession numbers, and patent applications cited in this specification are herein incorporated by reference as if each individual publication or patent application were specifically and individually indicated to be incorporated by reference.

WHAT IS CLAIMED IS:

- 1 1. A method of detecting an ovarian cancer-associated transcript in a cell
2 from a patient, the method comprising contacting a biological sample from the patient with a
3 polynucleotide that selectively hybridizes to a sequence at least 80% identical to a sequence
4 as shown in Tables 1-26.
- 1 2. The method of claim 1, wherein the biological sample comprises
2 isolated nucleic acids.
- 1 3. The method of claim 2, wherein the nucleic acids are mRNA.
- 1 4. The method of claim 2, further comprising the step of amplifying
2 nucleic acids before the step of contacting the biological sample with the polynucleotide.
- 1 5. The method of claim 1, wherein the polynucleotide comprises a
2 sequence as shown in Tables 1-26.
- 1 6. The method of claim 1, wherein the polynucleotide is immobilized on
2 a solid surface.
- 1 7. The method of claim 1, wherein the patient is undergoing a therapeutic
2 regimen to treat ovarian cancer.
- 1 8. The method of claim 1, wherein the patient is suspected of having
2 ovarian cancer.
- 1 9. An isolated nucleic acid molecule consisting of a polynucleotide
2 sequence as shown in Tables 1-26.
- 1 10. The nucleic acid molecule of claim 9, which is labeled.
- 1 11. An expression vector comprising the nucleic acid of claim 9.
- 1 12. A host cell comprising the expression vector of claim 11.
- 1 13. An isolated polypeptide which is encoded by a nucleic acid molecule
2 having polynucleotide sequence as shown in Tables 1-26.

- 1 14. An antibody that specifically binds a polypeptide of claim 13.
- 1 15. The antibody of claim 14, further conjugated to an effector component.
- 1 16. The antibody of claim 15, wherein the effector component is a
2 fluorescent label.
- 1 17. The antibody of claim 15, wherein the effector component is a
2 radioisotope or a cytotoxic chemical.
- 1 18. The antibody of claim 15, which is an antibody fragment.
- 1 19. The antibody of claim 15, which is a humanized antibody
- 1 20. A method of detecting an ovarian cancer cell in a biological sample
2 from a patient, the method comprising contacting the biological sample with an antibody of
3 claim 14.
- 1 21. The method of claim 20, wherein the antibody is further conjugated to
2 an effector component.
- 1 22. The method of claim 21, wherein the effector component is a
2 fluorescent label.
- 1 23. A method for identifying a compound that modulates an ovarian
2 cancer-associated polypeptide, the method comprising the steps of:
3 (i) contacting the compound with an ovarian cancer-associated polypeptide,
4 the polypeptide encoded by a polynucleotide that selectively hybridizes to a sequence at least
5 80% identical to a sequence as shown in Tables 1-26; and
6 (ii) determining the functional effect of the compound upon the polypeptide.
- 1 24. A drug screening assay comprising the steps of
2 (i) administering a test compound to a mammal having ovarian cancer or a cell
3 isolated therefrom;
4 (ii) comparing the level of gene expression of a polynucleotide that selectively
5 hybridizes to a sequence at least 80% identical to a sequence as shown in Tables 1-26 in a

- 6 treated cell or mammal with the level of gene expression of the polynucleotide in a control
7 cell or mammal, wherein a test compound that modulates the level of expression of the
8 polynucleotide is a candidate for the treatment of ovarian cancer.

(19) World Intellectual Property
Organization
International Bureau



(43) International Publication Date
27 December 2002 (27.12.2002)

PCT

(10) International Publication Number
WO 2002/102235 A3

- (51) International Patent Classification⁷: **C12Q 1/68**, (81) Designated States (*national*): AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CO, CR, CU, CZ, DE, DK, DM, DZ, EC, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, OM, PH, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TN, TR, TT, TZ, UA, UG, US, UZ, VN, YU, ZA, ZM, ZW.
- (21) International Application Number: PCT/US2002/019297
- (22) International Filing Date: 18 June 2002 (18.06.2002)
- (25) Filing Language: English
- (26) Publication Language: English
- (30) Priority Data:
60/299,234 18 June 2001 (18.06.2001) US
60/315,287 27 August 2001 (27.08.2001) US
60/317,544 5 September 2001 (05.09.2001) US
60/350,666 13 November 2001 (13.11.2001) US
60/372,246 12 April 2002 (12.04.2002) US
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- (72) Inventors; and
- (73) Inventors/Applicants (*for US only*): MACK, David, H. [US/US]; 2076 Monterey Avenue, Menlo Park, CA 94025 (US); GISH, Kurt, C. [US/US]; 40 Peregó Terrace #2, San Francisco, CA 94131 (US).
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- (84) Designated States (*regional*): ARIPO patent (GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZM, ZW), Eurasian patent (AM, AZ, BY, KG, KZ, MD, RU, TJ, TM), European patent (AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, TR), OAPI patent (BF, BJ, CF, CG, CI, CM, GA, GN, GQ, GW, ML, MR, NE, SN, TD, TG).
- Published:
— with international search report
— before the expiration of the time limit for amending the claims and to be republished in the event of receipt of amendments
- (88) Date of publication of the international search report: 3 February 2005
- For two-letter codes and other abbreviations, refer to the "Guidance Notes on Codes and Abbreviations" appearing at the beginning of each regular issue of the PCT Gazette.*

(54) Title: METHODS OF DIAGNOSIS OF OVARIAN CANCER, COMPOSITIONS AND METHODS OF SCREENING FOR MODULATORS OF OVARIAN CANCER

(57) Abstract: Described herein are genes whose expression are up-regulated or down-regulated in ovarian cancer. Related methods and compositions that can be used for diagnosis and treatment of ovarian cancer are disclosed. Also described herein are methods that can be used to identify modulators of ovarian cancer.

INTERNATIONAL SEARCH REPORT

International application No.

PCT/US02/19297

A. CLASSIFICATION OF SUBJECT MATTER

IPC(7) : C12Q 1/68; C07H 21/04
 US CL : 435/6, 91.1; 536/23.1

According to International Patent Classification (IPC) or to both national classification and IPC

B. FIELDS SEARCHED

Minimum documentation searched (classification system followed by classification symbols)

U.S. : 435/6, 91.1; 536/23.1

Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched

Electronic data base consulted during the international search (name of data base and, where practicable, search terms used)
 Please See Continuation Sheet

C. DOCUMENTS CONSIDERED TO BE RELEVANT

Category *	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
X	WU, D. et al. Characterization and Molecular Cloning of a Putative Binding Protein for Hepatitis-binding Growth Factors. The Journal of Biological Chemistry. 05 September 1991, Vol. 266, No. 25, pages 16778-16785, see especially page 16778, col. 1, page 16783, Fig. 7, Fig. 8.	1-5, 9-12
Y	US 5,700,637 A (SOUTHERN) 23 December 1997 (23.12.1997) see whole document.	6
Y		6

☐ Further documents are listed in the continuation of Box C.☐ See patent family annex.*** Special categories of cited documents:**

- "A" document defining the general state of the art which is not considered to be of particular relevance
- "E" earlier application or patent published on or after the international filing date
- "L" document which may throw doubts on priority claim(s) or which is cited to establish the publication date of another citation or other special reason (as specified)
- "O" document referring to an oral disclosure, use, exhibition or other means
- "P" documents published prior to the international filing date but later than the priority date claimed

- "T" later document published after the international filing date or priority date and not in conflict with the application but cited to understand the principle or theory underlying the invention
- "X" document of particular relevance: the claimed invention cannot be considered novel or cannot be considered to involve an inventive step when the document is taken alone
- "Y" document of particular relevance: the claimed invention cannot be considered to involve an inventive step when the document is combined with one or more other such documents, such combination being obvious to a person skilled in the art
- "Δ" document member of the same patent family

Date of the actual completion of the International search

08 November 2004 (08.11.2004)

Name and mailing address of the ISA/US

Mail Stop PCT, Attn: ISA/US
 Commissioner for Patents
 P.O. Box 1450
 Alexandria, Virginia 22313-1450
 Facsimile No. (703) 305-3230

Date of mailing of the International search report

Authorized officer
 Jonathan S. Sifton
 Telephone No. 571-272-0500

INTERNATIONAL SEARCH REPORT

International application No.

PCT/US02/19297

Box I Observations where certain claims were found unsearchable (Continuation of Item 1 of first sheet)

This international report has not been established in respect of certain claims under Article 17(2)(a) for the following reasons:

1. ☐ Claim Nos.:
because they relate to subject matter not required to be searched by this Authority, namely:

2. ☐ Claim Nos.:
because they relate to parts of the international application that do not comply with the prescribed requirements to such an extent that no meaningful international search can be carried out, specifically:

3. ☐ Claim Nos.:
because they are dependent claims and are not drafted in accordance with the second and third sentences of Rule 6.4(a).

Box II Observations where unity of invention is lacking (Continuation of Item 2 of first sheet)

This International Searching Authority found multiple inventions in this international application, as follows:
Please See Continuation Sheet

1. ☐ As all required additional search fees were timely paid by the applicant, this international search report covers all searchable claims.
2. ☐ As all searchable claims could be searched without effort justifying an additional fee, this Authority did not invite payment of any additional fee.
3. ☐ As only some of the required additional search fees were timely paid by the applicant, this international search report covers only those claims for which fees were paid, specifically claims Nos.:

4. ☒ No required additional search fees were timely paid by the applicant. Consequently, this international search report is restricted to the invention first mentioned in the claims; it is covered by claims Nos.: 1-12, directed to heparin binding growth factor binding protein

Remark on Protest ☐ The additional search fees were accompanied by the applicant's protest.
☐ No protest accompanied the payment of additional search fees.

INTERNATIONAL SEARCH REPORT

BOX II. OBSERVATIONS WHERE UNITY OF INVENTION IS LACKING

Groups 1-12000, claim(s) 1-12, drawn to nucleic acids and methods of detecting nucleic acids. It is noted that each group named above corresponds to each of the genes or nucleic acids set forth in tables 1-26. Therefore, if applicant does not choose to pay additional fees for search, Group 1 and claims 1-12 will be searched to the extent that they apply to heparin binding growth factor. If applicant wishes to elect and pay for additional groups for search, applicant is requested to indicate which nucleic acid from tables 1-26 are elected.

Groups 12001-24000, claim(s) 13 and 23, drawn to polypeptides and methods of detecting polypeptides. It is noted that each group named above corresponds to proteins encoded by each of the genes or nucleic acids set forth in tables 1-26. Therefore, if applicant wishes to elect and pay for additional groups for search, applicant is requested to indicate which nucleic acid from tables 1-26 are elected.

Groups 24001-36000, claim(s) 14-22, drawn to antibodies and methods of using antibodies. It is noted that each group named above corresponds to an antibody that binds a protein encoded by each of the genes or nucleic acids set forth in tables 1-26. Therefore, if applicant wishes to elect and pay for additional groups for search, applicant is requested to indicate which nucleic acid from tables 1-26 are elected.

Groups 36001-48000, claim(s) 24, drawn to drug screening assays. It is noted that each groups named above correspond to detection of gene expression of each of the genes or nucleic acids set forth in tables 1-26. If applicant wishes to elect and pay for additional groups for search, applicant is requested to indicate which nucleic acid from tables 1-26 are elected.

The inventions listed as Groups 1-48000 do not relate to a single general inventive concept under PCT Rule 13.1 because, under PCT Rule 13.2, they lack the same or corresponding special technical features for the following reasons: The products claimed in groups 1-12000 (see e.g., claim 1) include genes or nucleic acid sequences which are both structurally and functionally unrelated to any of the other nucleic acids in the tables. As such the products of groups 1-12000 do not represent a contribution over the prior art, the claims lack a special technical feature that is the same as or that corresponds to a special technical feature of the other claimed inventions. Thus there is no special technical feature linking the recited Groups, as would be necessary to fulfill the requirement for unity of invention.

Groups 1-36000 are additionally drawn to multiple distinct products lacking the same or corresponding special technical features. The nucleic acids of Groups 1-12000 are composed of nucleotides and function in, e.g., methods of nucleic acid hybridization or amplification. The polypeptides of groups 12001-24000, which are composed of amino acids are structurally distinct molecules from polynucleotides or antibodies and can function in, e.g., catalysis of reactions. While the inventions of both groups 12001-24000 and groups 24001-36000 are polypeptides, in this instance the polypeptides of groups 12001-24000 are single chain molecules whereas the polypeptides of groups 24001-36000 encompasses antibodies including IgG which comprises 2 heavy and 2 light chains containing constant and variable regions, and including framework regions which act as a scaffold for the 6 complementarity determining regions (CDRs) that function to bind an epitope, and can function, e.g., in eliciting an immune response. Thus the polypeptides of groups 12001-24000 and the antibodies of groups 24001-36000 are structurally distinct molecules. As the products of the different sets of groups differ from each other in structure, function, and effect, they do not belong to a recognized class of chemical compounds, or have both a "common property or activity" and a common structure, as would be required to show that the inventions are "of a similar nature".

Further, the methods of Groups 36001-48000 do not require either the peptides of groups 12001-24000 or the antibodies of groups 24001-36000. Further, the methods of groups 36001-48000 (involve administering a test compound) have different objectives and require different process steps than the methods or nucleic acids of groups 1-12000. Further, the methods of groups 1-12000 do not require the method steps of groups 36001-48000. In addition to differences in objectives, effects, and method steps, it is again noted that the claims of the present groups are not directed to the detection or identification of molecules having the same or common special technical feature, for the reasons discussed above.

INTERNATIONAL SEARCH REPORT

PCT/US02/19297

Continuation of B. FIELDS SEARCHED Item 3:
medline, caplus, NCBI
search terms: heparin binding growth factor binding protein